

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 25, 2006, 21:43:01 ; Search time 6217.24 Seconds
(without alignments)
4242.296 Million cell updates/sec

Title: US-10-070-794a-30

Perfect score: 2403

Sequence: 1 MSFLEGENSSWSPAVTSS.....LSDIQLVLSPAGIDALGA 464

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Zgapop 6.0 , Zgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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3: gb.env.*

4: gb.om.*

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6: gb.pat.*

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8: gb.pr.*

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10: gb.sts.*

11: gb.sy.*

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13: gb.vi.*

14: gb.htg.*

15: gb.pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2403	100.0	1470	6	AX814738 Sequence
2	2403	100.0	2115	6	AX099802 Sequence
3	2403	100.0	2115	8	AF214519 Homo sapi

4	2398	99.8	1597	8	BC098277	Homo sapi
5	2398	99.8	1599	8	BC098102	Homo sapi
6	2398	99.8	1647	6	AX281582	Sequence
7	2394	99.6	2109	6	AX099776	Sequence
8	2390	99.5	1597	8	BC098255	Homo sapi
9	2390	99.5	1597	8	BC098306	Homo sapi
10	2372	98.7	2290	8	HS2429977	Homo sapi
11	2013	83.8	1873	6	AX398333	Sequence
12	2011	83.7	1873	6	AX099800	Sequence
13	2011	83.7	1873	6	AX398331	Sequence
14	2011	83.7	2022	6	AX099804	Sequence
15	2011	83.7	2023	4	AF214520	Sus scrofa
16	2011	83.7	2256	4	AY264345	Sus scrofa
17	2010	83.6	1540	9	AF525500	Mus muscu
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20	2007	83.5	1873	6	AX398339	Sequence
21	2005	83.4	1873	6	AX398335	Sequence
22	2002	83.3	1867	6	AX099774	Sequence
23	2000	83.2	1518	6	AX814740	Sequence
24	1888	78.6	1322	4	AY376689	Equus cab
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28	1276	53.1	9100	6	AX814742	Sequence
29	1275	53.1	26000	6	AX814795	Sequence
30	1275	53.1	1570	6	CQ714782	Sequence
31	1231	51.2	2679	5	CT025503	Xenopus t
32	1231	51.2	2214	5	BC043738	Xenopus l
33	1188	49.5	10480	9	AY263402	Mus muscu
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39	1100	45.8	1938	5	AJ720277	Gallus ga
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ALIGNMENTS

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AUTHORS	AX814738.1	AX814738.1	GI:39103937	1470 bp	DNA	linear	PAT 05-DEC-2003
TITLE	AX814738.1	AX814738.1	GI:39103937	1470 bp	DNA	linear	PAT 05-DEC-2003
JOURNAL	AX814738.1	AX814738.1	GI:39103937	1470 bp	DNA	linear	PAT 05-DEC-2003
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ORIGIN

Alignment Scores:
Pred. No.: 1,41e-135 Length: 1470
Score: 2403.00 Matches: 464
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-070-794A-30 (1-464) x AX814738 (1-1470)

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Qy 41 ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60
Db 196 GTGGAGGAAGGGAGCCACAGGTGAGGGGAGAGGTCCCGGTCCAGGCCCACTGCTGAG 255
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AX099802
LOCUS Sequence 29 from Patent WO0120003.
DEFINITION AX099802
ACCESSION AX099802.1 GI:13538836
VERSION
KEYWORDS Homo sapiens (human)
SOURCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Anderson, L., Looft, C., Kalm, E., Milan, D., Robic, A.,
Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., le Roy, P. and
Chardon, P.
TITLE Variants of the gamma chain of ampk, dna sequences encoding the
same, and uses thereof
JOURNAL Patent: WO 0120003-A 29 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
Anderson, L., Looft, C., Kalm, E., Milan, D., Robic, A.,
Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., le Roy, P. and
Chardon, P.
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US-10-070-794A-30 (1-464) x AX099802 (1-2115)

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ACCESSION AF214519
VERSION AF214519.1 GI:8215681
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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REFERENCE 1 (bases 1 to 2115)
AUTHORS Milan, D., Jeon, J.T., Looft, C., Amarger, V., Robic, A., Thelander, M., Rogel-Gaillard, C., Paul, S., Iannuccelli, N., Rask, L., Ronne, H., Lundstrom, K., Reinsch, N., Gellin, J., Kalm, E., Roy, P.L., Chardon, P. and Andersson, L.
TITLE A mutation in PRKAG3 associated with excess glycogen content in pig skeletal muscle
JOURNAL Science 288 (5469), 1248-1251 (2000)
PUBMED 10818001
REFERENCE 2 (bases 1 to 2115)
AUTHORS Milan, D., Jeon, J.T., Looft, C., Amarger, V., Robic, A., Thelander, M., Rogel-Gaillard, C., Paul, S., Gellin, J., Lundstrom, K., Reinsch, N., Kalm, E., Le Roy, P., Chardon, P. and Andersson, L.
TITLE Direct Submission

JOURNAL Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish University of Agricultural Sciences, BMC box 597, Uppsala 751 24, Sweden

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ORIGIN

Alignment Scores:
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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US-10-070-794A-30 (1-464) x AF214519 (1-2115)

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Qy 41 ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60
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RESULT 4

BC098277

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

BC098277 1597 bp mRNA linear PRI 02-JUL-2005
Homo sapiens protein kinase, AMP-activated, gamma 3 non-catalytic
subunit, mRNA (cDNA clone MGC:119344 IMAGE:40005886), complete cds.
BC098277.1 GI:67514270
MGC.
Homo sapiens (human)


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BC098102 1599 bp mRNA linear PRI 23-JUN-2005
LOCUS BC098102
DEFINITION Homo sapiens protein kinase, AMP-activated, gamma 3 non-catalytic
subunit, mRNA (cDNA clone MGC:119342 IMAGE:40005880), complete cds.
ACCESSION BC098102
VERSION BC098102.1 GI:66990059
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 1599)
AUTHORS Klausner,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeb,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.P., Caavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Ustin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,

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Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 1599)
NIH MGC Project
Direct Submission
Submitted (03-JUN-2005) National Institutes of Health, Mammalian
Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-x@mail.nih.gov
Tissue Procurement: Baylor Human Genome Sequencing Center
cDNA Library Preparation: Baylor Human Genome Sequencing Center
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
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Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc.mgc@hgrl.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
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McDowell,J., Pearson,R., Stantropop,S., Thomas,P.J., Touchman,J.W.,
Tsurgon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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ORIGIN

Alignment Scores:
 Pred. No.: 3,11e-135 Length: 1599
 Score: 2398.00 Matches: 463
 Percent Similarity: 99.78% Conservative: 0
 Best Local Similarity: 99.78% Mismatches: 1
 Query Match: 99.79% Indels: 0
 DB: 8 Gaps: 0

US-10-070-794A-30 (1-464) x BC098102 (1-1599)

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 VERSION AX281582.1 GI:16608833
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 SOURCE Homo sapiens
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 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 REFERENCE 1
 AUTHORS Andersson, L., Luthman, H. and Marklund, S.
 TITLE Variants of the human amp-activated protein kinase gamma 3 subunit
 JOURNAL Patent: WO 0177305-A 5 18-OCT-2001;
 Arexis AB (SE)

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ORIGIN

Alignment Scores:
Pred. No.: 3,21e-135 Length: 1647
Score: 2398.00 Matches: 463
Percent Similarity: 99.78% Conservatives: 0
Best Local Similarity: 99.78% Mismatches: 1
Query Match: 99.79% Indels: 0
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US-10-070-794A-30 (1-464) x AX281582 (1-1647)

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RESULT 7

AX099776 2109 bp DNA linear PAT 02-APR-2001
LOCUS Sequence 3 from Patent WO0120003.
DEFINITION AX099776
ACCESSION AX099776
VERSION AX099776.1 GI:13538810

KEYWORDS Homo sapiens (human)

SOURCE

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE

1. Anderson, L., Looft, C., Kalm, E., Milan, D., Robic, A.,
Rogel-Gallard, C., Iannuccelli, N., Gellin, J., le Roy, P. and
Chardon, P.

1. Variants of the gamma chain of ampk, dna sequences encoding the
same, and uses thereof

Patent: WO 0120003-A 3 22-MAR-2001;

INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;

Anderson, Looft, Christian (DE) ; Kalm, Ernst (DE)

Location/Qualifiers

FEATURES

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ORIGIN

Alignment Scores:

Pred. No.: 7,39e-135 Length: 2109
 Score: 2394.00 Matches: 462
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 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.63% Indels: 0
 DB: 6 Gaps: 0

US-10-070-794A-30 (1-464) x AX099776 (1-2109)

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 Qy 463 GlyAla 464
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 DEFINITION subunit mRNA (cdna clone MGC:119343 IMAGE:4005983), complete cds.
 BC098255
 ACCESSION BC098255.1 GI:67514300
 VERSION MGC.
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1597)
 AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F.,
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 Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
 Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E.,
 Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
 Mammalian Gene Collection Program Team
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 CONSRMT
 TITLE Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 JOURNAL
 PUBMED 12477932

REFERENCE	2	(bases 1 to 1597)																									
AUTHORS	NIH MGC Project																										
CONSTRM	Direct Submission																										
TITLE	Submitted (10-JUN-2005) National Institutes of Health, Mammalian																										
JOURNAL	Gene Collection (MGC), Bethesda, MD 20892-2590, USA																										
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov																										
COMMENT	Contact: MGC help desk Email: cgabs-remail.nih.gov Tissue Procurement: Baylor Human Genome Sequencing Center cDNA Library Preparation: Baylor Human Genome Sequencing Center cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site: http://www.nisc.nih.gov/ Contact: nisc_mgc@hgrl.nih.gov Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vost, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, J.-H. and Green, E.D.																										
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Pred. No.:	9,39e-135	Length:	1597																								
Score:	2390.00	Matches:	462																								
Percent Similarity:	99.57%	Conservative:	0																								
Best Local Similarity:	99.57%	Mismatches:	2																								
Query Match:	99.46%	Indels:	0																								
DB:	8	Gaps:	0																								
	1	MetSerPheLeuGluGlnGluAenSerSerTrpProSerProAlaValThrSerSer	20																								
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	21	SerGluArgIleArgGlyLysArgAlaLysAlaLeuArgTrpThrArgGlnLysSer	40																								
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RESULT 9

BC098306
 DEFINITION Homo sapiens protein kinase, AMP-activated, gamma 3 non-catalytic subunit, mRNA (CDNA clone MGC:119345 IMAGE:40005888), complete cds.
 ACCESSION BC098306
 VERSION BC098306.1 GI:67514235
 KEYWORDS MGC.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 1597)
 AUTHORS Klausner, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Strausberg, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.B., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Abramson, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., McKernan, K.J., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalios, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
 Mammalian Gene Collection Program Team
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

CONSRMT
 TITLE human and mouse cDNA sequences
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 PUBMED 12477932
 REFERENCE 2 (bases 1 to 1597)

NIH MGC Project
 Direct Submission
 Submitted (10-JUN-2005) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Baylor Human Genome Sequencing Center
 cDNA Library Preparation: Baylor Human Genome Sequencing Center
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (fLNL)
 cDNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc_mgc@hghri.nih.gov

Akhter, N., Ayèle, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskripop, S., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stankriopop, S., Thomas, P.J., Touchman, J.W., Tauregon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L., H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/fLNL at: <http://image.llnl.gov>
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ORIGIN

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 Score: 2390.00 Matches: 462
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 Query Match: 99.46% Indels: 0
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US-10-070-794A-30 (1-464) x BC098306 (1-1597)

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ACCESSION AJ249977
VERSION AJ249977.1 GI:6688200
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1. Cheung, P.C., Salt, I.P., Davies, S.P., Hardie, D.G. and Carling, D. Characterization of AMP-activated protein kinase gamma-subunit isoforms and their role in AMP binding
AUTHORS Biochem. J. 345 Pt 3, 659-669 (2000)
JOURNAL 1698692
PUBMED 2 (bases 1 to 2290)
TITLE Carling, D.
AUTHORS Direct Submission
JOURNAL Submitted (12-OCT-1999) Carling D., Cellular Stress Group, MRC Clinical Sciences Centre, Hammersmith Hospital, DuCane Road, London, W12 0NN, UNITED KINGDOM
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 DEFINITION Sequence 3 from Patent WO0220850.
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 VERSION AX398333.1 GI:21261108
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 Novel p-kag3 alleles and use of the same as genetic markers for
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 Query Match: 6 Gaps: 2
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ACCESSION AX099800
VERSION AX099800.1 GI:13538834
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Sub.
REFERENCE 1
AUTHORS Andersson, L., Looft, C., Kalm, E., Milan, D., Robic, A.,
Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., le Roy, P. and
Chardon, P.
TITLE Variants of the gamma chain of ampk, dna sequences encoding the
same, and uses thereof
JOURNAL Patent: WO 0120003-A 27 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)
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Query Match: 83.63% Indels: 2
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QY 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspPro--- 79
DB 181 TCCACCGGGCAGGAGGCCACATTCCTCCCAAGGCCACACCTTGGCCCAAGCGCTCCCTTG 240
QY 80 AlaGlyValGlyThrProProThrGlyTTPAspCysLeuProSerAspCysThrAlaSer 99
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QY 140 AlaProPheProLysLeuGlyTTPAspGluLeuArgLysProGlyAlaGlnIleTyr 159
DB 418 GTGCTGTATCCAGCTGGGCTGGGATGATGAGCTGCAGAAAGCGGGGGCCAGGTCTAC 477
QY 160 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 179
DB 478 ATGCATCTCATGAGGAGGACACCTGTACGATGCCATGGCAGCAGCTCCAAACTGGTC 537
QY 180 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 199
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QY 200 ArgAlaAlaProLeuTrpAspSerLysGlyGlnSerPheValGlyMetLeuThrIleThr 219
DB 598 CGAGCGCACCTTGTGGGACAGCAAGCAGAGCTTCGTGGGATGCTGACCATCACA 657
QY 220 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 239
DB 658 GACTTCATCTGGTGTGCAACCGCTATTACAGGTCCTCCCTGGTCCAGATCTACGAGATT 717
QY 240 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 259
DB 718 GAAGAACTAAGATTGAGACTGGAGGAGATCTACCTTCAAGCTGCTTCAAGCCTCTG 777
QY 260 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 279
DB 778 GTCTCCATCTCTCCATGACAGCTGTCTGAAGCTGTCTAGGCCCTCATCAAGAACCG 837
QY 280 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 299
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QY 300 LysArgLeuLeuLysPheLeuHisIlePheCysSerLeuLeuProArgProSerPheLeu 319
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QY 320 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 339
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QY 340 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 359
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QY 380 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 399
DB 1138 GCTGCCCAACAACATACACACCTGGACATGAATGTGGGAGAAGCCCTGAGGACGCG 1197
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QY 420 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 439
DB 1258 GACCGGATTTCCGGGAACAGGTGACCCGCTGGTCTCGTGGATGAGACCCAGCACCTT 1317
QY 440 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 459
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QY 460 AspAlaLeuGlyAla 464
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AX398331 LOCUS 1873 bp DNA linear PAT 27-MAY-2002
DEFINITION Sequence 1 from Patent WO0220850.
ACCESSION AX398331
VERSION AX398331.1 GI:21261106
KEYWORDS Sus scrofa (pig)
SOURCE Sus scrofa
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
REFERENCE 1
AUTHORS Rothschild,M.F., Ciobanu,D.C., Malek,M. and Plastow,G.
TITLE Novel prkag3 alleles and use of the same as genetic markers for
reproductive and meat quality traits
JOURNAL Patent: WO 0220850-A 1 14-MAR-2002;
Iowa State University Research Foundation, Inc. (US)
FEATURES
source 1. .1873
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Alignment Scores: 6.91e-112 Length: 1873
Pred. No.: 2011.00 Matches: 400
Score: 90.11% Conservative: 19
Percent Similarity: 90.11% Mismatches: 44
Best Local Similarity: 86.02% Indels: 2
Query Match: 83.69% Gaps: 2
DB: 6
US-10-070-794A-30 (1-464) x AX398331 (1-1873)
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Db	61	TCGAAGAAGCCATGGGACAGGGGAAACAGGCCCTCTAGATGGCAAGGAGGAGGAGAT	120
Qy	41	ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu	60
Db	121	GTAGAGAAAGGGGGGCTCCGGGCCGAGGGAAGTCCCGAGTCCAGGCCAGTGTGCTGAG	180
Qy	61	SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspPro---	79
Db	181	TCCACCGGGCAGGAGGCCACATTCCTCCCAAGGCCACACCCCTTG3CCCAAGCGCTCCCTTG	240
Qy	80	AlaGlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSer	99
Db	241	GCCGAGGTGGACAACCCCCCAACAGAGCGGGACATCTCCCTCTCACTGTGCAGCTCA	300
Qy	100	AlaAlaGlySerSerThrAspValGluLeuAlaThrGluPheProAlaThrGluAla	119
Db	301	GCCTCCGACTCCAACACAGACCATCTGGATCTGGGCATAGAGTTCTCAGCCTCGGCGGG	360
Qy	120	TrpGluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGln	139
Db	361	TCGGGGGATGAGCTT--GGGCTGGTGGAAAGAAAGCCAGCCCGCTGCCCATCCCCAGAG	417
Qy	140	AlaProPheProLysLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnIleTyr	159
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Qy	200	ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr	219
Db	598	CGAGCGGACCTTTGTGGACAGACAGACAGAGCTTCGTGGGGATGCTGACCATCACA	657
Qy	220	AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle	239
Db	658	GACTTCATCTTGGTGTGCACCGCTATTACAGGTCCGCCCTCTGGTCCAGATCTACGAGATT	717
Qy	240	GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu	259
Db	718	GAAGAACAATAGATTGAGACTGGAGGGAGATCATCCTTCAAGGCTGCTTCAAGCCTCTG	777
Qy	260	ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg	279
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Db	838	ATCCACCGCCTCGCGGTCCTGGACCCCTGCTCCGGGGCTGTGCTCCACATCCTCACACAT	897
Qy	300	LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu	319
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Qy	320	TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu	339
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Qy	340	ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro	359
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Qy	380	AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg	399
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Qy	400	ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIle	419
Db	1198	ACACTGTGCTGGAGGCGTCTCTCTCCAGCCCCACGAGACCTTGGGGGAAGTCATT	1257
Qy	420	AspArgTleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu	439
Db	1258	GACCGATTGTCCGGGAACAAGTGCACCGCTGTGTCTCGTGGATGAGACCCAGCACCTT	1317
Qy	440	LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle	459
Db	1318	CTGGGCGTGTGTCCCTCTCTGACATCTTCAGGCTCTGTGTCTCAGCCCTGCTGGAATT	1377
Qy	460	AspAlaLeuGlyAla 464	
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DEFINITION	Sequence 31 from Patent WO0120003.		
ACCESSION	AX099804		
VERSION	AX099804.1	GI:13538838	
KEYWORDS	Sus scrofa (pig)		
SOURCE	Sus scrofa		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.		
REFERENCE	1		
AUTHORS	Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A., Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy,P. and Chardon,P.		
TITLE	Variants of the gamma chain of ampk, dna sequences encoding the same, and uses thereof		
JOURNAL	Patent: WO 0120003-A 31 22-MAR-2001; INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ; Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)		
FEATURES	Location/Qualifiers		
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Pred. No.:	7.53e-112	Length:	2022
Score:	2011.00	Matches:	400
Percent Similarity:	90.11%	Conservative:	19
Best Local Similarity:	86.02%	Mismatches:	44
Query Match:	83.69%	Indels:	2
DB:	6	Gaps:	2
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Qy	21	SerGluArgIleArgGlyLysArgArgAlaLysAlaLeuArgTrpThrArgGlnLysSer	40
Db	211	TCGAAAGAGCCATGGGGACCAGGGGAACAGCGCTCTAGATGACAAGGCAGGAGGAT	270
Qy	41	ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu	60
Db	271	GTAGAGGAAGGGGGCGCTCCGGGCCCGAGGGAAGGTCCCGATCCAGGCCAGTTGCTGAG	330

Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspPro--- 79
Dy 331 TCCACCGGCGAGGAGGACATTCCTCCCAAGGCCACACCTTTGGCCCAAGCGCTCCCTTG 390
Qy 80 AlaGlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSer 99
Dy 391 GCCAGGTGGACACCCCGGAGAGGAGGAGGACATCTCCCTCTGATCTGACGCTCGCGCGG 450
Qy 100 AlaAlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAla 119
Dy 451 GCCTCCGACCTCCACACAGACCATCTGGATCTGGCATAGAGTTCTCAGCCTCGCGCGG 510
Qy 120 TrpGluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGln 139
Dy 511 TCGGGGATGAGCTT---GGGCTGGTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 567
Qy 140 AlaProPheProLysLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnIleTyr 159
Dy 568 GTGCTGTACCCAGGCTGGGCTGGGATGATGAGCTGCAGAGCGCGGCGGCGGAGGCTAC 627
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Dy 1348 ACATGTGTCTGGAAGGCGCTCTTCTTCTGCGAGCCCGGAGGAGGAGGAGGAGGAGG 1407

Qy 420 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValLeuValLeuValLeuVal 439
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Qy 440 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 459
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LOCUS Sus scrofa AMP-activated protein kinase gamma subunit (PRKAG3)
DEFINITION mRNA, complete cds.
ACCESSION AF214520
VERSION AF214520.2 GI:29812509
KEYWORDS Sus scrofa (pig)
SOURCE Sus scrofa
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 2023)
AUTHORS Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M., Rogel-Gallard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H., Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P. and Andersson,L.
TITLE A mutation in PRKAG3 associated with excess glycogen content in pig skeletal muscle
JOURNAL Science 288 (5469), 1248-1251 (2000)
PUBMED 10818001
REFERENCE 2 (bases 1 to 2023)
AUTHORS Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Rogel-Gallard,C., Paul,S., Gellin,J., Lundstrom,K., Reinsch,N., Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish University of Agricultural Sciences, BMC box 597, Uppsala 751 24, Sweden
REFERENCE 3 (bases 1 to 2023)
AUTHORS Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Rogel-Gallard,C., Paul,S., Gellin,J., Lundstrom,K., Reinsch,N., Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.
TITLE Direct Submission
JOURNAL Submitted (11-APR-2003) Dept Animal Breeding and Genetics, Swedish University of Agricultural Sciences, BMC box 597, Uppsala 751 24, Sweden
REMARK Sequence update by submitter
COMMENT On Apr 11, 2003 this sequence version replaced gi:8215683.
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ORIGIN

Alignment Scores:
Pred. No.: 7,54e-112 Length: 2023
Score: 2011.00 Matches: 400
Percent Similarity: 90.11% Conservative: 19
Best Local Similarity: 86.02% Mismatches: 44
Query Match: 83.69% Indels: 2
DB: 4 Gaps: 2

US-10-070-794A-30 (1-464) x AF214520 (1-2023)

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Db	271	GTAGAGGAAGGGGGCCCTCCGGGCCGAGGAAAGGTCCCACTCAGGCCCACTGGCTGAG	330
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Qy	140	AlaProPheProLysLeuGlyTrpAspAspGluLeuArgLysProGlyValaGlnIleTyr	159
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Db	688	ATCTTCGACACCATCTGAGATCAAGAAGGGCTTCTTTGGCCCTGGTGGCCAAAGCGCTC	747
Qy	200	ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr	219
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Qy	220	AspPheIleLeuValLeuHisArgTyrTrpArgSerProLeuValGlnIleTyrGluIle	239
Db	808	GACTTCATCTTGGTGTGCACCGCTATTACAGGTCCCGCTGGTCCAGATCTTACGAGATT	867
Qy	240	GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu	259
Db	868	GAAGAACAATAAGATTGAGACCTGGAGGGGAGATCTACCTTCAAGGCTGTCTTCAAGCCTCTG	927
Qy	260	ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg	279
Db	928	GTCTCCATCTCTCCCAATGACAGCCTGTTTCGAAGCTGTCTACGCCCTCATCAAGAACCGG	987

Qy	280	IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis	299
Db	988	ATCACCGCTTCGGGTCTCGGACCTGTCTCGGGGCTGTGTCCACACATCTCCACACAT	1047
Qy	300	LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu	319
Db	1048	AAGCGGCTTCTCAAGTTCCTGCACATCTTTGGCACCTGTGTGGCCGGCTCTCTCTCTC	1107
Qy	320	TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGlu	339
Db	1108	TACCGCACCATCCAAAGATTTGGGCATCGGCACATTCGAGACTTGGCCGGTGTCTGGAA	1167
Qy	340	ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuPro	359
Db	1168	ACGGCGCCCATCTGACCGCCTGGACATCTTCTGGACCGGGCTGTGTCTGCGCTGCT	1227
Qy	360	ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu	379
Db	1228	GTGGTCAACGAAACTGGACAGGTAGTGGGCTCTTACTCTCGCTTGTATGTATCCACCTG	1287
Qy	380	AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg	399
Db	1288	GCTGCCCAACAAACATACAAACCTCGACATGAATGTGGAGAAAGCCCTGAGGACGCG	1347
Qy	400	ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIle	419
Db	1348	ACACTGTGTCTGGAAAGCGTCTCTTCTGTCAGGCCCAAGAGACTTGGGGGAAGTCAAT	1407
Qy	420	AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu	439
Db	1408	GACCGGATTTGTCGGGAAACAGGTGCACCGCTGTGTCTGTGGATGAGACCCAGACCTT	1467
Qy	440	LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle	459
Db	1468	CTGGCGCTGTGTCTCTCTGACATCTTCAGGCTCTGGTGTCTCAGCCCTGTCTGGAAAT	1527
Qy	460	AspAlaLeuGlyAla	464
Db	1528	GATCCCTTCGGGGCC	1542

Search completed: January 26, 2006, 01:18:34
Job time : 6250.24 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 25, 2006, 21:45:36 ; Search time 4619.48 Seconds
(without alignments)
4699.486 Million cell updates/sec

Title: US-10-070-794A-30

Perfect score: 2403
Sequence: 1 MSFLEQNSSSWSPAVTSS.....LSDILQALVLSPIGIDALGA 464

Scoring table: BLOSUM62 Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPTO_spool_P/US10070794/runat_24012006.164415.8798/app.query.fasta_1.1102
-DB=EST_QPWT-fastcap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCT=0 -LOOPEXT=0
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-DOCALIGN=200 -THRESHOLD=500 -MINLEN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_hcc.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_est7.*
9: gb_gss1.*
10: gb_gss2.*
11: gb_gss3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2281	94.9	1470	11	DQ030935 Homo sapi
2	2055	85.5	1470	11	DQ030936 Pan trogl
3	2010	83.6	2256	4	AK036585 Mus muscu
c 4	1239	51.6	754	6	CD628194
c 5	1177	49.0	796	6	CD628192
6	1154	48.0	799	6	CD628195
7	1121.5	46.7	805	6	CD628193

8	1113	46.3	2839	4	AK032238	Mus muscu
9	1097	45.7	1990	4	CR861174	Pongo pyg
10	1094	45.5	2058	4	BC079017	Rattus no
11	1043.5	43.4	824	8	CX313244	JGI X2T90
12	1017	42.3	1136	5	EX403964	BM922418
13	1017	42.3	1144	5	EX421925	BM922418
14	1017	42.3	1561	4	CR604823	full-leng
15	1017	42.3	1577	4	CR608916	full-leng
16	1017	42.3	1584	4	CR613967	full-leng
17	1017	42.3	1600	4	CR596899	full-leng
18	1017	42.3	1610	4	CR612109	full-leng
19	1017	42.3	1648	4	CR620523	full-leng
20	1016.5	42.3	1006	1	AL513784	AL513784
21	1006	41.9	1015	3	BM907915	AGENCOURT
22	1004	41.8	900	10	AY420782	Mus muscu
23	1004	41.8	978	1	AL533446	AL533446
24	1003	41.7	900	10	AY420780	Homo sapi
25	991.5	41.3	1912	4	CNSOGLSJ	CR724269 Tetraodon
26	989	41.2	1623	4	CR611774	full-leng
27	982	40.9	1081	1	AL554278	AL554278
28	977	40.7	1096	5	EX424876	BM922418
29	972.5	40.5	1023	1	AL555228	AL555228
30	964	40.1	1062	1	AL524822	AL524822
31	960	40.0	929	1	AL548987	AL548987
32	955	39.7	1085	3	BM548053	AGENCOURT
33	946	39.4	857	8	DR866220	JGI_CABG8
34	941	39.2	944	5	BQ954908	BQ954908
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36	924	38.5	937	5	EX845992	EX845992
37	915.5	38.1	1070	3	BQ224866	AGENCOURT
38	913	38.0	845	8	DN067954	JGI_CABD4
39	913	38.0	850	8	DR880606	DR880606
40	913	38.0	870	8	DN069094	DN069094
41	910	37.9	1134	3	BM922418	BM922418
42	909	37.8	922	6	CA982776	CA982776
43	909	37.8	1314	8	DN731086	DN731086
44	908	37.8	809	7	CV561269	CV561269
45	906	37.7	937	1	AL552459	AL552459

ALIGNMENTS

RESULT 1

DQ030935

LOCUS

DEFINITION

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.

DQ030935 Homo sapiens PRKAG3 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

DQ030935 GI:66882139

GSS.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 1470)

Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B.,

Hubisz, M.J., Fledel-Alon, A., Tanenbaum, D.M., Civallo, D.,

White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

A Scan for Positively Selected Genes in the Genomes of Humans and

Chimpanzees

(er) PLOS Biol. 3 (6), E170 (2005)

2 (bases 1 to 1470)

Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B.,

Hubisz, M.J., Fledel-Alon, A., Tanenbaum, D.M., Civallo, D.,

White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,

Rockville, MD 20850, USA

This sequence was made by sequencing genomic exons and ordering

them based on alignment. Translation starts at the beginning of

alignment.

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Alignment Scores:
Pred. No.:      8.27e-196      Length:      1470
Score:          2281.00        Matches:    443
Percent Similarity: 95.47%      Conservative: 0
Best Local Similarity: 95.47%      Mismatches: 21
Query Match:     94.92%         Indels:     0
DB:              11           Gaps:       0

US-10-070-794A-30 (1-464) x DQ030935 (1-1470)
Qy      1 MetSerPheLeuGluGlnGluAsnSerSerTrpProSerProAlaValThrSerSer 20
Db      76 ATGAGCTTCTTAGAGCAAGAAACAGCAGCTCATGGCCATCACCAGCTGTGACCAAGC 135
Qy      21 SerGluArgIleArgGlyeArgAlaLysAlaLeuArgTfThrArgGlnLysSer 40
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Qy      41 ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60
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Qy      61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla 80
Db      256 TCCACCGGGCTGGAGGCCACATTCCTCCCAAGACCACACCCCTTGGCTCAAGCTGATCTGCC 315
Qy      81 GlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSerAla 100
Db      316 GGGGTGGGCACTCCACCAACAGGGTGGAGCTGCCCTCCCTCTGAGTGTACAGCCCTCAGCT 375
Qy      101 AlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTrp 120
Db      376 GCAGGCTCCAGCAGATGATGTGAGCTGGCCAGCGAGTTCACGACCACAGAGGCGCTGG 435
Qy      121 GluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGlnAla 140
Db      436 GAGTGTGAGCTAGAAAGGCTGCTGGAAGAGAGGCGCTGCCCTGTGCTGTCCCGCAGGCC 495
Qy      141 ProPheProLysLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnIleTyMet 160
Db      496 CCATTTCCAAAGCTGGGTGGGATGACCAACTGCGGAAACCCGGCGCCAGATCTACATG 555
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Qy      201 AlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAsp 220
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261 SerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIle 280
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281 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 300
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301 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 320
976 CGCTGTCTCAAGTTCCTGCACATCTTTGGTTCCTGCTGCCCGGCCCTCTCTCTCTAC 1035
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361 ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeuAla 380
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421 ArgIleAlaArgGluGlnValHisArgLeuValLeuValLeuGluThrGlnHisLeuLeu 440
1336 AGGATTCCTCGGAGCAGGTACACAGGTGCTGTGTAGTGACAGAGACCCAGCATCTCTTG 1395
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461 AlaLeuGlyAla 464
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RESULT 2
DQ030936
LOCUS
DEFINITION
Pan troglodytes PRKAG3 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION
DQ030936
VERSION
DQ030936.1 GI:66882140
KEYWORDS
GSS.
SOURCE
Pan troglodytes (chimpanzee)
ORGANISM
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Pan.
REFERENCE
1 (bases 1 to 1470)
Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civallo,D.,
White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
(ser) PLoS Biol. 3 (6), E170 (2005)
15869325
2 (bases 1 to 1470)
Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civallo,D.,
White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
Direct Submission
Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
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them based on alignment. Translation starts at the beginning of alignment.

FEATURES

source Location/Qualifiers
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 /mol_type="genomic DNA"
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ORIGIN

Alignment Scores:

Pred. No.: 2,59e-175 Length: 1470
 Score: 2055.00 Matches: 405
 Percent Similarity: 87.72% Conservat: 2
 Best Local Similarity: 87.28% Mismatches: 57
 Query Match: 85.52% Indels: 0
 DB: 11 Gaps: 0

US-10-070-794A-30 (1-464) x DQ030936 (1-1470)

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 Db 76 ATGAGCTTCNAGAGCAAGAAACAGCANTCTCATGGCCATCACCAGCTGTGACAGCAGC 135
 Qy 21 SerGluArgileArgGlyLysArgAlaAlaLeuArgTrpThrArgGlnLysSer 40
 Db 136 TCAGAAAGATCCGCGGAAACGAGAGGCCCAAGCCTCGAGATGGACAGGAGAGCGG 195
 Qy 41 ValGluGluGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60
 Db 196 GTGGAAGAGAGGAGCACCAGGCTCAGGGGAGAGGAGGAGGAGGAGGAGGAGGAGG 255
 Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAaspProAla 80
 Db 256 NNN 315
 Qy 81 GlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSerAla 100
 Db 316 NNNNGGGCACTCCACCAACAGGNTGGAGTGCTCTCCCTCTGACTGTACAGCCTCAGCT 375
 Qy 101 AlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTrp 120
 Db 376 GCAGGCTCCAGCAGACATGATGTGGAGCTGCCACCGAGTTCCACGACACAGAGGCGTGG 435
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 Qy 141 ProPheProLysLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnIleTyrMet 160
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 Db 976 CGCTGCTCAAGTTCCTGACATCTTTGGTTCCTGCTGCCCGGCCCTCTCTCTCTAC 1035
 Qy 321 ArgThrIleGlnAaspLeuGlyIleGlyThrPheArgAaspLeuAlaValValLeuGluThr 340
 Db 1036 CGCACTATCCAAAGATTGGGCATCGGCACATTCGAGAGCTTGGTGTGGTGGAGACA 1095
 Qy 341 AlaProIleLeuThrAlaLeuAaspIlePheValAaspArgValSerAlaLeuProVal 360
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 Qy 401 LeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAasp 420
 Db 1276 CTATGTCTGGAGGAGTCTCTTCTGTCAGCCACGAGAGCTTGGGGAGTGTGATCGAC 1335
 Qy 421 ArgIleAargGluGlnValHisArgLeuValLeuValAaspGluThrGlnHisLeuLeu 440
 Db 1336 AGATTGTCTGGAGAGGAGTACAGCTGTGTGTAGTGGACGAGACCCAGCATCTCTTG 1395
 Qy 441 GlyValValSerLeuSerAaspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAasp 460
 Db 1396 GGGGTGTCTCTCTCTCCGACATCTCTGAGCAGCTGTGTGCTGAGCCCTGTGCGATCAT 1455
 Qy 461 AlaLeuGlyAla 464
 Db 1456 GCCCTCGGGGCC 1467

RESULT 3
 AK036585
 LOCUS
 DEFINITION
 AK036585 2256 bp mRNA linear HTC 03-APR-2004
 Mus musculus adult male bone cDNA, RIKEN full-length enriched
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 GAMMA-3 SUBUNIT (AMPK GAMMA-3 CHAIN) (AMPK GAMMA3) homolog [Homo
 sapiens], full insert sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 AK036585.1 GI:263331523
 HTC; CAP trapper.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 1
 AUTHORS
 TITLE
 JOURNAL
 PUBLISHED
 REFERENCE
 2
 AUTHORS
 TITLE
 JOURNAL
 PUBLISHED
 REFERENCE
 3
 TITLE
 JOURNAL
 PUBLISHED
 REFERENCE

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
 11042159

AUTHORS
Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsu, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Tshikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.

TITLE
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL
Genome Res. 10 (11), 1757-1771 (2000)

REFERENCE
11076861

AUTHORS
4

TITLE
The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

JOURNAL
Functional annotation of a full-length mouse cDNA collection

REFERENCE
Nature 409, 685-690 (2001)

AUTHORS
5

TITLE
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

JOURNAL
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

REFERENCE
Nature 420, 563-573 (2002)

AUTHORS
6 (bases 1 to 2256)

TITLE
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kohji, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numata, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saich, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.

TITLE
Direct Submission

JOURNAL
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/
Location/Qualifiers

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/clone="9830138C07"
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107. 1576

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ORIGIN

Alignment Scores: 5.92e-171 Length: 2256
Pred. No.: 2010.00 Matches: 399
Score: 89.25% Conservative: 16
Percent Similarity: 85.81% Mismatches: 48
Best Local Similarity: 83.65% Indels: 2
Query Match: 4 Gaps: 2
DB:

US-10-070-794A-30 (1-464) x AK036585 (1-2256)

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Qy 21 SerGluArgIleArgGlyLysArgArgAlaLysAlaLeuArgTrpThrArgGlnLysSer 40
Db 239 TCAGAAAGAACCTGTGCCATACGGGGAGTCCAGGCTCCAGATGAGCAGACAGAGGCCC 298
Qy 41 ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60
Db 299 GTAGAGGAGCAGAACCAACCCAGGTTTGGGAGAGGTTGCCAGTCCAGACCAAGCTGTGAG 358
Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspPro--- 79
Db 359 TCCACAGGAGGAGGAGGAGCCACATTCCTCCGAGAGCCACACCTTGGCTCAAGCTGTTCCTTG 418
Qy 80 AlaGlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSer 99
Db 419 GCTGAAGGGAGAGACTCCCCACAGAGGTGGAGCTGTCTTGGCCGACTGTGCAGCCTCA 478
Qy 100 AlaAlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAla 119
Db 479 GCAGGGGGCTCCAGCAGAGGTGAGTGCAGTGCATAGCAGTATGCCAGGCCAGGCCAGAGGCC 538
Qy 120 TrpGluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGln 139
Db 539 TGGGACTGTGAGCTGGAGAGGCTTGGGAGAGGAGGAGGCTCTCTCTGTGTCATCCCAAG 598
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Db 599 GCCCCACTTCTCGGCGCTGAGTTGGGATCAGCAACTTCAGAAAGCCCGGAGGCCAGGCTTAC 658
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Qy 180 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 199
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Qy 220 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 239
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Db 899 GAAGAACAATAAGATTGAGACCTTGGAGGAGGAGATCTACCTACAGAGGCTGTCTCANGCTCTA 958
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Qy 420 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 439
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RESULT 4
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DEFINITION 56028554H1 FLP Homo sapiens cDNA, mRNA sequence.

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VERSION CD628194.1 GI:40276460
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 754)
Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
PUBMED 15203218

COMMENT
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.

FEATURES
source location/Qualifiers
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ORIGIN

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Query Match: 51.56% Indels: 2
DB: 6 Gaps: 0

US-10-070-794A-30 (1-464) x CD628194 (1-754)

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Qy 138 oGlnAlaProPheProLysLeuGlyTyrAspAspGluLeuArgLysProGlyAlaGlnI 158
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Qy 158 eTyrMetArgPheMetGlnGlnHisThrCysTyrAspAlaMetAlaThr-SerSerLysL 178
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Qy 198 lyValArgAlaAlaProLeuTyrAspSerLysLysGlnSerPheValGlyMetLeuThrI 218
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Qy 218 leThrAspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrG 238
Db 450 TCACTGACTTCATCTCTGCTGCTGCTACTACAGTCCCCCTGCTGGTCCAGATCTATG 391
Qy 238 luIleGluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysP 258
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Qy 258 roLeuValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrleuIleLysA 278
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Qy 278 snArgIleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuT 298
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Qy 298 hrHisLysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerP 318
Db 210 CACACAAACGCTGTCTCAAGTTCCTGCACATCTTTGGTTCCTGCTGCCCGGCCCTCT 151
Qy 318 heLeuTyrArgThrIleGlnAspIleGlyIleGlyThrPheArgAspLeuAlaValL 338
Db 150 TCCTCTACCGCACTATCCAAAGATTTGGGATCGGCACATTCGCGAGACTTGCTGTGG 91
Qy 338 euGluThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaL 358
Db 90 TGGGGACAGACCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 31
Qy 358 euProValValAenGluCysGlyGlnVal 367
Db 30 TGCCTGTGGTCAACGAATGTGGTCAAGGTC 2

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RESULT 5

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CD628192
VERSION CD628192.1 GI:40276458
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens


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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 796)
Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
15203218
COMMENT
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
FEATURES
Location/Qualifiers
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Best Local Similarity: 93.94% Mismatches: 9
Query Match: 48.98% Indels: 8
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QY 130 uArgProAlaLeuCysLeuSer-ProGlnAlaPro---PheProLysLeuGlyTrp-Asp 148
Db 723 GAGGCTGCCCTGTGCTGTCCCGCAGGGGCCATGTTCGCCAAGCTTGGCGCTGGGGAT 664
QY 149 AspGlu---LeuArgLysProGlyAlaGlnIle-TyrMetArgPheMetGlnGluHisTh 167
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QY 167 rCysTyrAspAlaMetAlaThrSerLysLeuValIlePheAspThrMetLeuGluIl 187
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QY 187 eLysLysAlaPhePheAlaLeuValAlaAsnGlyValArgAlaAlaProLeuTrpAspSe 207
Db 543 CAAGAAGGCTTCTTTGCTCTGTGGTGGCAACCGTGTGGGGCAGCCCTCTATGGGACAG 484
QY 207 r-LysLysGlnSerPheValGlyMetLeuThrIleThrAspPheIleLeuValLeuHisA 227
Db 483 CAAGAAGCAGAGCTTTTGGGGATGCTGACCATCACTGACTTCATCTCTGGTGGTGCATC 424
QY 227 tGlyTyrArgSerProLeuValGlnIleTyrGluIleGluGlnHisLysIleGluThrT 247
Db 423 GCTACTACAGTTCCTCCCTGGTCCAGATCTATGAGATTGAACAACATAGATTGAGACT 364
QY 247 rPArgGluIleTyrLeuGlnGlyCysPheLysProLeuValSerIleSerProAsnAspS 267
Db 363 GGAGGGAGATCTACCTGCAAGGCTGCTTCAAGCCTCTGGTCTCCATCTCTCTCTAATGATA 304
QY 267 rLeuPheGluAlaValTyrThrLeuIleLysAsnArgIleHisArgLeuProValLeuA 287
Db 303 GCCTGTGTGAAGCTGTCTACACCTCATCAAGAACCGGATCATCGCTCGCTGTCTCTG 244
QY 287 spProValSerGlyAsnValLeuHisIleLeuThrHisLysArgLeuLeuLysPheLeuH 307
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Db 123 GCATCGGCACATTCGAGACTTGGCTGTGTGGAGACAGACCCATCTGACTGCAC 64
QY 347 euAspIlePheValAspArgValSerAlaLeuProValValAsnGluCysGlyGlnV 367
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QY 367 al 367
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DEFINITION S6028562J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD628195
VERSION CD628195.1 GI:40276461
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 799)
Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
15203218
COMMENT
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
FEATURES
Location/Qualifiers
1..799
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Alignment Scores:
Pred. No.: 5,31e-94 Length: 799
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Best Local Similarity: 96.12% Mismatches: 7
Query Match: 48.02% Indels: 1
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QY 21 SerGluArgIleArgGlyLysArgAlaLysAlaLeuArgTyrThrArgGlnLysSer 40
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QY 41 ValGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60
Db 224 GTGGGGGAAGGGAGCCACAGGTTCAGGGGAAAGTCCCGGTCCAGGCCAGCTGCTGAG 283
QY 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla 80
Db 284 TCCACCGGGCTGGAGGCCACATTCGCCAAGACCAACCCCTTGGCTCAAGCTGATCTCTGCC 343

```


TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
11042159
3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishire, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
11076861
4
The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2839)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saichou, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216]
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/
Location/Qualifiers
1. .2839
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/db_xref="taxon:10090"
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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CDS

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KIEFWELVLOETFKPLVNISPDASLFDVAVSLINKIHLRPVIDISGNALYLTHK
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2839
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Query Match: 46.32% Indels: 45
DB: 4 Gaps: 7
US-10-070-794a-30 (1-464) x AK032238 (1-2839)
Qy 13 ProSerProAlaValThrSerSerSerGluArgIleArgGlyLysArgAlaLysAla 32
Db 321 CCTTCCCGCGTACAGCTACACATGTTTCGAGTCTTGATATGTTTCACCTGTCTACGTCT 380
Qy 33 ---LeuArgTrpThrArgGlnLysSerValGluGluGluGluProProGlyGlnGlu 51
Db 381 TCTGTGGCCACAGTACTCATGAAGCGCTTTGGAAGTCTCAGGGGCGACCAAGAACCAA 440
Qy 52 GlyProArgSerArgProThrAlaGluSerThrGlyLeuGluAlaThrPhe----- 68
Db 441 GGACCAAAACCGAAGCACCACCGCGCGCCAGTCCGACCCCATGCGCTTTTGGCTCCAG 500
Qy 69 -----ProLysThrThrProLeuAlaGlnAlaAspPro----- 79
Db 501 CGTCTCTCTTCTCCGTCAACACACCCACCAAGTGACCAAGCAGCACCATTTCCCTCGGA 560
Qy 80 -----AlaGlyValGlyThrProThrProThrGlyTrpAspCys----- 91
Db 561 GTCCTACAGCAGGAGCGCTGACACCCAGAGCGCGCATCTATGCTTCTCGTCCCTCC 620
Qy 92 -----LeuPro-----SerAspCysThrAlaSerAlaAlaGly-Se 103
Db 621 AGACACTGGGCGCGCTTCTGCTGGCTTCAGAGCCAGCGCGACCTCGCTGGCATC 680
Qy 103 rSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTrpGluCyeG 123
Db 681 CCCGACATACCATGCTCCTTTGAGAACTGCGGTGCGCGCGCGCGCGCGCGCGGA 740
Qy 123 uLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGlnAlaProPhePr 143
Db 741 A---GCCGCGCATGCTGGAG----- 756
Qy 143 oLysLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnIleTrMetArgPheMe 163
Db 757 -AGCTGGAGTTCAGGAGGAAGCAGAGACTCAGAAAGTGGCGTTTATATGCGATTCAT 815
Qy 163 tGlnGluHisThrCysTrpAspAlaMetAlaThrSerSerLysLeuValIlePheAspTh 183
Db 816 GAGGTCAACACAGTGTATGACATGCTTCCCAACAGGTTCAAAGCTGTGTGTCTTCGACAC 875
Qy 183 rMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaLeuGlyValArgAlaAlaPr 203
Db 876 TACGTTCAGAGTCAAAAAGGCTCTTTCCTTGGTAGCAACAGGAGTCCGTCGCGCGCC 935
Qy 203 oLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAspPheIleLe 223

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Db	697	TCGTCCTCCCGGACAGGAGGAGGTTCTGCCGCTCTCCCTCCAGAGCCGAC	756
Qy	98	AlaSerAlaAlaGlySerThr-----AspAspValGluLeuAlaThr	112
Db	757	AGGCCTCCACTGGCATCACCAACACACTATGCTCCCTCCAAAGCGCGCGCGCG	816
Qy	113	GluPheProAlaThrGluAlaTrpGluCysGluLeuGluGlyLeuLeuGluGluArgPro	132
Db	817	GCCCTGGGACCGCGGAAGCC-----GGCATGCTGGAG-----	849
Qy	133	AlaLeuCysLeuSerProGlnAlaProPheProLysLeuGlyTyrAspAspGluLeuArg	152
Db	850	-----AAGCTGGAGTTCGAGGAGCAAGTAGAA	876
Qy	153	LysProGlyAlaGlnIleTyrMetArgPheMetGlnGluHisThrCysTyrAspAlaMet	172
Db	877	GACTCAGAAAGTGGTGTATCATCGGATTCATGAGTCCACCAAGTGTATGACATCGTT	936
Qy	173	AlaThrSerSerLysLeuValIlePheAspThrMetLeuGluIleLysLysAlaPhePhe	192
Db	937	CCAAACCAAGTTCAAAGCTTGTTGCTCTTGATACATACATACCAAGTGTATGACATCGTT	996
Qy	193	AlaLeuValAlaAsnGlyValArgAlaAlaProLeuTyrAspSerLysLysGlnSerPhe	212
Db	997	GCTTTGGTAGCAACGGGTCCGAGCGCGCTGTGGGAGATGAATAAACAAGTTT	1056
Qy	213	ValGlyMetLeuThrIleThrAspPheIleLeuValLeuHisArgTyrTyrArgSerPro	232
Db	1057	GTAGGAATGCTAACAAATTACAGATTTTCATAAATACATACATACATATAAATACCT	1116
Qy	233	LeuValGlnIleTyrGluIleGluHisLysIleGluThrTrpArgGluIleTyrLeu	252
Db	1117	ATGTGTACAGATTTATGAATTAGAGCAACATAAATAATGAACATGCGAGGAGCTTTATTTA	1176
Qy	253	GlnGlyCysPheLysProLeuValSerIleSerProAsnAspSerLeuPheGluAlaVal	272
Db	1177	CAAGAAACATTTAAGCCTTTAGTGAAATATATCTCGAGATGACAGCTCTCGATGCTGTA	1236
Qy	273	TyrThrLeuIleLysAsnArgIleHisArgLeuProValLeuAspProValSerGlyAsn	292
Db	1237	TACTCTTGATCAAAATAAATAATCCACAGATTTGCCGTTATTGACCTTATCAGTGGGAT	1296
Qy	293	ValLeuHisIleLeuThrHisLysArgLeuLysPheLeuHisIlePheGlySerLeu	312
Db	1297	GGCCTTTATATACCTACCCACAAAAGAAATCCTCAAGTTCCTCCAGCTTTTATGTCTGAT	1356
Qy	313	LeuProArgProSerPheLeuTyrArgThrIleGlnAspLeuGlyIleGlyThrPheArg	332
Db	1357	ATGCCAAAGCCCTTCATGAAGCAGAACCTGGATGAGCTTGGAAATAGGAACATACCAC	1416
Qy	333	AspLeuAlaValValLeuGluThrAlaProIleLeuThrAlaLeuAspIlePheValAsp	352
Db	1417	AACATTGCTTCATACATCCAGACACTCCCATCATCAAGGCTTCAACATATTTGTGAA	1476
Qy	353	ArgArgValSerAlaLeuProValValAsnGluCysGlyGlnValValGlyLeuTyrSer	372
Db	1477	AGACGAATATCAGCTCTGCTGCTGTGGATGAGTCAGGAAAAAGTTGTAGATATTATTCC	1536
Qy	373	ArgPheAspValIleHisLeuAlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerVal	392
Db	1537	AAATTGATGATTAATTAATCTCTGCTGAGAAAACATACATTAACCTAGATATCAGTG	1596
Qy	393	GlyGluAlaLeuArgGlnArgThrLeuCysLeuGluGlyValLeuSerCysGlnProHis	412
Db	1597	ACCCAGGCTTCAGCACCGTTCACAGTATTTTGAAGGTGTTGTGAAGTGAATAAGCTG	1656
Qy	413	GluSerLeuGlyGluValIleAspArgIleAlaArgGluGlnValHisArgLeuValLeu	432
Db	1657	GAATACTGGAGACCATTTGTGACAGAATAGTAAGAGCTGAGGTCATCGCTGGTGGTG	1716
Qy	433	ValAspGluThrGlnHisLeuLeuGlyValValSerLeuSerAspIleLeuAlaLeu	452

1717 GCCAATGACGACATAGTATTGTGGGTATTATTTCCTGTGCAGACATTTCTGCAGCCCTG 1776

453 ValLeuSerProAlaGly 458

1777 ATCTTCACACGACGAGT 1794

RESULT 10

BC079017

LOCUS

DEFINITION

BC079017

VERSION

KEYWORDS

SOURCE

ORGANISM

BC079017.1 GI:50927344

HTC.

Rattus norvegicus (Norway rat)

Rattus norvegicus

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

1 (bases 1 to 2058)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heien, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uedin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullen, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywicki, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

2 (bases 1 to 2058)

Director MGC Project.

Direct Submission

Submitted (02-AUG-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapbs-remail.nih.gov

Tissue Procurement: Howard Jacobs

CNA Library Preparation: Express Genomics

CNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

CNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: <http://www-shgc.stanford.edu>

Contact: (Dickson, Mark) mcd@paxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>

Series: IRAP Plate: 182 Row: m Column: 20

This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein

This clone has the following problem: frame shifted.

Location/Qualifiers

1. .2058

/organism="Rattus norvegicus"

/mol_type="mRNA"

FEATURES

source

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/db_xref="taxon:10116"
/clone="IMAGE:7113709"
/tissue_type="Testis, rat (Brown Norway)"
/clone_lib="NIH MGC_237"
/lab_host="DH10B"
/notes="Vector: pExpress1"

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ORIGIN

Alignment Scores:

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Pred. No.:      6,05e-88      Length:      2058
Score:          1094.00      Matches:      234
Percent Similarity: 65.00%      Conservative: 91
Best Local Similarity: 46.80%      Mismatches: 115
Query Match:      45.53%      Gaps:      60
DB:              4          Indels:      10

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US-10-070-794A-30 (1-464) x BC079017 (1-2058)

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Qy      4 LeuGluGlnGluAenSerSerTrpProSerProAlaValThrSerSerGluArg 23
Db      280 CTTCCAGAGGACTCTTCTCCAGGGGGCCCCCAGCCCGCCCTCCAGCCCTGTGTCTGCTC 339

Qy      24 IleArgGlyLysArgAlaLysAlaLeuArgTrpThrArgGlnLysSerValGluGlu 43
Db      340 CTGTGAGGCCCAAGATGAGCCTGGCTCCCAAACTGTGTCCCGTTCTCTTACCAGAA 399

Qy      44 GlyGluProGlyGlnGlyGluGlyProArgSerArgProThrAla-----Glu 60
Db      400 TCCCTCCA-----CGCTCTCCAGCCGGATGAGTTTCAGTGGGATCTTCCGC 447

Qy      61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAseProAla 80
Db      448 TCCTCATCCAAAGAGTCTTCG---CCCAACTCCAAACCG-----TCTACCTCTTCCCGGG 498

Qy      81 GlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSerAla 100
Db      499 GGCATCAGGTTCTC-----TTCTCGGGTCCAGAAACCTCCAGCGTC 540

Qy      101 AlaGlySerSerThrAspValGluLeuAlaThrGluPhePro---AlaThrGluAla 119
Db      541 TCCTCTCTCCATCAACACCCACCAGTGAACCAAGCAGCAGCCATTTCCCTCGAGTCC 600

Qy      120 TrpCysGluLeuGluGlyLeuLeuGluGluArg-----Glu 131
Db      601 TACAAGCAGGAGCTGAA---CGCTAGAAAGCGCGCATCTATGCTCTCTCATCCCCACCG 657

Qy      132 -----ProAlaLeuCysLeuSerProGlnAlaPro----- 141
Db      658 GACACCGCCAGCGCTCTGCTGGCTTCCAGAGCCCGGTTCGCGTCTCTGCGCATCT 717

Qy      141 ----- 141
Db      718 CCCACACCATGCTCTCTTTGAGAACCGCGGCTGGCGGCGCCCGGACCCCGGAA 777

Qy      142 -----PheProLysLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnIle 158
Db      778 GCGCGCATGCTGGAGAGCTGAGTTCAGGAGGAA---GAAAGACTCAGAGAGTGGCGTT 834

Qy      159 TyrMetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeu 178
Db      835 TATATGCGATTGATGAGGTACACAGTGTATGACATCTGTTCAACCACTCAAGCTT 894

Qy      179 ValIlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGly 198
Db      895 GTTGTCTTCGACACTAGCTTGCAGTTAAAGAGCTTCTTTGCTTTGGTAGCCACCGA 954

Qy      199 ValArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIle 218
Db      955 GTCCGTGCGCGCGCTGTGGGAAAGTAAAGACAGAGCTTCGTAGGAATGCTCAAAAT 1014

Qy      219 ThrAspPheIleLeuValLeuHisArgTyrTrpArgSerProLeuValGlnIleTyrGlu 238
Db      1015 ACAGATTTCATAAACATACATACACAGATACTATAAAATCCCCCAGGTGGTACAGATTATGAA 1074

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Qy      239 IleGluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysPro 258
Db      1075 TTGGAGGAACATAAGATTGAAACGTGGAGGAACTGACTTTACAAGAAACCTTCAAGCCT 1134

Qy      259 LeuValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsn 278
Db      1135 TTGGTGAATATCTCTCCAGATGCGAGCCTTCTTCATGCTGTATATCTCGTTGATCAAAAT 1194

Qy      279 ArgIleHisArgLeuProValLeuAspProValSerGlyAenValLeuHisIleLeuThr 298
Db      1195 AATATCCACAGATTGCGAGTTATTGACCTATCATGTGGGATGACACTTTATATTAATACC 1254

Qy      299 HisLysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPhe 318
Db      1255 CACAAAGAAATCCTCAAGTTCTCCAGCTTTTATGTCTGACATGCCAAAGCCCGCCTTC 1314

Qy      319 LeuTyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeu 338
Db      1315 ATGAAGCAGAACCTGGATGAGCTCGGAATAGGAACATATCACATATTGCTTCAATTCAC 1374

Qy      339 GluThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeu 358
Db      1375 CCGAATACCCCATCATCAAGCCTTGAACATCTTTGTGGAGACCGGATATCTGCGCTG 1434

Qy      359 ProValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHis 378
Db      1435 CCTGTGTGTGATGATGAGTCCAGAAAGTTGTAGATATTACTTCCAAGTTTGTATTAAT 1494

Qy      379 LeuAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGln 398
Db      1495 CTTGCTGCTGAGAAACGTACAATAACCTAGACATCATCGGTGACCCGCGCTCGACAC 1554

Qy      399 ArgThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluVal 418
Db      1555 CGTCAAGTATTGTTAGGGGTGGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 1614

Qy      419 IleAspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHis 438
Db      1615 GTGGACAGATAGTGTAGAGCGAGGTCCATCGGTGGTGGTGGTGGTGGTGGTGGTGGT 1674

Qy      439 LeuLeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGly 458
Db      1675 ATTGTGGTATTATCTCTCTGTGACATCTCTGCAAGCCCTGATCTCTCACACCAAGCAGT 1734

RESULT 11
LOCUS   CX313244
DEFINITION JGI_XZT9073.fwd NIH_XGC_tropad5 Xenopus tropicalis cDNA clone
IMAGE:7586968 5', mRNA sequence.
ACCESSION CX313244
VERSION   CX313244.1 GI:57041698
KEYWORDS EST.
SOURCE    Xenopus tropicalis (western clawed frog)
ORGANISM Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 824)
Richardson, P., Lucas, S., Rokhsar, D., Dettler, J.C., Ng, D.C.,
Brokstein, P., and Lindquist, E.A.
DOE Joint Genome Institute
Unpublished (2004)
Other ESTs: JGI_XZT9073.rev
Contact: Lindquist, E.A., Richardson, P.
DOE Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925 296 5600
Fax: 925 296 5710
Email: cdna@jgi-psf.org
Tissue Procurement: Richard M. Harland Laboratory, University of
California, Berkeley: http://tropicalis.berkeley.edu/home
cDNA Library Preparation: Richard M. Harland Laboratory, University

```


of California, Berkeley
 DNA Sequencing: DOE Joint Genome Institute: <http://www.jgi.doe.gov>
 Clone Distribution: I.M.A.G.E. Consortium/LLNL:
<http://image.llnl.gov>
 Naming Conventions: EST name is generated by the concatenation of
 the JGI Clone id and the direction of sequencing. The suffix 'fwd'
 indicates a forward sequencing read of the insert. It does not
 necessarily reflect the orientation of the insert.
 Plate: X27 0093 row: a column: 14
 High quality sequence stop: 775.

FEATURES

Location/Qualifiers
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 /organism="Xenopus tropicalis"
 /mol_type="mRNA"
 /db_xref="taxon:8364"
 /clones="IMAGE:7586968"
 /tissue_type="whole embryo"
 /dev_stage="tadpole (st. 36-41)"
 /lab_host="E. coli XL1-Blue derivative, Stratagene
 Electroten-Blue"
 /clone_lib="NIH_XGC_tropTad5"
 /note="Vector: pCS108; Site 1: SalI; Site 2: NotI; Tadpole
 library constructed by Russell B. Fletcher in R. Harland's
 lab using poly A RNA and oligo dt primers (Invitrogen
 SuperScript Plasmid System for cDNA Synthesis and
 Cloning). SalI (5' end) -NotI (3' end) cDNA was inserted
 into vector pCS108
 (http://mcb.berkeley.edu/labs/harland/pages/plasmids.html).
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ORIGIN

Alignment Scores:
 Pred. No.: 5.83e-84 Length: 824
 Score: 1043.50 Matches: 202
 Percent Similarity: 84.29% Conservative: 34
 Best Local Similarity: 72.14% Mismatches: 37
 Query Match: 43.42% Indels: 7
 DB: 8 Gaps: 1

US-10-070-794A-30 (1-464) x CX313244 (1-824)

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Qy 143 ProlysLeuGlyTTPAspAspGluLeuArgLysProGlyAlaGlnIleTyrMetArgPhe 162
Db 2 CCAGATCTGGGGAGAT-----GCCGGCTTTCATGAGTTC 40

Qy 163 MetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValIlePheAsp 182
Db 41 ATGATGAAGAACTGCTGTACGACGCCATCTCTACAGCTGCAAGTTGGTGGTTTGAC 100

Qy 183 ThrMetLeuGluIleLysLysAlaPheAlaLeuValAlaAsnGlyValArgAlaLa 202
Db 101 ACCACCTGCGAGATAAAGAGCGTTCTGGCACTGGTGGCAATGGAGTACGGGACGC 160

Qy 203 ProLeuTTPAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAspPheile 222
Db 161 CCTCTATGGGACAGCAAGCAGCAGCTTTGTGGGAATGCTCACCATCACCAGCTTCATC 220

Qy 223 LeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGluGlnHis 242
Db 221 AACATCTCGACCGATACACAGGCGCCCTGGTTCAGATATACGAAGTGGAGGAGCAT 280

Qy 243 LysIleGluThrTTPArgGluIleTyrLeuGlnGlyCysPheLysProLeuValSerIle 262
Db 281 AAAATAGAGACATGGAGAGAGTTTACCTGCAAGTTCTTTCAAGCCATTATCTATATC 340

Qy 263 SerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIleHisArg 282
Db 341 TCCCCAGCAGACAGCGCTTTCCACCGCTGTATATTCATTTATCAAGATAAGATCCACCG 400

Qy 283 LeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLysArgLeu 302
Db 401 CTGCCAGTAATGATCCCATATCCGGAACATCCTCGCATATCTTACGCACAAACGTCCTC 460
  
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Qy 303 LeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyrArgThr 322
Db 461 CTCAAGTTCCTCCACTCTGTTGGAGACACTCTCCCAAGGCCACGGTCTTTCGAGAAGACC 520

Qy 323 IleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGluThrAlaPro 342
Db 521 ATCTGGAGTTGGGCATCGGCACCTTTAGGATGTGGCAGTCGTGGAGGACTCTCTCTCT 580

Qy 343 IleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProValValAsn 362
Db 581 GTCTCAACAGCACTGTAATCTTTGTAGAGAGAGAGATTTCCTCCCTCCCGGTGGTGAAT 640

Qy 363 GluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeuAlaAlaGln 382
Db 641 GATCTGGCGAGGTGGTGGAGCTCTATTCCCGTTTGTATGATATACACTTGGGCACAG 700

Qy 383 GlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThrLeuCys 402
Db 701 AAGATCTATAACAACCTGGATATCAGCGTACGAGATGCCCTGGCGTTCTCTCGAGT 760

Qy 403 LeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValIleAspArgIle 422
Db 761 ATTGAGGGGCTCTCATGTGTACCCCATGAAAGTCTGGAGGTGGTCAATTGATCGAATT 820
  
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RESULT 12

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BX403964 1136 bp mRNA linear EST 01-MAY-2004
LOCUS BX403964 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
DEFINITION CL0BB0072F11 5-PRIME, mRNA sequence.
ACCESSION BX403964
VERSION BX403964.2 GI:46925338
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
  
```

Full-length cDNA libraries and normalization
 Unpublished (2001)
 On May 13, 2003 this sequence version replaced gi:30635099.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: secre@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
 was not normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
 This sequence belongs to sequence cluster 5712.f
 For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?s=CL0BB0072F11RPI&c=6712.f>.

FEATURES

Location/Qualifiers
 1..1136
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clones="CL0BB0072F11"
 /tissue_type="NEUROBLASTOMA"
 /clone_lib="Homo sapiens NEUROBLASTOMA"
 /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
 with a NotI-oligo(dT) primer. Five prime end enriched,
 double-strand cDNA was digested with Not I and cloned into
 the Not I and EcoRV sites of the pCMVSPORT 6 vector.
 Library was not normalized."

ORIGIN

Alignment Scores:
 Pred. No.: 2.39e-81 Length: 1136
 Score: 1017.00 Matches: 193
 Percent Similarity: 82.55% Conservative: 53


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Best Local Similarity: 64.77% Mismatches: 52
Query Match: 42.32% Indels: 0
DB: 5 Gaps: 0
US-10-070-794A-30 (1-464) x BX403964 (1-1136)

QY 158 IletyMetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLys 177
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Db 73 GTGTATATCTTCATCAAGTCTCATCGCTGCTATGACCTGATTCACCAAGCTCCAAA 132
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 178 LeuValIlePheAspThrMetLeuGluIleLysAlaPhePheAlaLeuValAlaAen 197
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 133 TTGGTGTATTGATGATGCTCCCTGACAGGAGAAAGCTTTTGTGGGATGCTAAC 192
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QY 198 GlyValArgAlaAlaProLeuTrpAspSerLysGlnSerPheValGlyMetLeuThr 217
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 193 GGTGTACAGCTGCCCTTATGGGATAGTAAGCAAGCTTTTGTGGGATGCTAAC 252
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QY 218 IletyMetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLys 237
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QY 238 GluIleGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLys 257
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QY 258 ProLeuValSerIleSerProAenAspSerLeuPheGluAlaValTyrThrLeuLys 277
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ORIGIN
Alignment Scores:
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Score: 1017.00 Matches: 193
Percent Similarity: 82.55% Conservative: 53
Best Local Similarity: 64.77% Mismatches: 52
Query Match: 42.32% Indels: 0
DB: 5 Gaps: 0
US-10-070-794A-30 (1-464) x BX421925 (1-1144)

QY 158 IletyMetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLys 177
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QY 178 LeuValIlePheAspThrMetLeuGluIleLysAlaPhePheAlaLeuValAlaAen 197
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QY 198 GlyValArgAlaAlaProLeuTrpAspSerLysGlnSerPheValGlyMetLeuThr 217
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QY 258 ProLeuValSerIleSerProAenAspSerLeuPheGluAlaValTyrThrLeuLys 277
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Db 373 CCCTGTTGCTGCATTTCTCTTAATGCCAGCTTGTGTGATGCTGTCTTCTTAATATCGG 432

KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (Bases 1 to 1144)
AUTHORS Li, W.B., Gruber, C., Jesses, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 13, 2003 this sequence version replaced gi:30638442.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 6712.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DH005DG11Q1&c=6712.f.
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Location/Qualifiers
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/clone="CS0DH005YN22"
/tissue_type="T CELLS (JURKAT CELL LINE)"
/cell_line="JURKAT CELL LINE"
/notes="Vector: pCMVSPORT 6; 1st strand cDNA was primed
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double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

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RESULT 13

BX421925

LOCUS

DEFINITION

clone CS0DH005YN22 5-PRIME, mRNA sequence.

ACCESSION

BX421925

VERSION

BX421925 Homo sapiens T CELLS (JURKAT CELL LINE) Homo sapiens cDNA
 1144 bp mRNA linear EST 01-MAY-2004
 clone CS0DH005YN22 5-PRIME, mRNA sequence.
 BX421925.2 GI:46925182

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Qy 278 AsnArgIleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeu 297
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Qy 298 ThrHisIysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSer 317
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Qy 398 GlnArgThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGlySerLeuGlyGlu 417
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RESULT 14
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LOCUS full-length cDNA clone CS0DK007YB02 of HeLa cells Cot 25-normalized
DEFINITION of Homo sapiens (human).
ACCESSION CR604823.1 GI:50485630
VERSION HTC; CNSLT_CDNA.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homindae; Homo.
1 (bases 1 to 1561)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1561)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
Location/Qualifiers
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FEATURES
source

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/tissue_type="HeLa cells Cot 25-normalized"
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Alignment Scores:
Pred. No.: 3.85e-81 Length: 1561
Score: 1017.00 Matches: 193
Percent Similarity: 82.55% Conservative: 53
Best Local Similarity: 64.77% Mismatches: 52
Query Match: 42.32% Indels: 0
DB: 4 Gaps: 0

US-10-070-794A-30 (1-464) x CR604823 (1-1561)

Qy 158 IleTyrMetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLys 177
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Qy 298 ThrHisIysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSer 317
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Qy 318 PheLeuTyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValVal 337
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RESULT 15	CR608916	1577 bp mRNA linear HTC 21-JUL-2004	374	CGCCTTTGCTGCATTTCTCCTAATGCCAGCTGTTTGTGCTGCTCTCTCATTAATTCGG
LOCUS	CR608916	full-length cDNA clone CS0DA012YB06 of Neuroblastoma of Homo sapiens (human).	278	AsnArgIleHisArgLeuProValSerGlyAsnValLeuHisIleLeu
DEFINITION	CR608916	HTC; CNSLT cDNA.	434	ACAAGATCCAGGCTGCCAGTTATTGACCAGAAATCAGGAATCACTTTGTACATCCCTC
ACCESSION	CR608916	GI:50489723	298	ThrHisLysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSer
VERSION	CR608916.1		494	ACCCACAAGCGCATCTCTGAAGTTCTCTCAAAATGTTTATCACTAGGTCCCAAGCCAGAG
KEYWORDS	CR608916	Homo sapiens (human)	318	PheLeuTyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaVal
SOURCE	CR608916	Homo sapiens	554	TTCATGTCCAAGTCTCTGGAAGAGCTACAGATTGGCACCTATGCGCAATATTCTATGTT
ORGANISM	CR608916	Homo sapiens	338	LeuGluThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAla
REFERENCE	CR608916	1 (bases 1 to 1577).	614	CGCACTTACCAACCCCGTCTATGTGGGTCTCTGGGGATTTTGTACACATCGAGTCTCAGCC
AUTHORS	CR608916	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.	358	LeuProValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIle
TITLE	CR608916	Full-length cDNA libraries and normalization	674	CTGCCAGTGTGGATGAGAAGGGCGCTGTGGTGACATCTACTCCAGTTTGATCTATC
JOURNAL	CR608916	Unpublished	378	HisLeuAlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArg
REMARK	CR608916	Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue 2 (bases 1 to 1577)	734	AATCTGGCAGCAGAAAGAACCTTACAACAACCTAGATGTATCTGTGACTAAAGCCTTGCAA
REFERENCE	CR608916	Genoscope.	398	GlnArgThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGlu
AUTHORS	CR608916	Genoscope.	794	CATCGATCATCACTACTTTGAGGGGTGTTCTCAAGTGCTTACCTGTCATGAGACTCTGGAGACC
TITLE	CR608916	Direct Submission	418	ValIleAspArgIleAlaAargGluGlnValHisArgLeuValLeuValAspGluThrGln
JOURNAL	CR608916	Submitted (20-JEY-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)	854	ATCATCAACAGCGTAGTGGAACGAGAGGTTTACCAGCTTGTAGTGTGGTGAATAATGAT
COMMENT	CR608916	1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.	438	HisLeuLeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSer
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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

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(without alignments)
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Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2010	83.6	1873	3	US-09-950-022A-7
4	2007	83.5	1873	3	US-09-950-022A-9
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11	1016.5	42.3	1576	3	US-09-101-146-63	Sequence 63, Appl
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c 24	151.5	6.3	1664976	3	US-09-692-570-1	Sequence 82286, A
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c 26	130.5	5.4	622	3	US-08-998-416-987	Sequence 3, Appli
c 27	130.5	5.4	2622	3	US-10-132-350-3	Sequence 1, Appli
c 28	130.5	5.4	2912	3	US-10-132-350-1	Sequence 2, Appli
c 29	130.5	5.4	3019	3	US-09-359-161-2	Sequence 1219, Ap
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c 45	117	4.9	4411529	3	US-09-103-840A-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-950-022A-3
; Sequence 3, Application US/09950022A

; Patent No. 6919177
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: Reproductive
; TITLE OF INVENTION: and Meat Quality Traits
; FILE REFERENCE: P04668US3
; CURRENT APPLICATION NUMBER: US/09/950,022A
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 21
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; SEQ ID NO 3
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; TYPE: DNA
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)-(1392)
; OTHER INFORMATION:
US-09-950-022A-3

Alignment Scores:

Pred. No.: 7.05e-192 Length: 1873
Score: 2013.00 Matches: 400
Percent Similarity: 90.11% Conservative: 19
Best Local Similarity: 86.02% Mismatches: 44
Query Match: 83.77% Indels: 2
DB: 3 Gaps: 2

US-10-070-794A-30 (1-464) x US-09-950-022A-3 (1-1873)

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QY 1 MetSerPheLeuGluGlnGluAsnSerSerTirProSerProAlaValThrSerSer 20
DB 1 ATGAGCTTCTTAGAGCAAGAGGAGAGCGTTCATGGCCATCCCGAGCTGTAAACACACAGC 60
QY 21 SerGluArgLleArgGlyLysArgAlaLysAlaLysAlaLeuArgTrpThrArgGlnLysSer 40
DB 61 TCAGAAAGAGCCATCGGACCGAGGACCAAGGCCCTCTAGATGGACCAAGCGAGGAGAT 120
QY 41 ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60
DB 121 GTAGAGGAAGGGGGCTTCGCGGCCCGAGGGAAGGTCCCCAGTCCAGGCCAGTTGCTGAG 180
QY 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspPro--- 79
DB 181 TCCACCGGCGAGGAGGCCACATTCGCCAAGGCCACACCTTGGGCCCAAGCGCTCCCTTG 240
QY 80 AlaGlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSer 99
DB 241 GCCGAGGTGGACAACCCCAACAGAGCGGAGACATCCTCCCTCTGACTGTGCAGCCTCA 300
QY 100 AlaAlaGlySerSerThrAspValGluLeuAlaThrGluPheProAlaThrGluAla 119
DB 301 GCCTCCGACTCCAAACAGACACATCTGGATCTGGGCATAGAGTTCTCAGCCCTCGCGGCG 360
QY 120 TrpGluCysGluLeuGluGlyLeuLeuGluArgProAlaLeuCysLeuSerProGln 139
DB 361 TCGGGGATGAGCTT---GGCTGTGTGAAGAGCAGCCCGCTGCCATCCCCAGAG 417
QY 140 AlaProPheProLysLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnLetyr 159
DB 418 GTGCTGTATACCCAGCGTGGGTGGATGATGAGCTGCAGAGCGCGGGCGCCAGGTCTAC 477
QY 160 MetArgPheMetGlnGluHisThrCysTrpAspAlaMetAlaThrSerSerLysLeuVal 179
DB 478 ATGCACCTTCATGCGAGGAGCACACCTGTACCATGCGGCGACGAGCTCCAAACTGTCTC 537
QY 180 IlePheAspThrMetLeuGluLleLysLysAlaPheAlaLeuValAlaAsnGlyVal 199
DB 538 ATCTTCGACACCATGCTGGAGATCAAGAGGCTTCTTTGGCCCTGGTGGCCCAAGCGGCTC 597
QY 200 ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 219
DB 598 CGAGCGGCACCTTTGTGGGACAGCAAGAGCAGAGCTTCGTGGGAGTCTGACCATCACA 657
QY 220 AspPheIleLeuValLeuHisArgTrpTrpArgSerProLeuValGlnLetyrGluIle 239
DB 658 GACTTTCATCTGTGCTGCGCGCTATTACAGGTCCCGGCTGGTCCAGATCTACAGATT 717
QY 240 GluGlnHisLysAlleGluThrTrpArgGluLetyrLeuGlnGlyCysPheLysProLeu 259
DB 718 GNAGAACATAGATTGAGACCTGGAGGAGATCTACCTTCAAGGCTGTCTCAGGCTCTG 777
QY 260 ValSerIleSerProAsnAspSerLeuPheGluAlaValThrLeuLleLysAsnArg 279
DB 778 GTCTCATCTCTCCCAATGACAGCCTGTTCGAAGCTGTCTAGCCCTCATCAAGAACCGG 837
QY 280 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleThrHis 299
DB 838 ATCCACCGGCTCCCGCTCGGACCTGTCTCGGGGCTGTGCTCCATCTCTCACAT 897
QY 300 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 319
DB 898 AAGCGGCTTCTCAAGTTCTCTGCACATCTTTGSCACCTGTCTCGCGGCGCTCTCTCTC 957
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QY 320 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 339
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QY 340 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 359
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QY 360 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 379
DB 1078 GTGGTCAACGAAATCGACAGGAGTGGGCTCTACTCTCGCTTGTATGTATCCACCTG 1137
QY 380 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 399
DB 1138 GCTGCCCAACAACATACACACCTGGACATGAATGTGGAGAGGCCCTGAGCAGCGG 1197
QY 400 ThrLeuCysLeuGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIle 419
DB 1198 ACATGTGTCTGGAAGGCGTCTTCTCTGCAGCCCCCAGAGACCTTGGGGGAAGTCAAT 1257
QY 420 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 439
DB 1258 GACCGGATTTCTCGGGGAACAGGTGCACCGCTGGTGTCTCGTGTATGAGACCCAGACCTT 1317
QY 440 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 459
DB 1318 CTGGGCGTGTGTGCTCTCTGACATCTTTCAGGCTCTGGTCTCAGCCCTGCTGGAAATT 1377
QY 460 AspAlaLeuGlyAla 464
DB 1378 GATGCCCTCGGGGCC 1392
RESULT 2
US-09-950-022A-1
; Sequence 1, Application US/09950022A
; Patent No. 6919177
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: No. 6919177e1 PRKAG3 Alleles and Use fo the Same as Genetic Mark
; TITLE OF INVENTION: Reproductive
; TITLE OF INVENTION: and Meat Quality Traits
; FILE REFERENCE: P04688US3
; CURRENT APPLICATION NUMBER: US/09/950,022A
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1873
; TYPE: DNA
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1392)
; OTHER INFORMATION:
US-09-950-022A-1
Alignment Scores:
Pred. No.: 1.12e-191 Length: 1873
Score: 2011.00 Matches: 400
Percent Similarity: 90.11% Conservative: 19
Best Local Similarity: 86.02% Mismatches: 44
Query Match: 83.69% Indels: 2
DB: 3 Gaps: 2
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US-10-070-794A-30 (1-464) x US-09-950-022A-1 (1-1873)

Qy 1 MetSerPheLeuGluGlnGluAAsnSerSerSerTrrProSerProAlaValThrSerSer 20
Db 1 ATGAGCTTCTTAGAGCAGGAGAGAGCGGTTCATGGCCATCCCGAGCTGTAAACACAGC 60

Qy 21 SerGluArgIleArgGlyLysArgArgAlaLysAlaLeuArgTrrThrArgGlnLysSer 40
Db 61 TCAGAAAGAGCCATGCGGACCAAGGGGAAACAGGCTCTAGATGACACAGGAGGAGAT 120

Qy 41 ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60
Db 121 GTAGAGAGAGGGGGCTCTCGGGCCCGAGGAGGCTCCCGAGTCCAGGCCAGGTGTGTGAG 180

Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspPro--- 79
Db 181 TCCACCGGGCAGGAGGCCACATTCCTCCAGGCCACACCTTGGCCCAAGCGCTCCCTTG 240

Qy 80 AlaGlyValGlyThrProProThrGlyTrrAspCysLeuProSerAspCysThrAlaSer 99
Db 241 GCCGAGGTGCAACACCCCAACAGAGCGGACATCTCCCTCTGACTGTGACGCTCA 300

Qy 100 AlaAlaGlySerSerThrAspValGluLeuAlaThrGluPheProAlaThrGluAla 119
Db 301 GCCTCCGACTCCAACACAGACCATCTGGATCTGGGCATAGAGTCTCAGCCTCGCGGGC 360

Qy 120 TrpGluCysGluGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGln 139
Db 361 TCGGGGATGAGCTT---GGGTGTGTGAAGAGAGCAGCCCGTGCCTCCACAGAG 417

Qy 140 AlaProPheProLysLeuGlyTrrAspAspGluLeuArgLysProGlyAlaGlnIleTyr 159
Db 418 GTGCTGTACCCAGCTGGCTGGATGATGATGATGATGATGATGATGATGATGATGATGAT 477

Qy 160 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 179
Db 478 ATGCACCTTCATGACGAGGACACCTCTGATGATGATGATGATGATGATGATGATGATG 537

Qy 180 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 199
Db 538 ATCTTCACACCATGCTGGAGATCAAGAGCCCTCTTTCCTCTGGTGGCCAGCGGCTC 597

Qy 200 ArgAlaAlaProLeuTrrAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 219
Db 598 CGAGCGCACCTTGTGGGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 657

Qy 220 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 239
Db 658 GACTTCATCTTGGTGTGCAACCGCTATTACAGGTCCCTCTGGTCCAGATCTACGAGAT 717

Qy 240 GluGlnHisLysIleGluThrTrrArgGluIleTyrLeuGlnGlyCysPheLysProLeu 259
Db 718 GAAGAACATAGATTGAGACTGGAGGAGATCTACCTTCAGGCTGCTTCAAGCCTCTG 777

Qy 260 ValSerIleSerProAsnAspSerLeuPheGluAlaValTrrThrLeuIleLysAsnArg 279
Db 778 GTCTCCATCTCTCCCAATGACAGCTGTTCGAGCTGTCTAGGCCCTCATCAAGAACCGG 837

Qy 280 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 299
Db 838 ATCCACCGCTGCGGGTCTGGACCCCTGTCTCGGGGCTGTGCTCCACATCTCCACAT 897

Qy 300 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 319
Db 898 AGCGGGTCTTCAAGTCTCTGCACATCTTTGGACACCTTGTGCGCCGCGCTCTCTCTC 957

Qy 320 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGlu 339
Db 958 TACGCAACCATCCAAAGATTTGGGCATCGGCACATTCGAGACTTGGCGGTGGTGGAA 1017

Qy 340 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 359
Db 1017

Db 1018 ACGGCGCCCATCTCTGACCGCAGCTGGACATCTTCGTGGACCGGCTGTGTCTGCGCTGCCT 1077

Qy 360 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 379
Db 1078 GTGGTCAACGAACTGGACAGGTAGTGGGCTCTACTCTCGCTTGTATGTATCCACCTG 1137

Qy 380 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 399
Db 1138 GCTGCCCAACAACATACACACCTGGACATGAATGTGGGAGAGCCCTTGAGCAGCGG 1197

Qy 400 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIle 419
Db 1198 AACTGTGTCTGAAGCGTCTTCTTCGACGCCACGAGACTTGGGGGAAGTCATT 1257

Qy 420 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 439
Db 1258 GACCGGATTTGTCGGGAACAGGTGCACCGCTGTGTCTGTGATGAGACCCAGCACCTT 1317

Qy 440 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 459
Db 1318 CTGGGCTGTGTCTCTCTGATCATCTTTCAGGCTCTGTGTGTCTGAGCCCTGCTGGAATT 1377

Qy 460 AspAlaLeuGlyAla 464
Db 1378 GATGCCCTCGGGGCC 1392

RESULT 3

US-09-950-022A-7

; Sequence 7, Application US/09950022A

; Patent No. 6919177

; GENERAL INFORMATION:

; APPLICANT: Rothschild, Max

; APPLICANT: Ciobanu, Dan

; APPLICANT: Malek, Massoud

; APPLICANT: Plastow, Graham

; TITLE OF INVENTION: No. 6919177el PRKAG3 Alleles and Use fo the Same as Genetic Mark

; TITLE OF INVENTION: Reproductive

; TITLE OF INVENTION: and Meat Quality Traits

; FILE REFERENCE: P04668US3

; CURRENT APPLICATION NUMBER: US/09/950, 022A

; PRIOR FILING DATE: 2001-09-10

; PRIOR APPLICATION NUMBER: 60/231045

; PRIOR FILING DATE: 2000-09-08

; PRIOR APPLICATION NUMBER: 60/260,239

; PRIOR FILING DATE: 2001-01-08

; PRIOR APPLICATION NUMBER: 60/299,111

; PRIOR FILING DATE: 2001-06-18

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 7

; LENGTH: 1873

; TYPE: DNA

; ORGANISM: Sus scrofa

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(1392)

; OTHER INFORMATION:

US-09-950-022A-7

Alignment Scores:

Pred. No.: 1,41e-191 Length: 1873

Score: 2010.00 Matches: 399

Percent Similarity: 90.11% Conservative: 20

Best Local Similarity: 85.81% Mismatches: 44

Query Match: 83.65% Indels: 2

DB: 3 Gaps: 2

US-10-070-794A-30 (1-464) x US-09-950-022A-7 (1-1873)

Qy 1 MetSerPheLeuGluGlnGluAAsnSerSerSerTrrProSerProAlaValThrSerSer 20
Db 1 ATGAGCTTCTTAGAGCAGGAGAGCGGTTCATGGCCATCCCGAGCTGTAAACACAGC 60

Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspPro--- 79
Db 181 TCCACCGGGAGGAGGACACATCCCAAGGCCACACCTTGGCCCAAGCGCTCCCTTG 240
Qy 80 AlaGlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSer 99
Db 241 GCCAGGTGGCAACACCCCAACAGAGCGGACATCCCTCCCTCTGACTGTGACGCTCA 300
Qy 100 AlaAlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAla 119
Db 301 GCCTCCGACTCCAAACAGACATCTGATCTGGGCATAGAGTTCTCAGCCCTCGCGGCG 360
Qy 120 TrpGluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGln 139
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Qy 140 AlaProPheProLysLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnIleTyr 159
Db 418 GTGCTGTATACCGGCTGGGCTGGGATGATGAGCTGCAGAGCGGGGGCCAGGTCTAC 477
Qy 160 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 179
Db 478 ATGCACCTTCATGCAGGAGCACCTCTGATGATGCCATGGCGACAGCTCCAACTGGTC 537
Qy 180 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 199
Db 538 ATCTTCGACACCATGCTGGAGATCAAGAGCGCTTCTTGGCCCTGGTGGCCAGCGGCTC 597
Qy 200 ArgAlaProLeuTrpAspSerLysGlnSerPheValGlyMetLeuThrIleThr 219
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Qy 220 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 239
Db 658 GACTTCATCTTGGTGGCTGACCGCTATTTACAGGTCCCTCCCTGGTCCAGATCTACGAGATT 717
Qy 240 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 259
Db 718 GAAGAACAATAGATTGAGACTGGAGGAGATCTACCTTCAGAGCTGCTTCAGGCTCTG 777
Qy 260 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 279
Db 778 GTCTCCATCTCTCCAAATGACAGCTGTTCGAGCTGTCTACGCGCTTCATCAAGACCGG 837
Qy 280 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 299
Db 838 ATCCACCGCTTCCCGGCTGGACCTGTCTCGGGGCTGTGTCCACATCTCCACACAT 897
Qy 300 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 319
Db 898 AAGCGGCTTCTCAAGTCTCTGCACATCTTTGGCACCTGTCTCGCCGCGCTCTCTTCTC 957
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Db 958 TACCGCACCATCCAAATTTGGGATCGGCACATTCGAGACTTGGCGGTGGTCTGGAA 1017
Qy 340 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 359
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Qy 360 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 379
Db 1078 GTGGTCAACGAACACTGCACAGTAGTGGCTCTACTCTCGCTTTGATGTATCCACTG 1137
Qy 380 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 399
Db 1138 GCTGCCCAACAAACATCAACACCATGCACATGAATGTGGAGAGCGCTTCGAGCGCG 1197
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Db 1198 ACACGTGTGTGGAGGCGCTCTTTCTGCGAGCCCAACAGACCTTGGGGGAGTCAATT 1257

Qy 420 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 439
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Db 1318 CTGGCGGTGTGTCTCTCTGACATCTTTCAGGCTCTGGTGTCTCAGCCCTGCTGGAATT 1377
Qy 460 AspAlaLeuGlyAla 464
Db 1378 GATGCCCTCGGGGCC 1392
RESULT 5
US-09-950-022A-5
; Sequence 5, Application US/09950022A
; Patent No. 6919177
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: No. 6919177el PRKAG3 Alleles and Use fo the Same as Genetic Mark
; TITLE OF INVENTION: Reproductive
; TITLE OF INVENTION: and Meat Quality Traits
; FILE REFERENCES: P04668US3
; CURRENT APPLICATION NUMBER: US/09/950,022A
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1873
; TYPE: DNA
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1392)
; OTHER INFORMATION:
US-09-950-022A-5
Alignment Scores:
Pred. No.: 4.48e-191 Length: 1873
Score: 2005.00 Matches: 399
Percent Similarity: 89.89% Conservative: 19
Best Local Similarity: 85.81% Mismatches: 45
Query Match: 83.44% Indels: 2
DB: 3 Gaps: 2
US-10-070-794A-30 (1-464) x US-09-950-022A-5 (1-1873)
Qy 1 MetSerPheLeuGluGlnGluAsnSerSerSerTrpProSerProAlaValThrSerSer 20
Db 1 ATGAGCTTCTTAGGCAAGAGAGAGAGCGCTTCAATGGCCATCCCGAGCTGTAAACCCAGC 60
Qy 21 SerGluArgIleArgGlyLysArgAlaLysAlaLeuArgTrpThrArgGlnLysSer 40
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Qy 41 ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60
Db 121 GTAGAGGAAGGGGGGCTCCGGGCCCGGAGGAAAGTCCCGAGTCCAGGCCAGTTGCTGAG 180
Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspPro--- 79
Db 181 TCACCGGCGAGGAGGCCACATTCGCCAAGGCCACACCTTGGCCCAAGCCGCTCCCTTG 240
Qy 80 AlaGlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSer 99

Db	241	CGCAGGTGACAAACCCCCCAACAGACGGGAGCATCTCCCTCTGACTGTGAGCGCTCA	300
Qy	100	AlaAlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAla	119
Db	301	GCCTCCGACTCCAACACAGACCATCTGGATCTGGCATAGAGTTCTCAGCCTCGCGGGCG	360
Qy	120	TrpGluCysGlnLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGln	139
Db	361	TCGGGGGATGAGCTT--GGCGTGTGGAAAGAACCCAGCCCGTGCCTATCCCCAGAG	417
Qy	140	AlaProPheProIysLeuGlyTrpAspAspGluLeuArgIysProGlyAlaGlnIleTyr	159
Db	418	GTGCTGTTACCCAGGCTGGGCTGGATGATGAGCTGCAGAAGCGGGGGCCCAAGGTCTAC	477
Qy	160	MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerIysLeuVal	179
Db	478	ATGCACATTTCATGCAGGAGCACACTGCTACGATGCCATGCGGACCACTCCAAACTGGTC	537
Qy	180	IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal	199
Db	538	ATCTTCGACACCATGCTGGAGATCAAGAAGCCCTTCTTTGCCCTGTGTGGCAACGCGCGTC	597
Qy	200	ArgAlaAlaProLeuTrpAspSerIysLysGlnSerPheValGlyMetLeuThrIleThr	219
Db	598	CGACGCGCACCTTTGTGGGACAGCAAGAAGCAGAGCTTCGTGGGGATGCTGACCATCAC	657
Qy	220	AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle	239
Db	658	GACTTCATCTTGTGTGTGCACCGCTATTACAGTTCCTCCCTGTGTCCAGATCTACGAGATT	717
Qy	240	GluGlnHisIysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheIysProLeu	259
Db	718	GAAGACATAGATTGAGACCTGCGAGGAGATCTACCTTCAAGSGCTGTTCAAGCCCTCTG	777
Qy	260	ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg	279
Db	778	GTCTCCATCTCTCCCAATGACAGAGCTGTTCGAAGCTGTCTACGCCCTCATCAAGAACC	837
Qy	280	IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis	299
Db	838	ATCCACCGCCTGCGCGTCTCGACCCCTGTCTCCGGGCTGTGTCTCCACATCTCCACAT	897
Qy	300	LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu	319
Db	898	AAGCGCTTCTCAAGTTCTCTGCACATCTTTGGCACCCCTGTCTGCCCGCGCCTCTCTCTC	957
Qy	320	TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu	339
Db	958	TACCGCACCATCCAAGATTTTGGGATCGGCACATTCGAGACTTGGCGCTGTGTGTGAA	1017
Qy	340	ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro	359
Db	1018	ACGGCGCCCATCTTGACCGCACTGGACATCTTCGTGGACCGCGCTGTCTGTGCTGCCT	1077
Qy	360	ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu	379
Db	1078	GTGGTCAACGAAACCTGGACAGTAGTGGCCCTCTACTCTCGCTTGTGATGATCCACCTG	1137
Qy	380	AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg	399
Db	1138	GCTGCCCAACAAACATACAAACACCTGGACATGAATGTGGGAGAAGCCCTGAGCAGCGG	1197
Qy	400	ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIle	419
Db	1198	ACACTGTGTCTGTGAAGGCGTCTTTCTTCGCAGCGCCACAGAGACTTGGGGGAAGTCA	1257
Qy	420	AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu	439
Db	1258	GACCGGATTGTCGGGGAACAGGTGCACCGCTGTGTCTGTGGATGAGACCCAGCACCTT	1317
Qy	440	LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle	459
Db	1318	CTGGGCGTGGTGTCTCTCTGACATCTCTCAGGCTCTGGTGTCTCAGCCCTGTGGAA	1377

Qy 460 AspAlaLeuGlyAla 464
Db 1378 GATGCCCTCGGGGCC 1392

RESULT 6

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US-09-949-016-2390
; Sequence 2390, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2390
; LENGTH: 1506
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2390

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Db 348 GACATCGTTCCAAACAGTTCAAAGCTTGTCTCTGTATACATACATACAGTTAAAG 407
Qy 190 AlaPheAlaLeuValAlaAsnGlyValArgAlaAlaProLeuTTPAspSerLysLys 209
Db 408 GCCTTCCTTGTGTAGCCAGCGGTGTCCAGACGCGCCACGTCGGAGAGTAAAAA 467
Qy 210 GlnSerPheValGlyMetLeuThrIleThrAspPheIleLeuValLeuHisArgTyr 229
Db 468 CAAAGTTTGTAGCAATGCTAAACATTAACATTTTCAATATACATACATACATAT 527
Qy 230 ArgSerProLeuValGlnIleTyrGluIleGlnHisLysIleGluThrTTPArgGlu 249
Db 528 AAATCACCTATGTTAGACATTTATGAATTAAGAACATAAAATTTGAACATGAGGAG 587
Qy 250 IleTyrLeuGlnGlyCysPheLysProLeuValSerIleSerProAsnAspSerLeuPhe 269
Db 588 CTTTATTACAGAAACATTTAAGCCTTGTAGTATATATCTCCAGATGCAGCTCTTC 647
Qy 270 GluAlaValTyrThrLeuIleLysAsnArgIleHisArgLeuProValLeuAspProVal 289
Db 648 GATGCTGTATCTCTTGTATCAAAATAAATCCACAGATTTGCCGTTATTGACCTATC 707
Qy 290 SerGlyAsnValLeuHisIleLeuThrHisLysArgLeuLeuLysPheLeuHisIlePhe 309
Db 708 AGTGGGAATGCATTTTATATATACCTACCAAAAGATCCCTCAAGTTCTCCAGCTTTT 767
Qy 310 GlySerLeuLeuProArgProSerPheLeuTyrArgThrIleGlnAspLeuGlyLeGly 329
Db 768 ATGCTGTATGTCAGAACCTGCTTATGAGCAGAACCTGGATGAGCTTGGNATAGA 827
Qy 330 ThrPheArgAspLeuAlaValLeuGluThrAlaProIleLeuThrAlaLeuAspIle 349
Db 828 ACGTACCACAAATGCTTCTTATACATCCACACACTCCCATCATCAAGCCTTGAACATA 887
Qy 350 PheValAspArgValSerAlaLeuProValValAsnGluCysGlyGlnValValGly 369
Db 888 TTGTGGAAAGACAAATATCAGCTCTGCTGTTGTGATGAGTCAAGAAAGTTGTAGAT 947
Qy 370 LeuTyrSerArgPheAspValIleHisLeuAlaAlaGlnGlnThrTyrAsnHisLeuAsp 389
Db 948 ATTATTCCTCAATTTGATGATTAATTAATCTGCTCTGAGAAACATCAATAACCTAGAT 1007
Qy 390 MetSerValGlyGluAlaLeuArgGlnArgThrLeuCysLeuGluGlyValLeuSerCys 409
Db 1008 ATCAGGTGACCCAGCCCTTCAGCACCGTTTCACAGTATTTTGAAGGTGTGTGAAGTC 1067
Qy 410 GlnProHisGluSerLeuGlyGluValIleAspArgIleAlaArgGluGlnValHisArg 429
Db 1068 AATAAGCTGGAATATCTGGAGACCATCTGTCGACAGAAATAGTAGAGCTGAGTCCATCG 1127
Qy 430 LeuValLeuValAspGluThrGlnHisLeuLeuGlyValValSerLeuSerAspIleLeu 449
Db 1128 CTGTGTGTGTAATGAGCAGATAGTATTGTGGGTATTATTTCCCTGTCTCGAATTCGT 1187
Qy 450 GlnAlaLeuValLeuSerProAlaGly 458
Db 1188 CAAGCCCTGATCTCTCACACAGCAGGT 1214

RESULT 7

US-08-878-989-14

; Sequence 14, Application US/08878989

; Patent No. 5885803

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Hillman, Jennifer L.

; APPLICANT: Corley, Neil C.

; APPLICANT: Guegler, Karl G.

; APPLICANT: Lal, Preeti

; APPLICANT: Goli, Surva K.

; APPLICANT: Shah, Purvi

; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN

; KINASES

NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,989
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0321 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 1435 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PENITUT01
CLONE: 1452972
US-08-878-989-14

Alignment Scores:

Pred. No.: 3,65e-99 Length: 1435
Score: 1088.00 Matches: 220
Percent Similarity: 71.39% Conservative: 72
Best Local Similarity: 53.79% Mismatches: 68
Query Match: 45.28% Indels: 49
DB: 2 Gaps: 6

US-10-070-794A-30 (1-464) x US-08-878-989-14 (1-1435)

Qy 52 GlyProArgSerArgProThrAlaGluSerThrGlyLeuGluAlaThrPheProLysThr 71
Db 1 GGCCCCAGCGCTGCGCGCGCGG----- 24
Qy 72 ThrProLeuAlaGlnAlaAspProAlaGlyValGlyThrProThrGlyTTPAspCys 91
Db 25 -----AGCCCGCGCGCGG---GACGAG 45
Qy 92 LeuProSerAspCysThrAlaSerAlaAlaGlySerThrAspAspValGluLeuAl 111
Db 46 CGTCGAGCGCTCATGC-----TGATCGCTGCTCTCTCTCCCTCAGCGCGCGCGG 99
Qy 111 aThrGluPheProAlaThrGluAlaThrGluCysGluLeuGluGlyLeuLeuGluAr 131
Db 100 GGCGCGCCCTGGGACCCCGGAGGCC-----GGCATGCTGGAG----- 136
Qy 131 gProAlaLeuCysLeuSerProGlnAlaProPheProLysLeuGlyTTPAspAspGlu-- 150
Db 137 -----AAGCTGGAGTTCGAGGACGAGC 159
Qy 151 -LeuArgLysProGlyAlaGlnIleTyrMetArgPheMetGlnGluHisThrCysTyrAs 170
Db 160 AGTAGAAGACTCAGAAAGTGGTGTGTATCATGCGATTATGAGGTTCACACAGTGTATGA 219


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Qy 114 PheProAlaThrGluAlaTrpGluCysGluLeuGluGlyLeuLeuGluAlaArgProAla 133
Db 14838 TTTTCTCTCTCTTTGATTGGGAG-----TTTTTATGTGAAGGAAGCTA 14882
Qy 134 LeuCysLeuSerProGlnAlaProPheProLysLeuGlyTrpAspAspGluLeuArgLys 153
Db 14883 CTAACATCCACCCTATGCAGAGACCCCA-----GAA 14915
Qy 154 ProGlyAlaGlnIleTyrMetArgPheMetGlnGlnHisThrCysTyrAspAlaMetAla 173
Db 14916 TCCAAACATACGGGTATACCTCTTCATGAAGTCTCATCGCTGCTATGACCTGATTCCTCC 14975
Qy 174 ThrSerSerLysLeuValIlePheAspThr----- 183
Db 14976 ACAAGCTCCAAATTTGGTTGATTATTTGATACAGTCCTCGCAGGGTGGGTGAATCTCTCTTTCC 15035
Qy 183 ----- 183
Db 15036 CTTCCCTTTGGAGCCTGTGGTTTAATACCTCTCATCTCATCTCATCTTAAGGGTAATA 15095
Qy 183 ----- 183
Db 15096 TCCTTATCTTCTGTGAAGTTAGTCTCATGTTTACCCAAACATGCCCAACACTGTTCCT 15155
Qy 184 -----Met-LeuGluI 187
Db 15156 TTTTATACAGTCCTGCCCTGTGGATTGGCTTTTATGATTATTACTGTCTTGGCTACAGGT 15215
Qy 187 eLysIysAlaPhePheAlaLeuAlaAsnGlyValArgAlaAlaProLeuTrpAspSe 207
Db 15216 GAAGAAAGCTTTTGTGCTTTGGTGACTAAACGGGTAGCAGCTGCCCTTTATGGGATAG 15275
Qy 207 rLysLysGlnSerPheVal----- 213
Db 15276 TAAGAGCAAGATTTTGTGGGTAAAGCAAAAGTTTCTGGAAACACAATATTATTGGCATCTT 15335
Qy 214 -----GlyM 215
Db 15336 GTGTGGGCGAGGAGACAAAGCTTCAGGCAGTGTCTGAGGGCTCTGTCTCTCTCTAGGCA 15395
Qy 215 etLeuThrIleThrAspPheIleLeuValLeuHisArgTyrTrpArgSerProLeu--- 233
Db 15396 TGCTGACCATCACTGATTTCATATATCTGACCGCTACTATATAATCAGC-CITGGTA 15454
Qy 233 ----- 233
Db 15455 AGGAACCTTAACCAATGACCAAAATCACTTCCCTGCCCTAAATCCCTCATTTCTCAATT 15514
Qy 233 ----- 233
Db 15515 CTTTTCTCCAAGCAAGCAGAGGGCTTAAGGAAGCAGAGATCAGGTCTCAAAATCT 15574
Qy 234 -----ValGlnIleTyrGluIleGluGlnHisLysIleGluThrTrpA 248
Db 15575 GTTGCTTCTGCTTCAGGTACAGATCTATAGCTAGAAGAACACAAAGATAGAAACTTGG 15634
Qy 248 rg----- 248
Db 15635 G-AGGTATGTAGAGAAATTTGGGTATATAAAGGATAAAGGATGGCGGGTTCTGGGAAAC 15693
Qy 249 -----GluIleTyrLeuGlnG 254
Db 15694 ACTTTTCCATGTGGTATTTTGTGACCCTATCCCTTTTCCCTTCAGAGGTGTATCTCCAGG 15753
Qy 254 lYcysPheLysProLeuValSerIleSerProAsn----- 265
Db 15754 ACTCCTTTAAACCGCTTGTGCAATTTCTCTTAATCCCGAGGTGAGTTCAGTTACCCATC 15813
Qy 265 ----- 265
Db 15814 TGTCCAAAAGCGGAAGAGATTTTGTTCATCAGCTAGCTAATGTCCTAGACACCCAGGGA 15873
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Qy 265 ----- 265
Db 15874 AAGGGGAAGAGAGAGAAAAGACACACACACACACACACACACACACACACACAC 15933
Qy 265 ----- 265
Db 15934 CACACACAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTTT 15993
Qy 265 ----- 265
Db 15994 AAGTCTGGCCTGTACACTGCCCCCTTCCCTAAACCATCATGTTTCCCTGTGTGACAATAC 16053
Qy 265 ----- 265
Db 16054 ACTGTATGACCTGTTTAAATCACCCCGCCGAGCACTGTGGAACTTATTATCTCCAC 16113
Qy 266 -----AspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIleHisArgLeuP 284
Db 16114 CCTCTCACAGCTTGTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 16173
Qy 284 roValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLysArgLeuLeuL 304
Db 16174 CAGTTATTGACCCAGAAATCAGGCAATCTTTGTATCATCTCTCACCCACCAAGCGCATTCGA 16233
Qy 304 ysPheLeuHisIlePhe----- 309
Db 16234 AGTTCCTCAAATTTGTGTAAAGTGTCTCTCAGCCAGTTCTTTTCTCTTTTTCATTG 16293
Qy 309 ----- 309
Db 16294 ATTGATTGATTGATTGATTGAAAAGAGAGAGAGGTCTCACTGTGTGCTCAGGCTAGTG 16353
Qy 309 ----- 309
Db 16354 TCAAACTCTGAGCTCAAGTGAATCCTCCGCTCAGCTCCCAAGTCTTAGGATTACAG 16413
Qy 309 ----- 309
Db 16414 GTGTGAGCACTGCATCCAGCCCACTCTTATTATTATTATTATTATTATTATTATTATTATT 16473
Qy 309 ----- 309
Db 16474 TTCTTACTCTGTGCCCAGGCTGCGTGCAGAGGGCTATCATGGCTCACTGCAGCCTCC 16533
Qy 309 ----- 309
Db 16534 AACCTCTTGTCTCAGGTGACCCCGACCTCAACCCCGAAGAGCTGGGACTACACGTG 16593
Qy 309 ----- 309
Db 16594 TGTACCAACACCTGGCTAATTTTGTGTATTTTATAGATAGAGTTTGGCATGT 16653
Qy 309 ----- 309
Db 16654 TGCCGAGCTGTCTCGAACTCTTGGGCTCAAGCAATATGTCCCTCAGCCTCCCAAAG 16713
Qy 309 ----- 309
Db 16714 TGCTGGGATTATAGGCATAAAGCCGCGCACCCAGCCCTTATTTCTAATATCTGGGTGG 16773
Qy 310 -----GlySerLeuLeu- 313
Db 16774 AGGGGTATCCAGGGTGGCTTTGGGTGCTTTGAAAGTTAAGCTGATGTTCTTTCTCTCA 16833
Qy 314 -----ProArgProSerPheLeuTyrArgThrIleGlnAspLeuGlyIleG 329
Db 16834 GATCACTCAGTTCCCAAG-CCAGAGTTTCATGTCCAGTCTCTGGAAGAGCTACAGATTG 16892
Qy 329 lYThrPheArgAspLeuAlaValLeuGluThrAlaProIleLeuThrAlaLeuAspI 349
Db 16893 GCACCTTAAACCAATATGCTATGGTTCGACCTACCCCTCTATGTGGTCTCTGGGA 16952
Qy 349 lePheValAspArgValSerAlaLeuProValValAsnGluCys----- 364
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|||||
16953 TTTTGTACAGTCAGTCAGCCCTGCAGCTGGTGGATGAGAA-GGGTGAGAGATTG 17011
364 ----- 364
17012 GGCAGAGGAGGGGAGAGATCCAGGCAAGTCAGGGTGGCTCTGGGAAGATCTGCTT 17071
364 ----- 364
17072 TCCCTCAGCTTAGCCAGGAGGTGATCTTATGATAGGGGAGCTTTAGATCCAGATC 17131
365 -----
17132 CTCCTACTAGCTGCTCTGCTCCCTAGGGCGTGGTGACATCTACTCCAAGTTG 17191
375 spValile-----GlyGlnValValGlyLeuTySerArgPheA 375
17192 ATGTTATCGTGAATGTTGAGGGTCTGGAGGTAGGAGTGGTGGGGGGGGGCAC 17251
377 ----- 377
17252 TGTAAATATGGAGGGGAGAGGAGTCTCTCTGTGATCTAAGGGTCTTAGAAGCTTC 17311
377 ----- 377
17312 CAGGCTTCAATCCTATTGAAAGGAATTGAATGAGTTGGGTGGCTGTGCTGAC 17371
377 ----- 377
17372 AATTGCCCTGATCCCTCTGTTGAGTTGGATGGTTCAGGGTTTGGAGGCTGCTCT 17431
378 -----HisLeuAlaAlaGlnInPheTyzA 386
17432 TGCTTCCCTGCAAGCTCTCTCTGCTCTCCCAAGATCTGGCAGCAGAAAGACCTACA 17491
386 snHisLeuApMetSerValGlyGluAlaLeuArgGlnArgThrLeuCysLeuGluGlyV 406
17492 ACAACCTAGATGATCTGTGACTAAAGCTTGCACATCGATCATCTTACTTTGAGGGTG 17551
406 alLeuSerCysGlnProHisGluSerLeuGlyGluValIleAspArgIleAla----- 423
17552 TTCTCAAGTGTACTCTGATGAGACTCTGGAGACCATCATCAACAGGCTAGT-GGAAGCA 17610
424 -----ArgGlu----- 425
17611 GAGTAGGGAGGCCAGCAACCCATAAGAGCTGAGGGGAGCAGCCTTGAGAGTGGGGTTT 17670
425 ----- 425
17671 GGCAAGGAGAGTAGGGGAGAGGGGCTTCCCTGAGGCCAGCACTAAACATTCCTTTCT 17730
426 -----GlnValHisArgLeuValLeuValValLeuValAspGluThrGlnHisLeuL 440
17731 CCCTTGTGCTGTGCGCAGTTCCAGCTTCCAGCTTGTAGTGGTGGATGATGATGTGTCA 17790
440 euGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSer 455
17791 AGGGAATTGTATCACTGTCTGACATCTCTGACGGCCCTGGTGTCTCACA 17837

RESULT 13

US-09-513-999C-1659
; Sequence 1659, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59, US2.REG
; CURRENT APPLICATION NUMBER: US/09/513.999C
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487

; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 1659

; LENGTH: 350
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 48..350
US-09-513-999C-1659

Alignment Scores:

Pred. No.: 3,06e-22 Length: 350
Score: 312.00 Matches: 57
Percent Similarity: 87.84% Conservative: 8
Best Local Similarity: 77.03% Mismatches: 9
Query Match: 12.98% Indels: 0
DB: 3 Gaps: 0

US-10-070-794A-30 (1-464) x US-09-513-999C-1659 (1-350)

Qy 158 IletyRmetArgPheMetGlnGluHisThrCysTyRaspAlaMetAlaThrSerSerLys 177
Db 129 GTGTATATCTTCCTTCATGAAGTCTCATCGCTGCTATGACCTATCCACAAAGCTCCAAA 188
Qy 178 LeuValIlePheAspThrMetLeuGluIleLysAlaPhePheAlaLeuValAlaAsn 197
Db 189 TTGGTGTATTTGATAGCTCCCTGCAGGTAGGAAGCTTTTGTGTTGGTACTTAAC 248
Qy 198 GlyValArgAlaAlaProLeuThrAspSerLysGlnSerPheValGlyMetLeuThr 217
Db 249 GGTGTACAGCTGCCCTTTATGGATAGTAAGAAGCAAGTTTGTGGCATCTGACC 308
Qy 218 IletRaspPheIleLeuValLeuHisArgTyTyRargSer 231
Db 309 ATCACTGATTCATCAATATCTTCGCCCTGCTACTATAATCA 350

RESULT 14

US-09-248-796A-4769
; Sequence 4769, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 4769
; LENGTH: 762
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-4769

Alignment Scores:
Pred. No.: 2,96e-16 Length: 762
Score: 258.00 Matches: 69
Percent Similarity: 50.00% Conservative: 55
Best Local Similarity: 27.82% Mismatches: 82
Query Match: 10.74% Indels: 42
DB: 3 Gaps: 8

US-10-070-794A-30 (1-464) x US-09-248-796A-4769 (1-762)

Qy 134 LeuCysLeuSerProGlnAlaProPheProLysLeuGlyTyRaspPheGluLeuArgLys 153
Db 52 TTGAGTTGTGCGCTGAA-----CAAATTGAACATGAC-----CAAAA 90

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QY 154 ProGlyAlaGlnIleTyrMetArgPheMetGlnGluHisThrCysTyrAspAlaMetAla 173
Db 91 ATTGGGATCAAGGCTATTCGATTATTTTCAAAAGCAAAACATCTTACGATGCTTACCT 150
QY 174 ThrSerSerLysLeuValIlePheAspThrMetLeuGluLeuLysAlaPhePheAla 193
Db 151 GTGAGTTATAGATAATTTGTTGGTACTTCAATTTGTTAGTGAATAAGTCAATAATATT 210
QY 194 LeuValAlaGlnGlyValArgAlaProLeuTyrAspSerLysLysGlnSerPheVal 213
Db 211 TTATTACAATAATATATGTTGACACCGTTATGGATTAACCAAAACATCCAGATTCGCT 270
QY 214 GlyMetLeuThrIleThrAspPheIleLeuValLeuHisArgTyrTyrArgSerPro--- 232
Db 271 GGATTGTTAATCATCGGATTTTATCAATGTGATCAACAATACTATTTACAATCCAGAA 330
QY 233 -----LeuValGlnIleTyrGluIleGluGln----- 241
Db 331 AAGTTTGAACATAGTTGATCACTAACAATGGGTGGTAAAGAGAAATTTGAAAAGCCATA 390
QY 242 -----HisLysIleGluThrTyrArgGluIleTyrLeuGlnGlyCysPheLysProLeu 259
Db 391 GGTGTAGATCAATCGAAACA----- 411
QY 260 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuLysLysArg 279
Db 412 GCATCAATACACCCATCTCAAGTCATATATCAAGCATGTGTCAAGATGTTGGAATCAAAA 471
QY 280 IleHisArgLeuProValLeuAspProValSerGlyAsn-----ValLeuHis 295
Db 472 GCTAGAGAAATCCCATTAATTAATGATGAAGATGAAAAAACTAAACCGTGAATTTGCTGTAGT 531
QY 296 IleLeuThrHisLysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArg 315
Db 532 GTGTAACTCAATACAGAAATTTGAATTTGTGGCTTG-----AATTGTAAGAA 582
QY 316 ProSerPheLeuTyrArgThrIleGlnAspLeu---GlyIleGlyThrPheArgAspLeu 334
Db 583 ACAGAAATGTTATTGAAACCCCTCAAGAAATTTGAGTGGTGGTGGTGAATTTG 642
QY 335 AlaValValLeuGluThrAlaProIleLeuThrAlaLeuAspIlePheValAspArg 354
Db 643 TCTACATGCTACTATGGACACACCTGTCTATGAAGTCATTCATTTATTAACTGAGAAATCT 702
QY 355 ValSerAlaLeuProValValAsn 362
Db 703 GTCTCTTCAATACCAATAGTCGAC 726
RESULT 15
US-09-016-434-194
; Sequence 194, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESS: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
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; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 194:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PENITUT01
; CLONE: 1452972
; US-09-016-434-194
Alignment Scores:
Pred. No.: 3,37e-15 Length: 269
Score: 240.00 Matches: 47
Percent Similarity: 77.27% Conservative: 21
Best Local Similarity: 53.41% Mismatches: 20
Query Match: 9.99% Indels: 0
DB: 3 Gaps: 0
US-10-070-794A-30 (1-464) x US-09-016-434-194 (1-269)
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Db 1 GCCTTCATACATCCAGACACTCCCATCATCAAGCCCTTGAACATATTTGTGGAAGACGA 60
QY 355 ValSerAlaLeuProValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPhe 374
Db 61 ATATCAGCTCTGCTGCTGTTGGATGAGTCAGGAAAAGTTGTAGATATTTATTCCAAATTT 120
QY 375 AspValIleHisLeuAlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGlu 394
Db 121 GATGTAATTAATCTGCTGCTGAGAAAACATACATAACCTAGATATACCGTGCACCCAG 180
QY 395 AlaLeuArgGlnArgThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSer 414
Db 181 GCCCTTCAGCACCGTTCACAGTATTTTGAAGGTGTTGTGAAGTGCATAAAGCTGGAATA 240
QY 415 LeuGlyGluValIleAspArgIle 422
Db 241 CTGGAGACCATCGTGGAGAGAATA 264
Search completed: January 26, 2006, 03:33:18
Job time : 274.939 secs
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 26, 2006, 01:18:45 ; Search time 997.992 Seconds
(without alignments)
3844.711 Million cell updates/sec

Title: US-10-070-794A-30

Perfect score: 2403
Sequence: 1 MSFLEQNSSSPSPAVTSS.....LSDIQLVLSPADIGALGA 464

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPTO_spool_p/US1007094/runat_24012006.164417.8900/app_query.fasta.1.1102
-DB=Published Applications NA_Main -QMTS=fastcap -SUFFIX=p2n.rnpbm
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct
-THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext
-HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US1007094 @CGN 1.1 2064 @runat_24012006.164417.8900 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DEBOP=6 -DELEXT=7

Database : Published Applications NA_Main:

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- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2403	100.0	1470	9	US-10-503-175-1
2	2398	99.8	1647	3	US-09-826-581-5
3	2398	99.8	1647	7	US-10-705-137-5
4	2398	99.8	2781	7	US-10-473-670-30
5	2372	98.7	2290	9	US-10-756-149-1235
6	2013	83.8	1873	3	US-09-950-022-3
7	2013	83.8	1873	10	US-11-075-134-3

8	2011	83.7	1873	3	US-09-950-022-1	Sequence 1, Appli
9	2011	83.7	1873	10	US-11-075-134-1	Sequence 1, Appli
10	2010	83.6	1873	3	US-09-950-022-7	Sequence 7, Appli
11	2010	83.6	1873	10	US-11-075-134-7	Sequence 7, Appli
12	2007	83.5	1873	3	US-09-950-022-9	Sequence 9, Appli
13	2007	83.5	1873	10	US-11-075-134-9	Sequence 9, Appli
14	2005	83.4	1873	3	US-09-950-022-5	Sequence 5, Appli
15	2005	83.4	1873	10	US-11-075-134-5	Sequence 5, Appli
16	2000	83.2	1518	9	US-10-503-175-3	Sequence 3, Appli
17	1276	83.1	9100	9	US-10-503-175-5	Sequence 5, Appli
18	1276	53.1	26000	9	US-10-503-039-1	Sequence 1, Appli
19	1094	45.5	2223	9	US-10-466-162-13	Sequence 13, Appli
20	1088	45.3	1435	3	US-09-769-970-14	Sequence 14, Appli
21	1082.5	45.0	1167	9	US-10-466-162-11	Sequence 11, Appli
22	1022.5	42.6	1578	6	US-10-305-720-1113	Sequence 1113, Ap
23	1022.5	42.6	1578	9	US-10-505-680-407	Sequence 407, App
24	1022.5	42.6	1578	9	US-10-466-162-15	Sequence 15, Appli
25	1017	42.3	1691	3	US-09-825-297-2	Sequence 2, Appli
26	904.5	37.6	989	3	US-09-826-581-2	Sequence 2, Appli
27	904.5	37.6	989	7	US-10-705-137-2	Sequence 2, Appli
28	886	36.9	1467	9	US-10-450-763-20069	Sequence 20069, A
29	884	36.8	3261	10	US-11-097-143-25526	Sequence 25526, A
30	766.5	31.9	11527	5	US-10-108-605-70	Sequence 70, Appli
31	766.5	31.9	39651	10	US-11-097-143-25525	Sequence 25525, A
32	758	31.5	547	7	US-10-276-774-261	Sequence 261, App
33	705.5	29.4	2303	9	US-10-450-763-20071	Sequence 20071, A
34	640.5	26.7	1722	3	US-09-826-581-3	Sequence 3, Appli
35	640.5	26.7	1722	7	US-10-705-137-3	Sequence 3, Appli
36	501	20.8	602	5	US-10-106-698-2295	Sequence 2295, Ap
37	408	17.0	765	6	US-10-264-237-248	Sequence 248, App
38	374.5	15.6	2314	8	US-10-739-930-1178	Sequence 1178, Ap
39	373.5	15.5	2339	8	US-10-425-115-2938	Sequence 2938, Ap
40	369.5	15.4	1533	7	US-10-425-114-8857	Sequence 8857, Ap
41	358.5	14.9	3077	7	US-10-424-599-44858	Sequence 44858, A
42	357	14.9	1402	7	US-10-437-963-66100	Sequence 66100, A
43	353	14.7	1507	7	US-10-425-114-29527	Sequence 29527, A
44	352	14.6	1014	3	US-09-826-581-4	Sequence 4, Appli
45	352	14.6	1014	7	US-10-705-137-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-10-503-175-1
; Sequence 1, Application US/10503175
; Publication No. US20050172348A1
; GENERAL INFORMATION:
; APPLICANT: Andersson, Leif
; TITLE OF INVENTION: Transgenic animals expressing prkag3
; FILE REFERENCE: 11145-020U51
; CURRENT APPLICATION NUMBER: US/10/503,175
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: PCT/IB03/00912
; PRIOR FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 60/353,430
; PRIOR FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1470
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1470)
; OTHER INFORMATION:
US-10-503-175-1

Alignment Scores: 2.73e-256 Length: 1470
Pred. No.: 2403.00 Matches: 464
Score: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-070-794A-30 (1-464) x US-10-503-175-1 (1-1470)

Qy 1 MetSerPheLeuGluGlnGluAAsnSerSerSerTrpProSerProAlaValThrSerSer 20
Db 76 ATGAGCTTCTTAGAGCAGAGAAACAGCAGCTCATGGCCATCACCAGCTGTGACAGCAGC 135

Qy 21 SerGluArgIleArgGlyLysArgAlaLysAlaLeuArgTrpThrArgGlnLysSer 40
Db 136 TCAGAAAGATCCCTGGGAAACGGAGGCCAAACCTTGAGATGGACAGGCAAGCTCG 195

Qy 41 ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60
Db 196 GTGGAGGAAGGGAGGCCACCAAGTCCAGGGGAGAGTCCCGGTCCAGGCCCAACTGCTGAG 255

Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla 80
Db 256 TCCACCGGGCTGGAGGCCACATCCCCAAGACCACACCCCTTGGCTCAAGCTGATCCCTGCC 315

Qy 81 GlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSerAla 100
Db 316 GGGTGGGCATCCACCAACAGGTGGGACTGCCTCCCTCTGACTGTACAGCCTCAGCT 375

Qy 101 AlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTrp 120
Db 376 GCAGGCTCCAGCAGATGATGTGGAGCTGGCCACGGAGTTCGCCAGGCCACAGAGGCTGG 435

Qy 121 GluCysGluLeuGluGlyLeuGluGluArgProAlaLeuCysLeuSerProGlnAla 140
Db 436 GAGTGTAGCTAGAGGGCTCTCTGGAAGAGGGCTGCCCCGTGCTGCCCTCCAGGCC 495

Qy 141 ProPheProLysLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnIleTyrMet 160
Db 496 CCAITTCACAGCTGGCTGGATGACGAACCTGGGAAACCCGGGCCAGATCTACATG 555

Qy 161 ArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValIle 180
Db 556 CGCTTCATGAGGAGCACACCTGTACGATGCCATGGCAACTAGTCTCCAACTAGTCATC 615

Qy 181 PheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyValArg 200
Db 616 TTCACACCATGCTGGAGATCAAGAGGCCCTCTTTGCTCTGGTGGCCACCGTGTGGCG 675

Qy 201 AlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAsp 220
Db 676 GCAGCCCTCTATGGGACAGCAAGACAGAGCTTTGTGGGATGCTGACCATCACTGAC 735

Qy 221 PheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGlu 240
Db 736 TTCATCTCTGCTGTCATCGCTACTACAGGTCCCGCCCTGGTCCAGATCTATGAGATTGAA 795

Qy 241 GlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeuVal 260
Db 796 CAACATAAGATTGACCTGGAGGGAGATCTACCTGCAAGGCTGCTTCAAGCCTCTGTC 855

Qy 261 SerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIle 280
Db 856 TCCATCTCTCTAATGATAGCTGTTTGAAGCTGTCTACACCTCATCAAGAACCGGATC 915

Qy 281 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 300
Db 916 CATCGCCTGCCTGTTCTTGACCCGGTGTGAGCAACAGTACTCCACATCTCTCACACAAA 975

Qy 301 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 320
Db 976 GCCTGCTCAAGTTCTGACACATCTTTGGTTCCTTGGCTGCCCGGCCCTCTCTCTAC 1035

Qy 321 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGluThr 340
Db 1036 CGCACTATCCAAAGTTTGGGCATCGGCACATTCCGAGACTTGGCTGTGGTGTGGAGACA 1095

Qy 341 AlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProVal 360
Db 1096 GCACCCATCTGACTGCATCGACATCTTTGTGGACCGGGTGTCTGTGCACTGCCTGTG 1155

Qy 361 ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeuAla 380
Db 1156 GTCAACGAATGTGGTCAGGTCGTGGGCTCTATTCCCGCTTTGATGTGATTCACTGGCT 1215

Qy 381 AlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr 400
Db 1216 GCCCAGCAAACTACACCACTGGCATGAGTGTGGGAGAAGCCCTTGAGGCGAGAGACA 1275

Qy 401 LeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAsp 420
Db 1276 CTATGCTGGAGGAGTCTTTCTGCCAGCCCCACAGAGCTTTGGGGGAAGTGTATCGAC 1335

Qy 421 ArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeu 440
Db 1336 AGGATTGCTCGGAGCAGGTACACAGGCTGGTCTAGTGGACGAGACCAGCATCTCTTG 1395

Qy 441 GlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAsp 460
Db 1396 GGGCTGGTCTCCCTCTCCGACATCTTCAGGCATGGTGTCTCAGCCCTGTGGCATCGAT 1455

Qy 461 AlaLeuGlyAla 464
Db 1456 GCCCTCGGGGCC 1467

RESULT 2
US-09-826-581-5
; Sequence 5, Application US/09826581
; Patent No. US20020142310A1
; GENERAL INFORMATION:
; APPLICANT: Andersson, Leif
; APPLICANT: Luthman, L. Holger
; APPLICANT: Marklund, Stefan
; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNIT
; FILE REFERENCE: 11145-007001
; CURRENT APPLICATION NUMBER: US/09/826,581
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 60/195,665
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1647
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (20)...(1486)
US-09-826-581-5

Alignment Scores:
Pred. No.: 1,17e-255 Length: 1647
Score: 2398.00 Matches: 463
Percent Similarity: 99.78% Conservative: 0
Best Local Similarity: 99.78% Mismatches: 1
Query Match: 99.79% Indels: 0
DB: Gaps: 0

US-10-070-794A-30 (1-464) x US-09-826-581-5 (1-1647)

Qy 1 MetSerPheLeuGluGlnGluAAsnSerSerSerTrpProSerProAlaValThrSerSer 20
Db 95 ATGAGCTTCTTAGAGCAGAGAAACAGCAGCTCATGGCCATCACCAGCTGTGACAGCAGC 154

Qy 21 SerGluArgIleArgGlyLysArgAlaLysAlaLeuArgTrpThrArgGlnLysSer 40
Db 155 TCAGAAAGATCCCTGGGAAACGGAGGCCAAAGCTTGAATGAGCAAGCGAGAGTCTG 214

Qy 41 ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60

395	CGAGGCTCCAGCACAGATGATGTGGAGCTGGCCACGAGATTCCAGAGCCACAGAGGCGCTGG	454
121	GluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGlnAla	140
455	GAGTGTGAGCTAGAAGCCCTGCTGGAAGAGAGCCCTGCCCTGTGCTGTGTCCCGCAGGCC	514
141	ProPheProIysLeuGlyTyrAspAspGluLeuArgLysProGlyAlaGlnIleTyrMet	160
515	CCATTTCCCAAGCTGGGCTGGATGACCAACTCGGAAACCGCGCGCCAGATCTACATG	574
161	ArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValIle	180
575	CGCTTCAATGCAGGAGCACACTGCTACGATGCCATGGCAACTAGCTCCAAAGCTAGTCATC	634
181	PheAspThrMetLeuGluIleLysAlaPhePheAlaLeuValAlaAsnGlyValArg	200
635	TTCCACACCATGCTGGAGATCAAGAGCCCTTCTTTGCTGTGGTGGCCAAAGGTGTGGCG	694
201	AlaAlaProLeuTyrAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAsp	220
695	GCAGCCCTCTATGGGACAGCAAGCAGAGCTTTGTGGCGATGTGCACCATCATCTGAC	754
221	PheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGlu	240
755	TTTCATCTCGTGTGCATCGCTACTACAGGTGCCCCCTGGTCCAGATCTATGAGATTGAA	814
241	GlnHisLysIleGluThrTyrArgGluIleTyrLeuGlnGlyCysPheLysProLeuVal	260
815	CAACATAGATTGAGACTGGAGGAGATCTACTCTGCAAGGCTGCTTCAAGCCTCTGGTC	874
261	SerIleSerProAsnAspSerPheGluAlaValTyrThrLeuLysAsnArgIle	280
875	TCCATCTCTCTAATGATAGCTGTGTTGAAGCTGTCTACACCTCATCAAGAACCCGATC	934
281	HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys	300
935	CATCGCCTCGCCTGTTCTTTGACCCGGTGTGAGGCAACGTACTCCACATCTCCACACAAA	994
301	ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr	320
995	CGCCTGTCTCAAGTCTCTGCACATCTTTGTTTCCCTGTCTGCCCGGCCCTCTCTCTCTAC	1054
321	ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGluThr	340
1055	CGCACTATCCAAGATTTGGGCATCGGCACATTCGAGACTTGGCTGTGGTGTCTGGAGACA	1114
341	AlaProfileLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProVal	360
1115	GCACCATCTGACTGCACTGGACATCTTTGTGACCGGGGTGTGTCTGCACATCGCCTGTG	1174
361	ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeuAla	380
1175	GTCAACGAATGTGGTTCAGGTCTGGGCCCTCTATTCCCGCTTTGATGTGATTCACCTGGCT	1234
381	AlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr	400
1235	GCCACAGCAACCTACACCACTGGACATGATGTGGGAGAAGCCCTGAGCGAGAGACA	1294
401	LeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAsp	420
1295	CTATGCTGGAGGAGTCTCTTCTCTGCCAGCCCCACGAGAGCTTTGGGGGAAGTATCGAC	1354
421	ArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeu	440
1355	AGGATTTGCTCGGGAGCAGGTACACAGCTGGTGTGTAGTGGACAGAGACCCAGCATCTCTTG	1414
441	GlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAsp	460
1415	GGCGTGGTCTCCCTCTCCGACATCTCTCAGGACATGGTGTCTCAGCCCTGCTGGCATCGAT	1474
461	AlaLeuGlyAla	464
1475	GCCTTCGGGGCC	1486

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RESULT 4
US-10-473-670-30
; Sequence 30, Application US/10473670
; Publication No. US20040110180A1
; GENERAL INFORMATION:
; APPLICANT: RECIPON, Shirley A.; BURRILL, John D.;
; APPLICANT: MARCUS, Gregory A.; ZINGLER, Kurt A.;
; APPLICANT: TANG, Y. Tom; THORNTON, Michael;
; APPLICANT: BOROWSKY, Mark L.; BAUGHN, Mariah R.;
; APPLICANT: BURFORD, Neil; LEE, Soo Yeun;
; APPLICANT: BANDMAN, Olga; HAFALIA, April J.A.;
; APPLICANT: YAO, Monique G.; RANKUMAR, Javalaxmi;
; APPLICANT: CHAWLA, Narinder K.; LU, Dyung Aina M.;
; APPLICANT: ARVIZU, Chandra S.; ISON, Craig H.;
; APPLICANT: DING, Li; LU, Yan;
; APPLICANT: GURURAJAN, Rajagopal.; WALSH, Roderick T.;
; APPLICANT: GANDHI, Ameenah R.; SWARNAKAR, Anita;
; APPLICANT: FORTSYNTH, Ian J.; YUE, Henry;
; APPLICANT: AU-YOUNG, Janice K.; ELLIOTT, Vicki S.;
; APPLICANT: LEE, Sally
; TITLE OF INVENTION: KINASES AND PHOSPHATASES
; FILE REFERENCE: PI-0398 USN
; CURRENT APPLICATION NUMBER: US/10/473,670
; CURRENT FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: PCT/US02/10818
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 60/282,119
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/283,588
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/283,759
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/285,589
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: US 60/287,037
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/287,036
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/288,608
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/288,712
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/289,909
; PRIOR FILING DATE: 2001-05-09
; Remaining Prior Application data removed - See File Wrapper
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PERL Program
; SEQ ID NO 30
; LENGTH: 2781
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7474666CB1
US-10-473-670-30

Alignment Scores:
Pred. No.: 2781
Score: 2.65e-255 Length: 2781
Percent Similarity: 2398.00 Matches: 463
Best Local Similarity: 99.78% Conservative: 0
Query Match: 99.78% Mismatches: 1
DB: 7 Indels: 0
Gaps: 0

US-10-070-794A-30 (1-464) x US-10-473-670-30 (1-2781)

QY 1 MetSerPheLeuGluGlnGluAsnSerSerTrpProSerPr
Db 96 ATGAGCTTCCTAGAGCAAGAAAAACAGCAGCTCATGGCCATCAC
QY 21 SerGluArgIleArgGlyLysArgAlaLysAlaLeuArgTr

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156 TCAGAAAGATCCCTGGGAAACCGAGGGCCAAAGCCCTTGAGATGAGACAGGACGAGTGC 215
41 ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60
216 GTGGAGGAGGAGGAGCCACAGAGTTCAGGGGAAAGTCCCGGTCCAGGCCAGCTGTGAG 275
61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla 80
276 TCCACCGGGCTGGAGGACACATTCCTCCCAAGACACACCTTTGGCTCAAGCTGTATCTCTGC 335
81 GlyValGlyThrProProThrGlyTyrAspCysLeuProSerAspCysThrAlaSerAla 100
336 GGGGTGGGCATCCACCAACAGGGTGGAGTGGCTCCCTCTGACTGTACAGCCCTCAGCT 395
101 AlaGlySerSerThrAspValGluLeuAlaThrGluPheProAlaThrGluAlaTyr 120
396 GCAGGCTCCAGCACAGATGATGTGGAGTGGCCACGGAGTTCCAGCCACAGAGGCTGG 455
121 GluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGlnAla 140
456 GAGTGTGAGCTAGAGGCTGCTGGAAGAGAGGCTGCTGCTGTGCTGCTGCTGCTGCTGCTG 515
141 ProPheProLysLeuGlyTyrAspAspGluLeuArgLysProGlyAlaGlnIleTyrMet 160
516 CCATTTCCCAAGCTGGGCTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 575
161 ArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValIle 180
576 CGCTTCATGCAGGAGCACACCTGTACGATGCCATGGCACTAGCTTCAAGCTAGTATC 635
181 PheAspThrMetLeuGluIleLysAlaPhePheAlaLeuValAlaAsnGlyValArg 200
636 TTCGACACCATGCTGGAGATCAAGAGGCTTCTTGTCTGTGGTGGCCAAACGGTGTGGG 695
201 AlaAlaProLeuTyrAspSerLysGlnSerPheValGlyMetLeuThrIleThrAsp 220
696 GCAGCCCTCTATGGGACAGCAAGAGCAGAGCTTTGTGGGAGTGCAGCATCAGTGC 755
221 PheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGlu 240
756 TTCACTCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 815
241 GlnHisLysIleGluThrTyrArgGluIleTyrLeuGlnGlyCysPheLysProLeuVal 260
816 CAACATAAGATGAGACCTGGAGGAGATCTACCTGCAAGGCTGCTTCAAGGCTCTGGTC 875
261 SerIleSerProLeuAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIle 280
876 TCCATCTCTCTAATGATAGCTGTTTGAAGCTGTCTACACCTTCATCAAGAACCGGATC 935
281 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 300
936 CATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 995
301 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 320
996 CGCTGCTCAAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1055
321 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGluThr 340
1056 CGCACTATCAAGATTGGGGCATCGGCACATTCGAGACTTGGCTGTGGTGGAGACA 1115
341 AlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProVal 360
1116 GCACCATCTGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTG 1175
361 ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeuAla 380
1176 GTCAACGAATGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1235
381 AlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr 400
1236 GCCCAGCAAACTTCAACACCTTGAATGATGAGTGGGAAAGCCCTTGGAGGACAGGACA 1295

401 LeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAsp 420
1296 CTATGCTGCGAGGAGTCTCTCTCTGTCAGCCACCCACGAGAGCTTGGGGGAAGTATCGAC 1355
421 ArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeu 440
1356 AGGATTGCTCGGAGCAGGTACACAGGCTGGTGTAGTGAGCAGAGACCCAGCATCTCTTG 1415
441 GlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAsp 460
1416 GGGTGGTCT 1475
461 AlaLeuGlyAla 464
1476 GCCTCGGGGCC 1487
RESULT 5
US-10-756-149-1235
; Sequence 1235, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; FILE REFERENCE: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
; CURRENT APPLICATION NUMBER: US/10/756,149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1235
; LENGTH: 2290
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-756-149-1235
Alignment Scores:
Pred. No.: 1,53e-252 Length: 2290
Score: 2372.00 Matches: 457
Percent Similarity: 99.35% Conservativity: 3
Best Local Similarity: 98.70% Mismatches: 3
Query Match: 98.71% Indels: 0
DB: Gaps: 0
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QY 1 MetSerPheLeuGluGlnGluAsnSerSerSerTyrProSerProAlaValThrSerSer 20
DB 97 ATGAGCTTCTAGAGCAAGAAACAGCAGCTCATGGCCATCAGCAGCTGTGACGAGCAGC 156
QY 21 SerGluArgIleArgGlyLysArgArgAlaValAlaLeuArgTyrThrArgGlnLysSer 40
DB 157 TCAGAAAGATCCGTGGAAACCGAGGCGCAAGCCCTTGAGATGGACAGGACGAAAGTCG 216
QY 41 ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60
DB 217 GTGGAGAGGGGAGGAGCCAGCAGCTCAGGGGGAGAGTCCCGGTCCAGGCCAGCTGTGAG 276
QY 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla 80
DB 277 TCCACCGGGCTGGAGGCGCACATTCCTCCACAGACACACCTTTGGCTCAAGCTGTATCTCTGCC 336
QY 81 GlyValGlyThrProProThrGlyTyrAspCysLeuProSerAspCysThrAlaSerAla 100
DB 337 GGGGTGGGCATCCACCAACAGGGTGGAGTGGCTCCCTCTCTCTCTCTCTCTCTCTCTCT 396
QY 101 AlaGlySerSerThrAspValGluLeuAlaThrGluPheProAlaThrGluAlaTyr 120
DB 397 GCAGGCTCCAGCACAGATGATGTGGAGTGGCCACGAGGTTCCAGGACACAGAGGCTGG 456
QY 121 GluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGlnAla 140

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Db 457 GAGTGTGAGCTAGAGGCGCTGCTGAAGAGAGGCGCTGCCCTGTGCTGTGCCCGCAGGCG 516
Qy 141 ProPheProLysLeuGlyTTrpAspAspGluLeuArgLysProGlyAlaGlnIleTyrMet 160
Db 517 CCATTTCACAGCTGGGCTGGGATGAGCAACTGGGAAACCCGGCGCCAGATCTCATG 576
Qy 161 ArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValIle 180
Db 577 CGCTTCATCGAGGAGCACACTGCTACGATGCCATGGCAACTAGCTCCAAGTAGTATC 636
Qy 181 PheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyValArg 200
Db 537 TTCGACACCATGCTGGAGATCAAGAGCGCTCTTCTGCTGTGGTGGCCAAAGGTGTGGG 696
Qy 201 AlaAlaProLeuTTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAsp 220
Db 697 GCAGCCCTCTATGGGACAGCAAGACAGAGCTTTGTGGGATGCTGACCATCACTGAC 756
Qy 221 PheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGlu 240
Db 757 TTCATCTCTGGTGCATCGCTACTACAGGTCCCGCTGGTCCAGATCTATGATTTGAA 816
Qy 241 GlnHisLysIleGluThrTTrpArgGluIleTyrLysGlnGlyCysPheLysProLeuVal 260
Db 817 CAACATAGATTGAGACTGGGGGAGATCTACTGCAAGGCTGCTTCAAGCCTCTGGTC 876
Qy 261 SerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIle 280
Db 877 TCCATCTCTCTAATATAGCTGTTTGAAGCTGCTTACACCTCATCAAGACCGGATC 936
Qy 281 HisArgIleProValLeuAspProValSerGlnValLeuHisLysIleLeuThrHisLys 300
Db 937 CATCGCTGCTGCTGCTTGAACCCGGTGCAGGACAGTACTCCACATCTCTCACACAAA 996
Qy 301 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 320
Db 997 CGCTGTCTCAAGTTCCTGCACATCTTTGGTTCCCTGCTGCCCGCGCCCTCTCTCTAC 1056
Qy 321 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGluThr 340
Db 1057 CGCATATTCACAGATTTGGGCATCGGCACATTCGGAGACTTGGCTGTGGTCTGGAGACA 1116
Qy 341 AlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuProVal 360
Db 1117 GCACCATCTCTGACTGCACATCTTTGTGACCGCGGTGTGTGCTGCTGCTGCTG 1176
Qy 361 ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeuAla 380
Db 1177 GTCAACGAATGTGGTCAAGTCTGCGGCTCTATTCCCGCTTTGATGTGATTCACCTGGCT 1236
Qy 381 AlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr 400
Db 1237 GCCCAGCAAACTACAACACCTGACATGATGTGGGAGAGCCCTCAGGAAAGAGGACA 1296
Qy 401 LeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAsp 420
Db 1297 CTATGTCTGGAGGGAGTCTCTTCTCCAGCCCGCCACGAGAGCTTGGGGAAGTATGATCAG 1356
Qy 421 ArgIleAlaArgGlnGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeu 440
Db 1357 AGGATTGCTCGGACAGAGTACACAGGCTGGTGTGTAGTGGACGAGACCCAGCATCTCTTG 1416
Qy 441 GlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAsp 460
Db 1417 GCGGTGCTCTCCTCTCGACATCTTTCAGGCACCTGCTGCTGCTGCTGCTGCTGCTGCTG 1476
Qy 461 AlaLeuGly 463
Db 1477 CCCTCGGGG 1485
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RESULT 6

US-09-950-022-3

; Sequence 3, Application US/09950022

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; Publication No. US20030017470A1
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: Novel PRKAG3 Alleles and Use for the Same as Genetic Markers for
; FILE REFERENCE: P04668US3
; CURRENT APPLICATION NUMBER: US/09/950,022
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1873
; TYPE: DNA
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1392)
US-09-950-022-3
Alignment Scores:
Pred. No.: 9,49e-213 Length: 1873
Score: 2013.00 Matches: 400
Percent Similarity: 90.11% Conservative: 19
Best Local Similarity: 86.02% Mismatches: 44
Query Match: 83.77% Indels: 2
DB: 3 Gaps: 2
US-10-070-794A-30 (1-464) x US-09-950-022-3 (1-1873)
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Qy 1 MetSerPheLeuGluGlnGluAsnSerSerSerTrpProSerProAlaValThrSerSer 20
Db 1 ATGAGCTTCTTAGAGCAAGGAGAGAGAGCGCTTCATGGCCATCCCGAGCTGTNACCACAGC 60
Qy 21 SerGluArgIleArgGlyLysArgArgAlaLysAlaLeuArgThrTrpArgGlnLysSer 40
Db 61 TCAGAAAGAGCCATGGGACCCAGGAGCCCTCTAGATGCACAAGGACGAGGAT 120
Qy 41 ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60
Db 121 GTAGAGGAAGGGGGGCTCCGGGCCCGAGGGAAGGTCCCAAGTCCAGGCCAGTTGCTGAG 180
Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspPro--- 79
Db 181 TCCACCGGGCAGGAGGGCCACATCCCAAGGCCACACCTTGGCCCAAGCGCTCCCTTG 240
Qy 80 AlaGlyValGlyThrProProThrGlyTTrpAspCysLeuProSerAspCysThrAlaSer 99
Db 241 GCCGAGGTGGACACCCCCCAACAGAGCGGACATCTCTCCCTCTGTACTGTGACCTCA 300
Qy 100 AlaAlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAla 119
Db 301 GCCTCCGACTCCAACACAGACCATCTGGATCTGGGCATAGAGTTTCTCAGCCTCGCGCGG 360
Qy 120 TrpGluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGln 139
Db 361 TCGGGGAGTAGCTT---GGGCTGTGGAAAGAGAGCCAGCCCGCTGCTCCCATCCCAAG 417
Qy 140 AlaProPheProLysLeuGlyTTrpAspAspGluLeuArgLysProGlyAlaGlnIleTyr 159
Db 418 GTGCTGTTACCCAGCTGGGCTGGGATGATGAGCTGCAGAGCCGCGGGGCGCCAGGTCTAC 477
Qy 160 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 179
Db 478 ATGCACCTTCATGAGGAGCACACCTGTGCTACGATGCCATGGCGACAGCTTCCAAATGGTTC 537
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Qy 180 IlePheAspThrMetLeuGluIleLysAlaPheAlaLeuValAlaAsnGlyVal 199
Db 538 ATCTTCGACACCATCTGGAGATCAAGAAGCCCTTCTTGGCCCTGGTGGCCAAACGGCGTC 597
Qy 200 ArgAlaAlaProLeuThrAspSerLysGlnSerPheValGlyMetLeuThrIleThr 219
Db 598 CGAGCGGCACCTTGTGGGACGACGACGAGCTTCGGGGGATGCTGACCATCACA 657
Qy 220 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 239
Db 658 GACTTCATCTGTGTGCTGCACCGCTATTACAGGTCCCCCTGGTCCAGATCTAGAGATT 717
Qy 240 GluGlnHisLysIleGluThrTyrArgGluIleTyrLeuGlnGlyCysPheProLeu 259
Db 718 GAAGAACAATAGATTGAGACCTGGAGGAGATCTACCTTCAAGGCTGCTTCAAGCCCTCTG 777
Qy 260 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 279
Db 778 GTCTCCATCTCTCCAAATGACAGCCTGTTCGAAGCTGTCTACGCCCTCATCAAGAACCGG 837
Qy 280 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 299
Db 838 ATCCACCGCCTGCCGCTCTGGACCTGTCTCCGGGCTGTGCTCCACATCTCTCACAT 897
Qy 300 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 319
Db 898 AAGCGGCTTCTCAAGTCTCTGCACATCTTGGCACCTGTCTGCCCGCCCTCTCTCTC 957
Qy 320 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGlu 339
Db 958 TACCGCACCATCCAAAGATTGGGGCATCGGCATCTCCGAGACTTGGCGCTGGTCTCGAA 1017
Qy 340 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 359
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Qy 360 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 379
Db 1078 GTGGTCAACGAACCTGGACAGGTAGTGGGCTCTACTCTGCTTTGTATGTATCCACCTG 1137
Qy 380 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 399
Db 1138 GCTGCCCAACAACAATCAACCACTGACATCTTCTGGACCGCGCTGTCTGGCTGCT 1197
Qy 400 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValIle 419
Db 1198 ACATGTGTGTGGAGGCTCTTCTTCTGCGAGCCCGACGAGACTTGGGGAGAGTCA 1257
Qy 420 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 439
Db 1258 GACCGGATTCTCCGGGAACAGGTGACCGCTGCTGCTGCTGGATGAGACCCAGCACCTT 1317
Qy 440 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 459
Db 1318 CTGGCGCTGTGTGCTCTCTGACATCTTCAAGCTCTGGTCTGCTGCTGCTGCTGCT 1377
Qy 460 AspAlaLeuGlyAla 464
Db 1378 GATGCCCTTCGGGGCC 1392

RESULT 7

US-11-075-134-3
; Sequence 3, Application US/11075134
; Publication No. US20050208551A1
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: Novel PRKAG3 Alleles and Use fo the Same as Genetic Markers for
; TITLE OF INVENTION: Reproductive
; TITLE OF INVENTION: and Meat Quality Traits

FILE REFERENCE: P04668US3
; CURRENT APPLICATION NUMBER: US/11/075,134
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: US/09/950,022
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1873
; TYPE: DNA
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1392)
; OTHER INFORMATION:
US-11-075-134-3
Alignment Scores:
Pred. No.: 9,49e-213 Length: 1873
Score: 2013.00 Matches: 400
Percent Similarity: 90.11% Conservative: 19
Best Local Similarity: 86.02% Mismatches: 44
Query Match: 83.77% Indels: 2
DB: 10 Gaps: 2
US-10-070-794A-30 (1-464) x US-11-075-134-3 (1-1873)

Qy 1 MetSerPheLeuGluGlnGluAsnSerSerTyrProSerProAlaValThrSerSer 20
Db 1 ATGAGCTTCTTAGAGCAAGGAGAGAGAGCCGTTCATGGCCATCCCGAGCTGTAAACCCAGC 60
Qy 21 SerGluArgIleArgGlyLysArgAlaLysAlaLeuArgTyrThrArgGlnLysSer 40
Db 61 TCAGAAAGAGCCATGGGGACAGGGGACCAAGGCTCTAGATGGACACAGGAGGAGAT 120
Qy 41 ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60
Db 121 GTAGAGGAGAGGGGGCTCCGGGGCCCGAGGAGAGGTCCCGAGTCCAGGCCAGTTGTCTGAG 180
Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspPro 79
Db 181 TCACCGGGGAGGAGGCGCATTTCCCAAGGCCACACCTTGGCCCAAGCGCTCCCTTG 240
Qy 80 AlaGlyValGlyThrProProThrGlyTyrAspCysLeuProSerAspCysThrAlaSer 99
Db 241 GCCGAGGTGGACAACCCCAACAGAGCGGGACATCTCTCCCTCTGACTGTGCAGCCTCA 300
Qy 100 AlaAlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAla 119
Db 301 GCCTCCGAGCTCCAAACACAGACCATCTGGATCTGGGATAGAGTTCTCAGGCTTCGGCGCG 360
Qy 120 TrpGluCysGluLeuGluLeuLeuGluGluArgProAlaLeuCysLeuSerProGln 139
Db 361 TCGGGGATGAGCTT---GGGCTGGTGGAGAGAGCCGCCCGCTGCCATCCCCAGAG 417
Qy 140 AlaProPheProLysLeuGlyTyrAspAspGluLeuArgLysProGlyAlaGlnIleTyr 159
Db 418 GTGCTGTTACCCAGGCTGGGCTGGGATGATGAGCTGCAGAAGCGGGGGCCAGGTCTAC 477
Qy 160 MetArgPheMetGlnGlnHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 179
Db 478 ATGCACCTTCATGCGAGGAGCACACCTGTCTAGATCGATGGCCATGGCCAGCTCAAACTG 537
Qy 180 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAenGlyVal 199
Db 538 ATCTTCGACACCATGCTGGAGATCAAGAAGGCTTCTTTTGGCCCTGGTGGCCAAACGGCGTC 597

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Qy 200 ArgAlaalaProLeuTrpAspSerLysAlaGlnSerPheValGlyMetLeuThrIleThr 219
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Qy 220 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluile 239
Db 658 GACTTCATCTGTGTGTCACCGCTATTACAGGTCCCGCTGCTCCAGATCTACGAGATT 717
Qy 240 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 259
Db 718 GAAGACATAAGATTGAGACCTGGAGGAGATCTACCTTCAAGGCTGCTTCAAGGCTCTG 777
Qy 260 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 279
Db 778 GTCTCCATCTCTCCCAATGACAGCGCTGTCTAGCGCCCTCATCAAGAACCGG 837
Qy 280 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 299
Db 838 ATCCACCGCCTGCGGCTCTGACCCCTGTCTCCGGGGCTGTGCTCCACATCTCCACAT 897
Qy 300 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 319
Db 898 AAGCGGCTCTCAAGATTCTGCACATCTTTGGCACCCTGTCTGCCCGCGCTCTCTCTC 957
Qy 320 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGlu 339
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Qy 340 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuPro 359
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Qy 380 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 399
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Qy 420 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 439
Db 1258 GACCGGATTGTCGGGAAACAGGTGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1317
Qy 440 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 459
Db 1318 CTGGGCGGTGGTCTCTGACATCTTCTAGGCTCTGGTCTGCTGCTGCTGCTGCTGCT 1377
Qy 460 AspAlaLeuGlyAla 464
Db 1378 GATGCCCTCGGGCC 1392

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RESULT 8

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US-09-950-022-1
; Sequence 1, Application US/09950022
; Publication No. US20030017470A1
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: Novel PKAG3 Alleles and Use fo the Same as Genetic Markers for
; TITLE OF INVENTION: Reproductive and Meat Quality Traits
; FILE REFERENCE: P04668US3
; CURRENT APPLICATION NUMBER: US/09/950,022
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239

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; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1873
; TYPE: DNA
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1392)
; US-09-950-022-1

Alignment Scores: 1.58e-212 Length: 1873
Pred. No.: 2011.00 Matches: 400
Score: 2011.00 Conservative: 19
Percent Similarity: 90.11% Mismatches: 44
Best Local Similarity: 86.02% Indels: 2
Query Match: 83.69% Gaps: 2
DB: 3

US-10-070-794A-30 (1-464) x US-09-950-022-1 (1-1873)

Qy 1 MetSerPheLeuGluGlnGluAsnSerSerTrpProSerProAlaValThrSerSer 20
Db 1 ATGAGCTTCTTAGAGCAGGAGAGAGCGGTCATGGCCATCCCGAGCTGTAAACCCAGC 60
Qy 21 SerGluArgIleArgGlyLysArgAlaLysAlaLeuArgTrpThrArgGlnLysSer 40
Db 61 TCAGAAAGAACCATGGGACACAGGGGAACAAAGGCCCTCTAGATGGACAGCAGGAGAT 120
Qy 41 ValGluGluGlyGluProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60
Db 121 GTAGAGGAAGGGGGGCTTCGGGGCCCGAGGGAAGGTCCCGAGTCCAGGCCAGTGTCTGAG 180
Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspPro--- 79
Db 181 TCCACCGGGCAGGAGGCGCACATTCGCCAAGGCCACACCCCTTGGCCCAAGCGCTCCCTTG 240
Qy 80 AlaGlyValGlyThrProProThrGlyTyrAspCysLeuProSerAspCysThrAlaSer 99
Db 241 GCCGAGGTGGACAAACCCCAACAGAGCGGACATCTCCCTCTCTGACTGTGCGAGCCTCA 300
Qy 100 AlaAlaGlySerSerThrAspValGluLeuAlaThrGluPheProAlaThrGluAla 119
Db 301 GCCTCCGACTCAACACAGACCATCTGGATCTGGGCATAGAGTCTCAGCCTCGCGCGCG 360
Qy 120 TrpGluCysGluLeuGluGlyLeuLeuGluArgProAlaLeuCysLeuSerProGln 139
Db 361 TCGGGGGATGAGCTT---GGGCTGGTGGAGAGAGAGCCAGCCCGTGGCCATCCCCAGAG 417
Qy 140 AlaProPheProLysLeuGlyTyrAspAspGluLeuArgLysProGlyAlaGlnIleTyr 159
Db 418 GTGCTGTTTACCAGGCTGGGCTGGGATGATGAGCTGCAGAGAGCGGGGGCCAGGCTCTAC 477
Qy 160 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 179
Db 478 ATGCATCTTCATGAGGAGACACACCTGCTACGATGCCATGGCGACAGCTCCAAACTGCTC 537
Qy 180 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 199
Db 538 ATCTTCGACACCATGCTGAGATCAAGAAGGCTTCTTTGGCTGGTGGCCAAACGCGCTC 597
Qy 200 ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 219
Db 598 CGAGCGGACCTTTGTGGGACAGCAAGAGAGAGAGCTTCTGGGGATGCTGACCATCACA 657
Qy 220 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluile 239
Db 658 GACTTCATCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 717
Qy 240 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 259

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Db 718 GAAGACATAGATTGAGACCTGGAGGAGATCTACCTTCAAGGCTGCTTCAAGCCCTG 777
Qy ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 279
Db GTCTCCATCTCTCCCAATGACAGCTGTTCGAAGCTGTCTAGCCCTCATCAAGACCG 837
Qy IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 299
Db ATCCACCGCTCTCCGCTGCTGACCTGTCTCCGGGCTGTCTCCACATCTCCACAT 897
Qy LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 319
Db AAGCGCTCTCAAGTCTCGACATCTTGGACCTGTCTCCCGGCTGTCTCTCTCTC 957
Qy TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 339
Db TACCGCACCATCCAAATTTGGGATTCGGGATTCGGGATTCGGGATTCGGGATTCGG 1017
Qy ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuPro 359
Db ACGCGGCTCATCTGACCGCATCTGACATCTTCTGTCGACCGCTGTCTGCTGCTG 1077
Qy ValValAsnGluCysGlyGlnValValGlyValGlyLeuTyrSerArgPheAspValIleHisLeu 379
Db GTGTCAACGAATCTGGACAGTAGTGGGCTCTTACTCTCTGCTTGTGTGTGATCC 1137
Qy AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 399
Db GCTGCCCAACAAACATACACCATCTGACATGATGTGGAGAGCCCTGAGCAGCGG 1197
Qy ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIle 419
Db AACTGTGTCTGGAAGGCTCTCTTCTCTGCGAGCCACAGACCTTGGGGAGTCA 1257
Qy AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 439
Db GACCGGATGTCTGGGAAACAGTGACCGCTGTGTGTGTGTGTGTGTGTGTGTGT 1317
Qy LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 459
Db CTGGGGTGTGTCTCTCTGACATCTCTGAGCTCTGTGTGTGTGTGTGTGTGTGT 1377
Qy AspAlaLeuGlyAla 464
Db GATGCCCTCGGGCC 1392

RESULT 9
US-11-075-134-1
; Sequence 1, Application US/11075134
; Publication No. US20050208551A1
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: Novel PRKAG3 Alleles and Use to the Same as Genetic Markers for
; TITLE OF INVENTION: Reproductive
; TITLE OF INVENTION: and Meat Quality Traits
; FILE REFERENCE: P04668US3
; CURRENT APPLICATION NUMBER: US/11/075,134
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: US/09/950,022
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1

LENGTH: 1873
TYPE: DNA
ORGANISM: Sus scrofa
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1392)
OTHER INFORMATION:
US-11-075-134-1
Alignment Scores:
Pred. No.: 1,59e-212 Length: 1873
Score: 2011.00 Matches: 400
Percent Similarity: 90.11% Conservative: 19
Best Local Similarity: 86.02% Mismatches: 44
Query Match: 83.69% Indels: 2
DB: 2 Gaps: 2
US-10-070-794A-30 (1-464) x US-11-075-134-1 (1-1873)

Qy 1 MetSerPheLeuGluGlnGluAsnSerSerTrpProSerProAlaValThrSerSer 20
Db 1 ATGAGCTTCTTAGAGCAAGGAGAGAGCGTTCATGGCCATCCCGAGCTGTAAACCA 60
Qy 21 SerGluArgIleArgGlyLysArgArgAlaLysAlaLeuArgTrpThrArgGlnLys 40
Db 61 TCAGAAAGAAAGCCATGCGGACCAAGGGAACAAGGCTCTAGATGGACAAGGAGG 120
Qy 41 ValGluGluGlyGluProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60
Db 121 GTAGAGNAGGGGGCTCCGGGCCCGAGGAGAGTCCCGAGTCCAGCTCAGGCCAG 180
Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspPro 79
Db 181 TCCACCGGCGAGGAGGCCACATCCCCAGGCCACACCTTGGCCCAAGCCGCTCC 240
Qy 80 AlaGlyValGlyThrProThrGlyTrpAspCysLeuProSerAspCysThrAlaSer 99
Db 241 GCGAGGTGGACAAACCCCAACAGAGCGGGACATCTCCCTCTGACTGTGACGCTCA 300
Qy 100 AlaAlaGlySerSerThrAspValGluLeuAlaThrGluPheProAlaThrGluAla 119
Db 301 GCCTCCGACTCAACACACAGACCATCTGGATCTGGGATAGAGTCTCAGCCTCG 360
Qy 120 TrpGluCysGluLeuGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGln 139
Db 361 TCGGGGATGAGCTT---GGGCTGGTGAAGAGAGCCAGCCCGTCCCATCCCCAG 417
Qy 140 AlaProPheProLysLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnIleTyr 159
Db 418 GTGCTGTACCCAGCTGGGCTGGGATGATGATGATGATGATGATGATGATGATGAT 477
Qy 160 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 179
Db 478 ATGCATTTTCATGAGGAGACACCTGTCTAGTGGCCATGGGACCACTCCAAACTG 537
Qy 180 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 199
Db 538 ATCTTCGACACCATCTGGAGATCAAGAGCCCTTCTTTCCTTGGTGGTGGTGGT 597
Qy 200 ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 219
Db 598 CGAGCGCACCTTGTGGGACAGCAAGAGCAGAGCTTCGTGGGATGCTGACCATACA 657
Qy 220 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 239
Db 658 GACTTATCTGT 717
Qy 240 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 259
Db 718 GAAGACATAGATTGAGACCTGGAGGAGATCTACCTTCAAGGCTGTCTCAAGCTCT 777
Qy 260 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 279

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Db 778 GTCTCCATCTCTCCATGACAGCCTGTTGAGAGCTGTCTACGCCCTCATCAAGAACCGG 837
Qy 280 ILeHisArgLeuProValLeuAspProValSerGlyAenValLeuHisIleLeuThrHis 299
Db 838 ATCCACCCGCTGCGGCTCTGGACCCCTGTCTCGGGGCTGTGCTCTCCACATCTCCACAT 897
Qy 300 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 319
Db 898 AAGCGGCTCTCAAGTCTCTGCACATCTTTGGCACCTTGTGGCCCTGTGCGCGCTCTCTCTC 957
Qy 320 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGlu 339
Db 958 TACCGCACCATCCAAAGATTGGGGCATCGGCACATTCGAGACTTGGCGGTGGTCTGGAA 1017
Qy 340 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 359
Db 1018 ACGCGGCCCTCTGACCGCACTGCACATCTTCGTGACCGCGTGTGTCTGCGCTGCCT 1077
Qy 360 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 379
Db 1078 GTGGTCAACGAACTGGACAGGTAGTGGGCTCTTACTCTGCTTTGATGTATCCACTG 1137
Qy 380 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 399
Db 1138 GCTGCCCAACAAATACACCACTTGACATGATGTGGAGAGGCCCTGAGCGACGGG 1197
Qy 400 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValIle 419
Db 1198 ACCTGTGTCTGGAAGGCTCTCTTCTCTCGCAGCCACGACACTTGGGGGGAAGTCATT 1257
Qy 420 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 439
Db 1258 GACCGGATTGTCGGGAACAGGTGCACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1317
Qy 440 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 459
Db 1318 CTGGCGTGGTGTCTCTCTGACATCTCTCAGGCTCTGGTGGTCTCAGCCCTGCTGGATT 1377
Qy 460 AspAlaLeuGlyAla 464
Db 1378 GATGCCCTCGGGGCC 1392
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RESULT 10
US-09-950-022-7
; Sequence 7, Application US/09950022
; Publication No. US20030017470A1
; GENERAL INFORMATION:
; APPLICANT: Rothechild, Max
; APPLICANT: Cibanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: Novel PRKAG3 Alleles and Use fo the Same as Genetic Markers for
; TITLE OF INVENTION: Reproductive and Meat Quality Traits
; FILE REFERENCE: P04668US3
; CURRENT APPLICATION NUMBER: US/09/950,022
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: '60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 1873
; TYPE: DNA
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1392)
US-09-950-022-7
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Alignment Scores:
Pred. No.: 2,05e-212 Length: 1873
Score: 2010.00 Matches: 399
Percent Similarity: 90.11% Conservative: 20
Best Local Similarity: 85.81% Mismatches: 44
Query Match: 83.65% Indels: 2
DB: Gaps: 2

US-10-070-794A-30 (1-464) x US-09-950-022-7 (1-1873)

Qy 1 MetSerPheLeuGluGlnGluAenSerSerTyrProSerProAlaValThrSerSer 20
Db 1 ATGAGCTTCTTAGAGCAAGAGAGAGAGCGGTTCATGTCATCCGAGCTGTAACCCAGCAG 60
Qy 21 SerGluArgIleArgGlyLysArgArgAlaLysAlaLeuArgTyrThrArgGlnLysSer 40
Db 61 TCAGAAAGAACCATGGGGACCAAGGGAAACAAGGCCCTCTAGATGGAGCAAGCGAGGAGAT 120
Qy 41 ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60
Db 121 GTAGAGAGAGGGGGCTCCGGGCCGAGGAGAGGTCCCCAGTCCAGCCAGTGTGTGAG 180
Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspPro--- 79
Db 181 TCCACGGGCGAGGAGGCCACATTCGCCAAGGCCACACCTTTGGCCCAAGCGCTCCCTTG 240
Qy 80 AlaGlyValGlyThrProProThrGlyTyrAspCysLeuProSerAspCysThrAlaSer 99
Db 241 GCGAGGTGAGCAACCCGCCAAGAGCGGGGACATCTCTCCCTCTGACTGTGACGCCCTCA 300
Qy 100 AlaAlaGlySerSerThrAspValGluLeuAlaThrGluPheProAlaThrGluAla 119
Db 301 GCCTCCGACTCCAAACACAGACCATCTGGATCTGGCATAGAGTTCTCAGGCTCGCGCGC 360
Qy 120 TrpGluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGln 139
Db 361 TCGGGGGATGAGCTT---GGGCTGGTGAAGAGAGAGCCAGCCCGTCCCATCCAGAG 417
Qy 140 AlaProPheProLysLeuGlyTyrAspAspGluLeuArgLysProGlyAlaGlnIleTyr 159
Db 418 GTGCTGTATCCAGGCTGGGCTGGGATGATGAGCTGCAGAGAGCGGGGGCCAGGTCTAC 477
Qy 160 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 179
Db 478 ATGCATCTTATGAGAGGACACACCTGTACGATGCCATGCCAGCCAGCTCCAAACTGTC 537
Qy 180 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 199
Db 538 ATCTTCGACACCATGCTGGAGATCAAGAAGGCCCTTCTTTGCCCTGGTGGCCAGCGCATC 597
Qy 200 ArgAlaAlaProLeuTyrAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 219
Db 598 CGAGCGGCACCTTTGTGGGACAGCAAGAGCAGAGCTTCGTGGGGATGCTGACCATACAC 657
Qy 220 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 239
Db 658 GACTTCTATCTGGTGTCTGACCGCTATTACAGTCCCGCTCCAGTCCAGATCTACGAGATT 717
Qy 240 GluGlnHisLysIleGluThrTyrArgGluIleTyrLeuGlnGlyCysPheLysProLeu 259
Db 718 GAAGAACATAAGATTGAGACCTGGAGGAGATCTACCTTCAAGGCTGCTTCAAGGCTCTG 777
Qy 260 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 279
Db 778 GTCTCCATCTCTCCCAATGACAGCGCTGTGGAAGCTGTCTAGCGCCTCATCAAGAACCGG 837
Qy 280 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 299
Db 838 ATCCACCCGCTGCGGCTCTGGAACCTGTCTCCGGGGCTGTGCTCCACATCTCCACAT 897
Qy 300 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 319
Db 898 AAGCGGCTCTCAAGTCTCTGACATCTTTGGCACCTTGTGGCACCTGTGCTGCTGCTGCTC 957
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Qy 320 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 339
 Db 958 TACCGCACCATCCCAAGATTTCGGCATCGGCACATTCGAGACTTGGCGTGTCTGGAA 1017
 Qy 340 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 359
 Db 1018 ACGGCGCCATCCCTGACCGCACTCGACATCTTCGTGGACCGCGGTGTCTGCGCTGCCT 1077
 Qy 360 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 379
 Db 1078 GTGGTCAACGAACTGACAGGTAGTGGCCCTCTACTCTCGCTTTGATGTATCCACTG 1137
 Qy 380 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 399
 Db 1138 GCTGCCCAACAACATACACCACTCGACATGAATGTGGAGAAGCCCTGAGGACGGG 1197
 Qy 400 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIle 419
 Db 1198 ACATGTGTCTGGAAAGCGTCCCTTTCTGCGCAGCCCAACGAGACCTTGGGGGAAGTCA 1257
 Qy 420 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 439
 Db 1258 GACCGGATTGTCGGGAACAGGTGCAACGGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 1317
 Qy 440 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 459
 Db 1318 CTGGCGGTGTGTCTCTGACATCCTTCAGGCTCTGTGTGTGTGTGTGTGTGTGTGTGT 1377
 Qy 460 AspAlaLeuGlyAla 464
 Db 1378 GATGCCCTCGGGGCC 1392

RESULT 11

US-11-075-134-7
 ; Sequence 7, Application US/11075134
 ; Publication No. US20050208551A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rothschild, Max
 ; APPLICANT: Ciobanu, Dan
 ; APPLICANT: Malek, Massoud
 ; APPLICANT: Plastow, Graham
 ; TITLE OF INVENTION: Novel PKRAG3 Alleles and Use for the Same as Genetic Markers for
 ; TITLE OF INVENTION: Reproductive
 ; TITLE OF INVENTION: and Meat Quality Traits
 ; FILE REFERENCE: P04668US3
 ; CURRENT APPLICATION NUMBER: US/11/075,134
 ; CURRENT FILING DATE: 2005-03-08
 ; PRIOR APPLICATION NUMBER: US/09/950,022
 ; PRIOR FILING DATE: 2001-09-10
 ; PRIOR APPLICATION NUMBER: 60/231045
 ; PRIOR FILING DATE: 2000-09-08
 ; PRIOR APPLICATION NUMBER: 60/260,239
 ; PRIOR FILING DATE: 2001-01-08
 ; PRIOR APPLICATION NUMBER: 60/299,111
 ; PRIOR FILING DATE: 2001-06-18
 ; NUMBER OF SEQ ID NOS: 21
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 7
 ; LENGTH: 1873
 ; TYPE: DNA
 ; ORGANISM: Sus scrofa
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(1392)
 ; OTHER INFORMATION:
 US-11-075-134-7
 Alignment Scores:
 Pred. No.: 2,05e-212 Length: 1873
 Score: 2010.00 Matches: 399
 Percent Similarity: 90.11% Conservative: 20
 Best Local Similarity: 85.81% Mismatches: 44

Query Match: 83.65% Indels: 2
 DB: 10 Gaps: 2
 US-10-070-794a-30 (1-464) x US-11-075-134-7 (1-1873)
 Qy 1 MetSerPheLeuGlnGlnAsnSerSerTrpProSerProAlaValThrSerSer 20
 Db 1 ATGAGCTTCTTAGAGCAAGGAGAGAGCGCTTATCGGCATCCCGAGGTGTAAACACCAAGC 60
 Qy 21 SerGluArgIleArgGlyLysArgArgAlaIleValLeuArgTrpThrArgGlnLysSer 40
 Db 61 TCAGAAAGAACCCATGCGGACCCAGGGGAAACAAGGCCCTCTAGATGGACAAGGACGAGAGAT 120
 Qy 41 ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60
 Db 121 GTAGAGGAAGGGGGCTCCGGGCCCGAGGGAGGTCCCGAGTCCAGGCCAGTGTGTGAG 180
 Qy 61 SerThrGlyLeuGluAlaThrPheProGlyThrThrProLeuAlaGlnAlaAspPro--- 79
 Db 181 TCCACCGGGGAGGAGGCCACATTCCTCCCAAGGCCACACCTTGGCCCAAGCGCTCCCTTGT 240
 Qy 80 AlaGlyValGlyThrProProThrGlyTyrAspCysLeuProSerAspCysThrAlaSer 99
 Db 241 GCCAGGTGGACAAACCCCAACAGAGCGGAGACATCTCTCCCTCTGACTGTGACGCTCA 300
 Qy 100 AlaAlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAla 119
 Db 301 GCCTCCGACTCCAAACACAGACCATCTGGATCTGGGCATAGAGTTCTCAGCCTCGGGCGG 360
 Qy 120 TrpGluCysGluLeuGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGln 139
 Db 361 TCGGGGGATGAGCTT---GGGCTGGTGAAGAGAGAGCAGCCCGCTGCCATCCCAAG 417
 Qy 140 AlaProPheProLysLeuGlyTyrAspAspGluLeuArgLysProGlyAlaGlnIleTyr 159
 Db 418 GTGCTGTATCCAGGCTGGGCTGGGATGATGAGCTGCAGAAAGCGGGGGCCAGGCTTAC 477
 Qy 160 MetArgPheMetGlnGlnHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 179
 Db 478 ATGCACCTTCATGACGAGGACACACTGCTAGCATGCCATGGGACCACTCCAACTGGTC 537
 Qy 180 IlePheAspThrMetLeuGluIleLysLysAlaPheAlaLeuValAlaAsnGlyVal 199
 Db 538 ATCTTCGACACCATGCTGGAGATCAAGAAGCCCTTCTTTGCCCTGTGTGGCAACGGCATC 597
 Qy 200 ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 219
 Db 598 CGAGCGGCACCTTTGTGGGACAGCAAGACGAGCTTCGTGGGATGCTGACCATCACA 657
 Qy 220 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 239
 Db 658 GACTTCATCTTGTGTGTGACCCCTATTACAGGTCCCCCTGTGTCCAGATCTACGAGATT 717
 Qy 240 GluGlnHisLysIleGluThrTrpArgGluIleTyrIleuGlnGlyCysPheLysProLeu 259
 Db 718 GAAGAACATAAGATTGAGACCTGGAGGAGATCTACCTTCAAGGCTGCTTCAAGGCTCTG 777
 Qy 260 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 279
 Db 778 GTCTCCATCTCTCCCAATGACGCTGTTCGAAGCTGTCTACGCCCTTCATCAAGAACCGG 837
 Qy 280 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 299
 Db 838 ATCCACCGCTCGCGGTCTGGACCTGTCTCGGGGGCTGTGTCCACATCTCTCACACAT 897
 Qy 300 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 319
 Db 898 AAGCGGCTTCTCAAGTTCTCTGCACATCTTTGGCACCTGTCTGCCCGGCCCTCTCTTCTC 957
 Qy 320 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGlu 339
 Db 958 TACCGCACCATCCCAAGATTTCGGCATCGGCACATTCGAGACTTGGCGTGTGTGTGGAA 1017

340	ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro	359
1018	ACGGCGCCCATCTGACCGACCTGGACATCTTGTTGGACCGGGTGTTCTGGCGCTGCCCT	1077
360	ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu	379
1078	GTGGTCAACGAACATGGACAGGTAGTGGGGCTCTACTCTGCCTTGTATGTATCCACCTG	1137
380	AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg	399
1138	GCTGCCCAACAACATACACCACTGGACATGAATGTGGGAGAACCTTGAGGACGCG	1197
400	ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValIle	419
1198	ACACTGTGCTGGGAAGCGTCTTCTTCGCAGCCCCACGAGACCTTGGGGGGAAGTCATT	1257
420	AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu	439
1258	GACCGGAATGTCCGGGAACAGGTGCACCGCTGTGTCTGTGGATGAGACCCAGCACCTT	1317
440	LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle	459
1318	CTGGGCGTGGTGTCCCTCTCTGACATCTTCAGGCTCTGTGTGCTCAGCCCTGCTGGAATT	1377
460	AspAlaLeuGlyAla	464
1378	GATGCCCTCGGGGCC	1392

RESULT 12

US-09-950-022-9
; Sequence 9, Application US/09950022
; Publication No. US20030017470A1
; GENERAL INFORMATION:
; APPLICANT: Rothechild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Matek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: Novel PRKAG3 Alleles and Use for the Same as Genetic Markers for
; TITLE OF INVENTION: Reproductive and Meat Quality Traits

Alignment Scores:		
Pred. No.:	4	41e-212
Score:	207.00	
Percent Similarity:	90.11%	
Best Local Similarity:	85.81%	
Query Match:	83.52%	
DB:	3	
Length:		1873
Matches:		399
Conservative:		20
Mismatches:		44
Indels:		2
Gaps:		2

US-10-070-794A-30 (1-464) x US-09-950-022-9 (1-1873)

[illegible]

Db 1138 GCTGCCCAACAAATACACACCTGACATGAATGTGGAGAGCCCTGAGGAGCGG 1197
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Db 1198 ACACGTGTCTGGAGAGGCTCTCTCTGCGACCCACAGAGACCTTGGGGAGTCAAT 1257
Qy 420 AsparGlieAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 439
Db 1258 GACCGGATGTGCGGGAAACAGGTGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1317
Qy 440 LeuGlyValValSerLeuSerAspGluGlnValHisArgLeuValLeuValSerProAlaGlyile 459
Db 1318 CTGGCGGTGGGTCTCTCTGACATCTCTCAGGCTCTGGTGTCTGAGCCCTGCTGGAAT 1377
Qy 460 AspaLaLeuGlyAla 464
Db 1378 GATGCCCTCGGGGCC 1392

RESULT 13

US-11-075-134-9
; Sequence 9, Application US/11075134
; Publication No. US20050208551A1
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: Novel PKRAG3 Alleles and Use fo the Same as Genetic Markers for
; TITLE OF INVENTION: Reproductive
; TITLE OF INVENTION: and Meat Quality Traits
; FILE REFERENCE: P04668U3
; CURRENT APPLICATION NUMBER: US/11/075,134
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: US/09/950,022
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 9
; LENGTH: 1873
; TYPE: DNA
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1392)
; OTHER INFORMATION:
US-11-075-134-9

Alignment Scores:
Pred. No.: 4,41e-212 Length: 1873
Score: 2007.00 Matches: 399
Percent Similarity: 90.11% Conservative: 20
Best Local Similarity: 85.81% Mismatches: 44
Query Match: 83.52% Indels: 2
DB: 10 Gaps: 2

US-10-070-794A-30 (1-464) x US-11-075-134-9 (1-1873)

Qy 1 MetSerPheLeuGluGlnGluAsnSerSerSerTrpProSerProAlaValThrSerSer 20
Db 1 ATGAGCTCTCTAGAGCAAGGAGAGCGGTTCATGGCCATCCCGAGCTGTAAACACGAGC 60
Qy 21 SerGluArgGlieArgGlyLysArgAlaLysAlaLeuArgTrpThrArgGlnLysSer 40
Db 61 TCAGAAAGACCATGGGACCGGACCAAGGACCTCTAGATGACAGGAGGAGGAT 120
Qy 41 ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60

Db 121 GTAGAGGAGGGGGCTCCGGGGCCCGAGGAAAGGTCCCAAGTCAGGCCAGTGTGCTGAG 180
Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspPro--- 79
Db 181 TCCACCGGGCAGGAGGCCACATTCCTCCNAGGCCACACCTTGGCCCAAGCGCTCCCTTG 240
Qy 80 AlaGlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSer 99
Db 241 GCCGAGGTGGACAAACCCCAACAGAGCGGGACATCTCCCTCTGACTGTGACGCTCA 300
Qy 100 AlaAlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAla 119
Db 301 GCCTCCCACTCCAAACACAGACCATCTGGATCTGGGCATAGAGTTCTCAGCCCTCGCGCG 360
Qy 120 TrpGluCysGluLeuGluGlyLeuLeuGluArgProAlaLeuCysLeuSerProGln 139
Db 361 TCGGGGATGAGCTT---GGCTGGTGGNAGAGCAGCCCGCTGCCATCCCAAG 417
Qy 140 AlaProPheProLysLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnIleTyr 159
Db 418 GTGCTGTATCCAGGCTGGGCTGGGATGATGAGCTGCAGAGCCGGGGCCAGGTCTAC 477
Qy 160 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 179
Db 478 ATGCACCTTCATGCAGGAGCACACCTGCTAGCATGCCATGGCGACGCTCCAAACTGGTC 537
Qy 180 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 199
Db 538 ATCTTCACACCATCTGGAGATCAGAGGCCCTCTTGGCCCTGGTGGCCACAGGCGTC 597
Qy 200 ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 219
Db 598 CAAGCGGCACCTTTGTGGGACAGCAAGACAGAGCTTGTGGGGATGCTGACCATCA 657
Qy 220 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleThrGluIle 239
Db 658 GACTTCATCTTGGTGTGTCACCGCTATTACAGGTCCCTCCCTGGTCCAGATCTACGAGAT 717
Qy 240 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 259
Db 718 GAAGAATAGATTGAGACTGGAGGAGATCTACCTTCAGGCTGCTCCAGGCTCTCAAGCCTCTG 777
Qy 260 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 279
Db 778 GTCTCCATCTCTCCCATGACAGCTGTTCGAAGCTGTCTAGGCCCTCATCAAGAACGG 837
Qy 280 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 299
Db 838 ATCCACCGCCTGCGGCTCTGGACCCCTGTCTCCGGGGCTGTGTCTCCACATCTCTCACAT 897
Qy 300 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 319
Db 898 AGCGGCTTCTCAAGTTCTCTGCACATCTTTGGCACCTGTCTGCCCGGCTCTCTCTCTC 957
Qy 320 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 339
Db 958 TACCGCACCATCCAAAGATTGGGCATCGGCACATTCGAGACTTGGCGGTGGTCTGGAA 1017
Qy 340 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 359
Db 1018 ACGGCGCCCATCTGACCGCAGCTGGACATCTTCTGGACCGGCTGTGTCTGCGCTGCT 1077
Qy 360 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 379
Db 1078 GTGTCAACGAACACTGGACAGGTAGTGGGCTCTTACTCTCGCTTTGATGTATCATCCTG 1137
Qy 380 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 399
Db 1138 GCTGCCCCAACAAACATACACACCTGGACATGAATGTGGGAGAGCCCTGAGGACGGG 1197
Qy 400 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValile 419

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Db 1198 ACATGTGTCTGGAGGGCTCCTTCTTCTGCGAGCCCGCCAGAGACCTTGGGGAGTGCATT 1257
Qy 420 AspArgLeuAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 439
Db 1258 GACCGGATTTCCGGAAACAGGTGCACCGCTGCTCGTGGATGAGACCCAGACCTT 1317
Qy 440 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuValLeuValLeuVal 459
Db 1318 CTGGCGGTGGTGTCTCTGACATCCTTCTGAGCTCTGAGCTCTGAGCCCTGCTGGAATT 1377
Qy 460 AspAlaLeuGlyAla 464
Db 1378 GATGCCCTTCGGGGCC 1392

RESULT 14
US-09-950-022-5
; Sequence 5, Application US/09950022
; Publication No. US20030017470A1
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: Novel PRKAG3 Alleles and Use fo the Same as Genetic Markers for
; TITLE OF INVENTION: Reproductive and Meat Quality Traits
; FILE REFERENCE: P04668US3
; CURRENT APPLICATION NUMBER: US/09/950,022
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 1873
; TYPE: DNA
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1392)
US-09-950-022-5

Alignment Scores:
Pred. No.: 7,36e-212 Length: 1873
Score: 2005.00 Matches: 399
Percent Similarity: 89.89% Conservative: 19
Best Local Similarity: 85.81% Mismatches: 45
Query Match: 83.44% Indels: 2
DB: 3 Gaps: 2

US-10-070-794a-30 (1-464) x US-09-950-022-5 (1-1873)
Qy 1 MetSerPheLeuGluGlnGluAsnSerSerTrrProSerProAlaValThrSerSer 20
Db 1 ATGAGCTTCTTAGACCAAGGAGAGAGCCGTTTCATGGCCATCCCGAGCTGTACACCACGAGC 60
Qy 21 SerGluArgIleArgGlyLysArgArgAlaLysAlaLeuArgTrrThrArgGlnLysSer 40
Db 61 TCAGAAAGAACCCATCTGGGACCCAGGGGAAACAAGGCTCTAGATGACCAAGGACGAGGAT 120
Qy 41 ValGluGluGlyGluProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60
Db 121 GTAGAGGAGGGGGCTTCGGGGCCGAGGAAAGTCCCCAGTCCAGGCCAGTTGCTGAG 180
Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspPro--- 79
Db 181 TCCACGGGCGAGGAGGCCACATTCGCCAAGGGCCACACCCCTTGGCCCAAGCCGCTCCCTTG 240
Qy 80 AlaGlyValGlyThrProProThrGlyTrrAspCysLeuProSerAspCysThrAlaSer 99
Db 1318 CTGGCGGTGGTGTCTCTGACATCCTTCTGAGCTCTGAGCTCTGAGCCCTGCTGGAATT 1377
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Db 241 GCCGAGGTGGACAACCCCAACAGAGCGGGACATCCTCCCTCTGACTGTGCAGCCTCA 300
Qy 100 AlaAlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAla 119
Db 301 GCCTCCGACTCCAAACACAGACCATCTGGATCTGGGCATAGAGTTCTCAGCCCTCGCGGCG 360
Qy 120 TrrPheCysGluGluGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGln 139
Db 361 TCGGGGGATGAGCTT---GGGCTGGTGAAGAGAGAGCAGCCCGCTGCCATCCCCAGAG 417
Qy 140 AlaProPheProLysLeuGlyTrrAspAspGluLeuArgLysProGlyAlaGlnIleTyr 159
Db 418 GTGCTGTTACCCAGGCTGGCTGGGATGATGAGCTGCAGAAGCGGGGGCCAGGCTCTAC 477
Qy 160 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 179
Db 478 ATGCACCTTCATGCGAGGAGCACACCTGCTAGCATGCCATGGCAGCCAGCTCCAAACTGGTC 537
Qy 180 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 199
Db 538 ATCTTCGACACCATGCTGGAGATCAGAGGCTTCTTTGCCCTGGTGGCCACCGGGCTC 597
Qy 200 ArgAlaAlaProLeuTrrAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 219
Db 598 CGAGCGGCACCTTTGTGGGACAGCAGCAGAGCTTCGTGGGGATGCTGACCATCACA 657
Qy 220 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 239
Db 658 GACTTCATCTTGGTGTGCACCGCTATTACAGGTCCCGCTTGGTCCAGATCTACAGAGATT 717
Qy 240 GluGlnHisLysIleGluThrTrrArgGluIleTyrLeuGlnGlyCysPheLysProLeu 259
Db 718 GAAGAACATATAGATTGAGACTCGAGGGAGATCTACTCTCAGGCTGCTTCAGGCTCTG 777
Qy 260 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 279
Db 778 GTCTCCATCTCTCCCAATGACAGCCTGTTGGAAGCTGTCTACGCCCTCATCAAGAACCGG 837
Qy 280 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 299
Db 838 ATCCACCGCTTCGCGGCTGCTGCGACCTGTCTCCGGGGCTGTGCTCCACATCTTCACAT 897
Qy 300 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 319
Db 898 AAGCGCTTCTCAAGTTCTCTGACATCTTTGGCACCTGCTGCCCGGCCCTCTCTCTCTC 957
Qy 320 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 339
Db 958 TACCGCACCATCCAAAGATTGGGCATCGGCACATTCGAGAGACTTGGCCGTGTGTCTGGA 1017
Qy 340 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuPro 359
Db 1018 ACGCGCCCATCTCTGACCGCATCTGTCGTCGAGCCGCGGTGTCTGCGCTGCTCT 1077
Qy 360 ValValAsnGluCysGlyValValGlyValGlyLeuTrrSerArgPheAspValIleHisLeu 379
Db 1078 GTGTGTCAACAGAACTGGACAGTAGTGGGCTCTACTCTCGCTTTGATGTATCCACCTG 1137
Qy 380 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 399
Db 1138 GCTGCCCAACAAACATACACACCTGGACATGAATGTGGGAGAGAGCCCTCAGGCGAGCGG 1197
Qy 400 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyValIle 419
Db 1198 ACATGTGTCTGGAGGGCTCTTCTTCCTGCCAGCCCGCCAGAGACCTTGGGGAGTGCATT 1257
Qy 420 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 439
Db 1258 GACCGGATTTCCGGGAAACAGGTGCACCGCTGCTGGTGTCTGCTGGATGAGACCCAGCCTT 1317
Qy 440 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 459
Db 1318 CTGGCGGTGGTGTCTCTGACATCCTTCTGAGCTCTGAGCTCTGAGCCCTGCTGGAATT 1377
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Qy 460 AspAlaLeuGlyAla 464
Db 1378 GATGCCCTCGGGGCC 1392

RESULT 15
US-11-075-134-5
; Sequence 5, Application US/11075134
; Publication No. US20050208551A1
; GENERAL INFORMATION:
; APPLICANT: Rothchild, Max
; APPLICANT: Ciohanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: Novel PKRAG3 Alleles and Use fo the Same as Genetic Markers for
; TITLE OF INVENTION: Reproductive
; TITLE OF INVENTION: and Meat Quality Traits
; FILE REFERENCE: P04668US3
; CURRENT APPLICATION NUMBER: US/11/075,134
; PRIOR FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: US/09/950,022
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1873
; TYPE: DNA
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1392)
; OTHER INFORMATION:
US-11-075-134-5

Alignment Scores:
Pred. No.: 7,36e-212 Length: 1873
Score: 2005.00 Matches: 399
Percent Similarity: 89.89% Conservative: 19
Best Local Similarity: 85.81% Mismatches: 45
Query Match: 83.44% Indels: 2
DB: 10 Gaps: 2

US-10-070-794A-30 (1-464) x US-11-075-134-5 (1-1873)

Qy 1 MetSerPheLeuGluGlnGluAsnSerSerSerTrpProSerProAlaValThrSerSer 20
Db 1 ATGAGCTTCTAGAGCAAGGAGAGCGGTCATGCGCCATCCCGAGCTGTAAACACCGAGC 60

Qy 21 SerGluArgIleArgGlyLysArgAlaLysAlaLeuArgTrpThrArgGlnLysSer 40
Db 61 TCAGAAAGAGCCATGCGGACCGAGGAAACAAAGGCCCTCTAGATGCACAGCGAGGAT 120

Qy 41 ValGluGluGlyGluProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60
Db 121 GTAGAGAGAGGGGGCCCTCGGGCCGAGGGAAGTCCCCAGTCCAGGCCCATGTTGCTGAG 180

Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspPro--- 79
Db 181 TCCACCGGGCAGGAGGCCACATTCGCCAAGGCCACACCTTGGCCCAAGCGCTCCCTTG 240

Qy 80 AlaGlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSer 99
Db 241 GCCGAGGTGGCAACACCCCAACAGAGCGGACATCTCCCTCTGACTGTGCGAGCTCA 300

Qy 100 AlaAlaGlySerSerThrAspValGluLeuAlaThrGluPheProAlaThrGluAla 119
Db 301 GCCTCCGACTCCAAACACAGACCATCTGGATCTGGGCATAGAGTTCTCAGCCCTCGGCGGC 360

Qy 120 TrpGluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGln 139
Db 361 TCGGGGGATGAGCTT---GGGCTGGTGAAGAGAGCCAGCCCGCTGCCATCCACAGAG 417

Qy 140 AlaProPheProLysLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnIleTyr 159
Db 418 GTGCTGTATACCCAGCTGGGCTGGGATGATGAGCTGCAGAAAGCCGGGGGCCACAGTCTAC 477

Qy 160 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 179
Db 478 ATGCACCTTCATGCAGGAGCACACCTGTACATGCCATGGCAGCCAGCTCCAAACTGGTC 537

Qy 180 IlePheAspThrMetLeuGluLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 199
Db 538 ATCTTCGACACCATGCTGGAGATCAAGAAGCCCTCTTTCCTGGTGGCCCAAGGGGCTC 597

Qy 200 ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 219
Db 598 CGAGCGGCACCTTTGTGGGACAGCAAGACAGAGCTTCGTGGGGATGCTGACCATCACA 657

Qy 220 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 239
Db 658 GACTTCATCTTGTGTGTCACCGCTATTACAGTCCCGCTGCTGCTCCAGATCTACAGATT 717

Qy 240 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 259
Db 718 GAAGAACATAAGATTGAGACCTGGAGGGAGATCTACCTTCAAGGCTGCTTCAAGCCCTCTG 777

Qy 260 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 279
Db 778 GTCTCCATCTCTCCCAATGACAGCTGTTCGAAGCTGTCTACGCCCTCATCAAGAACCGG 837

Qy 280 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 299
Db 838 ATCCACCGCTTGGCGTCTGGACCTGTCTCCGGGGCTGTGCTCCACATCTCCACAT 897

Qy 300 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 319
Db 898 AAGCGGCTTCTCAAGTTCTTGCCACATCTTTGGCACCTGTCTGCCCGCGCTCTCTCTC 957

Qy 320 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGlu 339
Db 958 TACCGCACCATCCCAAGATTGGGCGATCGGCACATTCGAGACTTGGCGCTGGTCTGGAA 1017

Qy 340 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 359
Db 1018 ACGCGCCCATCTGACCGCACTGGACATCTTGTGGACCGGCTGTCTGCGCTGCTCT 1077

Qy 360 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 379
Db 1078 GTGGTCAACGAAACTGGACAGGTAGTGGGCTCTCTACTCTCGCTTTGATGTGATCCACTG 1137

Qy 380 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 399
Db 1138 GCTGCCCAACAAACATACACACCATCCGATGAATGTGGGAGAGCCCTGAGCGAGCGG 1197

Qy 400 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyValIle 419
Db 1198 ACATGTGTCTGGAAGCGCTTCTTCTGCGAGCCCAAGAGACCTTTGGGGAAGTCAAT 1257

Qy 420 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 439
Db 1258 GACCGGATGCTCCGGGAACAGGTGACCGCTGGTGTCTGCTGGATGAGAGCCAGACCTT 1317

Qy 440 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 459
Db 1318 CTGGCGGTGGTGTCCCTCTCTGACATCTTTCAGGCTCTGTGTGCTCAGCCCTGTGTGAATT 1377

Qy 460 AspAlaLeuGlyAla 464
Db 1378 GATGCCCTCGGGGCC 1392

Search completed: January 26, 2006, 07:59:56
Job time : 1031.99 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 26, 2006, 03:26:13.; Search time 1080.05 Seconds
(without alignments)
356.862 Million cell updates/sec

Title: US-10-070-794A-30

Perfect score: 2403

Sequence: 1 MSFLEQNSSSWSPAVTSS.....LSDIQLVLSPAGIDALGA 464

Scoring table:

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6059551 seqs, 415333918 residues

Total number of hits satisfying chosen parameters: 12119102

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Published Applications NA New -QNT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=DIOSUM62
-TRANS=human40.cdi -LIST=45 -DALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10070794 @CGN 1 1 352 @runat 24012006 164418 8933
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-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA New:
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2: /cgn2_6/ptodata/1/pubpna/US06 NEW PUB.seq:
3: /cgn2_6/ptodata/1/pubpna/US07 NEW PUB.seq:
4: /cgn2_6/ptodata/1/pubpna/PTC NEW PUB.seq:
5: /cgn2_6/ptodata/1/pubpna/US09 NEW PUB.seq:
6: /cgn2_6/ptodata/1/pubpna/US10 NEW PUB.seq:
7: /cgn2_6/ptodata/1/pubpna/US11 NEW PUB.seq:
8: /cgn2_6/ptodata/1/pubpna/US11 NEW PUB.seq:
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11: /cgn2_6/ptodata/1/pubpna/US60 NEW PUB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1023	42.6	1628	8	US-11-136-527-2210
2	500.5	20.8	1321	7	Sequence 2210, Ap
3	500.5	20.8	1321	7	US-10-750-185-28770
4	461.5	19.2	568	8	Sequence 28770, A
5	461.5	19.2	568	8	US-11-128-061-330
6	461.5	19.2	568	8	Sequence 330, App
7	461.5	19.2	568	8	US-11-128-061-3972
					Sequence 3972, Ap
					Sequence 330, App
					Sequence 3972, Ap

Sequence 79, Appl
Sequence 851, App
Sequence 454, App
Sequence 465, App
Sequence 466, App
Sequence 38, Appl
Sequence 1, Appl
Sequence 55, Appl
Sequence 5005, Ap
Sequence 327, App
Sequence 85, Appl
Sequence 9, Appl
Sequence 17, Appl
Sequence 7, Appl
Sequence 38, Appl
Sequence 1, Appl
Sequence 955, App
Sequence 933, App
Sequence 45911, A
Sequence 82, Appl
Sequence 7875, Ap
Sequence 3779, Ap
Sequence 52488, A
Sequence 8239, Ap
Sequence 49, Appl
Sequence 6, Appl
Sequence 124, App
Sequence 75, Appl
Sequence 48, Appl
Sequence 4, Appl
Sequence 12, Appl
Sequence 37, Appl
Sequence 38, Appl
Sequence 230, App
Sequence 30, Appl
Sequence 60819, A

ALIGNMENTS

RESULT 1

US-11-136-527-2210
; Sequence 2210, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2210
; LENGTH: 1628
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2210

Alignment Scores:
Pred. No.: 7.86e-77 Length: 1628
Score: 1023.00 Matches: 196
Percent Similarity: 79.75% Conservative: 56
Best Local Similarity: 62.03% Mismatches: 64
Query Match: 42.57% Indels: 0
DB: 8 Gaps: 0
US-10-070-794A-30 (1-464) x US-11-136-527-2210 (1-1628)

Db 700 ACTCTTTGGGATCCTCTGGACTGTAGCGGTACAGGCTTCTGTCCANGGACTTCCAG 759
 Qy 375 -----AapValIleHisLeuAlaAala 381
 Db 760 GCAAGAACACTAGAGTGGGTACCATTCTCTTCAGTGATGTATCCATCAGGCAGCA 819
 Qy 382 GlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThrLeu 401
 Db 820 TAAAGATCTACCAACACCTAGATGTGCTGTAGTCAAGGCCCTGAAAAATCGATCACAG 879
 Qy 402 CysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAspArg 421
 Db 880 TACTTTAAATGACTTCAAGTCGACCTGATGAGGCTCTGGAGACTTCTCAGCAGG 939
 Qy 422 IleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuGly 441
 Db 940 CTAGTGAAGCAGGAGTCAACCGACTCGTGGTGGTGGATGAGATGTGATCAAGGGA 999
 Qy 442 ValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSer 455
 Db 1000 ACTGTATACCATCTGTCTCCTGTAGACCCCTGGTGTCTACA 1041

RESULT 3

US-10-750-623-28770
 ; Sequence 28770, Application US/10750623
 ; Publication No. US20050287531A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MMI GENOMICS, INC.
 ; APPLICANT: DENISE, Sue K.
 ; APPLICANT: KERR, Richard
 ; APPLICANT: ROSENFELD, David
 ; APPLICANT: HOLM, Tom
 ; APPLICANT: BATES, Stephen
 ; APPLICANT: FANTIN, Dennis
 ; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
 ; FILE REFERENCE: MM1100-1
 ; CURRENT APPLICATION NUMBER: US/10750,623
 ; PRIOR FILING DATE: 2003-12-31
 ; PRIOR FILING DATE: 2003-12-31
 ; PRIOR FILING DATE: 2002-12-31
 ; NUMBER OF SEQ ID NOS: 64922
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 28770
 ; LENGTH: 1321
 ; TYPE: DNA
 ; ORGANISM: Bovine 19866880603844
 US-10-750-623-28770

Alignment Scores:

Pred. No.: 1.57e-32 Length: 1321
 Score: 500.50 Matches: 136
 Percent Similarity: 53.27% Conservative: 43
 Best Local Similarity: 40.48% Mismatches: 89
 Query Match: 20.83% Indels: 69
 DB: 7 Gaps: 5

US-10-070-794A-30 (1-464) x US-10-750-623-28770 (1-1321)

Qy 168 CysTyrAspAlaMetAlaThrSerSerLysLeuValIlePheAspThrMetLeuGluIle 187
 Db 101 TGTATGACCTGAGTCTCACAAGCTCCAAATTTGGTGTATTTGTCTACTTCCCTGCAGGTA 160
 Qy 188 LysLysAlaPhePheAlaLeuValAlaAsnGlyValAlaProLeu-TrpAspSe 207
 Db 161 TACAG-----TTGCCCTTCTGGATAC 184
 Qy 207 rLysLysGlnSerPheValGlyMetLeuThrIleThrAspPheIleLeuValLeuHisAr 227
 Db 185 TAAAGAACAGGAGCTTGTGGCATTGATATACCAATTTTCATCAATATCTGCACTA 244
 Qy 227 gTyrTyrArgSerProLeuVal-GlnIleTyrGluIleGluGlnHisLysIleGluThrT 247
 Db 245 TTACTATATGACGCTTGGTTCAGAGCTATGAGCTGGGAAGATACAAAATAGAACTT 304

Qy 247 rPargGluIleTyrLeuGlnGlyCysPheLysProLeuValSerIleSerProAsnAsps 267
 Db 305 GAAAGAGGTGTATATACAGGACTCTTTAAACACCATTGTCTGCTATTTCTTCTTAATGCCA 364
 Qy 267 erLeuPheGluAlaValTyrThrIleLysAsnArgIleHisArgLeuProValLeuA 287
 Db 365 ACTTGTATATGCTGTCTTTTCATTAATTCAGAACAGATCCACAGGCTGCCAGTTGTTG 424
 Qy 287 spProValSerGlyAsnValLeuHisIleLeuThrHisLysArgLeuLysPheLeuH 307
 Db 425 ACCAGATACAGCAACATCTTGTACACCTCCACCAAGTGCATTTCTATGTTCTCTCA 484
 Qy 307 islePheGlySerLeuLeuProArgProSerPheLeuTyrArgThr-IleGlnAspLeu 326
 Db 485 AAGTGTATACCTAGAGCTCTT-AAGCCAGAAATTCATGTCTAAGTCTTAATAGAAGAT--- 540
 Qy 327 GlyIleGlyThrPheArgAspLeuAlaValValLeuGluThrAlaProIleLeuThAla 346
 Db 541 -----TAGCTTCTATGCCAGCATTTGCCATGTTCTGCATCTATGACCCCTGACACGGCT 594
 Qy 347 LeuAspIlePheValAspArgArgValSerAlaLeuProValValLeuGluCysGlyGln 366
 Db 595 CTGGCATC-----TCTGTACAGGATCTGCCA---GTGAATGAGGAAGGTCAG 639
 Qy 367 ValValGlyLeuTyrSerArgPhe----- 374
 Db 640 GTGGTGAACATCTATTCCACATTTGATGTTATCTGTGCTAAGTCACCTTTCAGTCAGCTCCA 699
 Qy 374 ----- 374
 Db 700 ACTCTTTGGGATCCTCTGGACTGTAGCGGTACAGGCTTCTGTCCATGGGACTTCCAG 759
 Qy 375 -----AapValIleHisLeuAlaAala 381
 Db 760 GCAAGAACACTAGAGTGGGTACCATTCTCTTCAGTGATGTATCCATCAGGCAGCA 819
 Qy 382 GlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThrLeu 401
 Db 820 TAAAGATCTACCAACACCTAGATGTGCTGTAGTCAAGGCCCTGAAAAATCGATCACAG 879
 Qy 402 CysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAspArg 421
 Db 880 TACTTTAAATGTAGCTTCAAGTCCGACCTGTCATGAGGCTCTGGAGACCTTTCTCAGCAGG 939
 Qy 422 IleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuGly 441
 Db 940 CTAGTGAAGCAGGAGTCAACCGACTCGTGGTGGTGGATGAGATGTGATCAAGGGA 999

RESULT 4

US-11-128-061-330
 ; Sequence 330, Application US/11128061
 ; Publication No. US20060003958A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Melville, Mark W.
 ; APPLICANT: Charlebois, Timothy S.
 ; APPLICANT: Mounts, William M.
 ; APPLICANT: Hann, Louane E.
 ; APPLICANT: Sinacore, Martin S.
 ; APPLICANT: Leonard, Mark W.
 ; APPLICANT: Brown, Eugene L.
 ; APPLICANT: Miller, Christopher P.
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
 ; FILE REFERENCE: 01997,027701
 ; CURRENT APPLICATION NUMBER: US/11/128,061
 ; CURRENT FILING DATE: 2005-05-11
 ; PRIOR APPLICATION NUMBER: US 60/570,425
 ; PRIOR FILING DATE: 2004-05-11

```
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 330
; LENGTH: 568
; TYPE: DNA
; ORGANISM: Cricetulus griseus
; US-11-128-061-330

Alignment Scores:
Pred. No.: 9.77e-30 Length: 568
Score: 461.50 Matches: 104
Percent Similarity: 59.32% Conservative: 36
Best Local Similarity: 44.07% Mismatches: 40
Query Match: 19.21% Indels: 57
DB: 8 Gaps: 2

US-10-070-794A-30 (1-464) x US-11-128-061-330 (1-568)

Qy 221 PheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGlu 240
Db 3 TTTATCAACATCTCTGCACCGATCTATAAGTCGCGCTTGGTGCAGATCTATGAACCTGAA 62
Qy 241 GlnHisIleValLeuThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeuVal 260
Db 63 GAACACAGATAGAAACTTGGAGAGAGTATACCTACAGGACTCTTTAGCCCTTGTGTC 122
Qy 261 SerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIle 280
Db 123 TGCATTTCTCCAAATGC-CAGATCACTGAG----- 151
Qy 281 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 300
Db 151 ----- 151
Qy 301 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 320
Db 152 -----TTCCCAAGCCAGAAATTCATGTC 175
Qy 321 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGluThr 340
Db 176 AAGTCTCTGGAAGAGCTACAGATTGGCACCCTATGCCAACATTCGTATGTCCTGCTACTACC 235
Qy 341 AlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProVal 360
Db 236 ACACCTGTCTATGTGGCTCTAGGCATCTTTGTACAGACCAGAGCTCTGCGCTGCTGTG 295
Qy 361 ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIle-HisLeuAl 380
Db 296 GTGATGAG-----AAAGAATTGGC 316
Qy 380 aAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgTh 400
Db 317 AGCAGAAAAGACCTATACAACTCGATATATCTGTGACAAAAGCTCTACAAACACCGGTC 376
Qy 400 rLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAs 420
Db 377 TCACCTACTTTGAGGGTGTCTCAAGTGTCTATCTACAGGAGACTCTGGAGACTATCATTA 436
Qy 420 PArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLe 440
Db 437 TAGACTGTGTGAGCAGAGGTTTACCGTCTGCTGTGGTGTGGATGAGACGAGTGTGTC 496
Qy 440 uGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSer 455
Db 497 GGGCATCGTATCGCTGTCGATATCTCGAGGCTCTGCTGTGCTCACA 542

RESULT 5
US-11-128-061-3972
; Sequence 3972, Application US/11128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
```

```
Db 437 TAGACTGTGGAGCAGAGTTTACCGTCTCGGTGGTGGATGAGAACGACGTGGTCAA 496
Qy 440 uGlyValSerLeuSerAspIleLeuGlnAlaLeuValLeuSer 455
Db 497 GGGCATCGTATCGTGTCCGATATCCTGCAGGCTCTGGTGTCTACA 542

RESULT 6
US-11-128-049-330
; Sequence 330, Application US/111128049
; Publication No. US20060010513A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR
; FILE REFERENCE: 01997.027700
; CURRENT APPLICATION NUMBER: US/11/128,049
; PRIOR FILING DATE: 2005-05-11
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 330
; LENGTH: 568
; TYPE: DNA
; ORGANISM: Cricetus griseus
US-11-128-049-330

Alignment Scores:
Pred. No.: 9.77e-30 Length: 568
Score: 461.50 Matches: 104
Percent Similarity: 59.32% Conservative: 36
Best Local Similarity: 44.07% Mismatches: 40
Query Match: 19.21% Indels: 57
DB: 8 Gaps: 2

US-10-070-794A-30 (1-464) x US-11-128-049-330 (1-568)
Qy 221 PheileuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluileGlu 240
Db 3 TTATCAACATCTGCGACCGATCTATAAGTCGGCTTGGTGAGATCTATGACTGAA 62
Qy 241 GlnHisLysIleGluThrTrpArgGluileTyrLeuGlnGlyCysPheLysProLeuVal 260
Db 63 GAACACAGATAGAACTTGGAGAGAGGTATACCTACAGACTCTCTTTAAGCCCTTGTC 122
Qy 261 SerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuileLysAsnArgIle 280
Db 123 TGCATTTCTCCAAATGC-CAGATCACTGAG----- 151
Qy 281 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 300
Db 151 ----- 151
Qy 301 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 320
Db 152 -----TTCCCAAGCCAGAAATTCATGTCT 175
Qy 321 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGluThr 340
Db 176 AAGTCTTGAAGAGCTACAGATTGGCACTATGGCAACATTGCTATGGTCCGTACTACC 235
Qy 341 AlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProVal 360
Db 236 ACACCTGTCTATGGCTTAGGCACTTTGTACAGACCGAGTCTCTGCCCTCGCTGTG 295
Qy 361 ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIle-HisLeuAl 380
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Db 296 GTGCATGAG-----AAAGAATTTGGC 316
Qy 380 aAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgTh 400
Db 317 AGCAGAAAAGACCTATAACACCTGGATATATCTGTGACAAAGCTCTACAAACCCGTC 376
Qy 400 rLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAs 420
Db 377 TCACACTTTGAGGGTGTCTCAAGTGTCTATCTACAGAGACTCTGGAGACTATCATTA 436
Qy 420 pArgIleAlaArgGlnGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLe 440
Db 437 TAGACTGTGGAGACGAGAGGTTCACCGTCTGGTGGTGGATGAGAACGACGTGGTCAA 496
Qy 440 uGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSer 455
Db 497 GGGCATCGTATCGTGTCCGATATCTGCAGGCTCTGGTGTCTACA 542
```

RESULT 7

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US-11-128-049-3972
; Sequence 3972, Application US/111128049
; Publication No. US20060010513A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR
; FILE REFERENCE: 01997.027700
; CURRENT APPLICATION NUMBER: US/11/128,049
; PRIOR FILING DATE: 2005-05-11
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3972
; LENGTH: 568
; TYPE: DNA
; ORGANISM: Cricetus griseus
US-11-128-049-3972
```

```
Alignment Scores:
Pred. No.: 9.77e-30 Length: 568
Score: 461.50 Matches: 104
Percent Similarity: 59.32% Conservative: 36
Best Local Similarity: 44.07% Mismatches: 40
Query Match: 19.21% Indels: 57
DB: 8 Gaps: 2
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US-10-070-794A-30 (1-464) x US-11-128-049-3972 (1-568)

```
Qy 221 PheileuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluileGlu 240
Db 3 TTATCAACATCTGCGACCGATCTATAAGTCGGCTTGGTGAGATCTATGACTGAA 62
Qy 241 GlnHisLysIleGluThrTrpArgGluileTyrLeuGlnGlyCysPheLysProLeuVal 260
Db 63 GAACACAGATAGAACTTGGAGAGAGGTATACCTACAGACTCTCTTTAAGCCCTTGTC 122
Qy 261 SerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuileLysAsnArgIle 280
Db 123 TGCATTTCTCCAAATGC-CAGATCACTGAG----- 151
Qy 281 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 300
Db 151 ----- 151
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Qy 301 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 320
Db 152 -----TTCCCAAGCCAGAAATTCATGCT 175
Qy 321 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGluThr 340
Db 176 AAGTCTCTGGAGAGCTACAGATTGGACCTATCCACATGCTATGTTCCGTACTACC 235
Qy 341 AlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProVal 360
Db 236 ACACCTGTCTATGTGGCTCTAGGCATCTTTGTACAGACCGAGTCTCTGCCCTGCCTGTG 295
Qy 361 ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIle-HisLeuAl 380
Db 296 GTGGATGAG-----AAGAATTTGGC 316
Qy 380 aAlaGlnGlnThrTyrZnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgTh 400
Db 317 AGCAGAAAGACCTATACACCTGGATATATCTGTGACAAAGCTCTACACACCGGTC 376
Qy 400 rLeuCysLeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValIleAs 420
Db 377 TCACCTACTTTCAGGGTGTCTCAAGTGTCTATCTACAGGAGACTCTGGAGACTATCAATAA 436
Qy 420 pArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLe 440
Db 437 TAGACTGGTGAAGCAGAGAGGTTCACCGCTCTGGTGGTGGATGAGAACGACGTGGTCAA 496
Qy 440 uGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSer 455
Db 497 GGGCATCGTATCGCTGCCGATATCTCGACGGCTCTGGTGTCTACA 542

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RESULT 8

```

US-11-041-776-79
; Sequence 79, Application US/11041776
; Publication No. US20050272057A1
; GENERAL INFORMATION:
; APPLICANT: ABRAHAMSEN, MITCHELL
; APPLICANT: FREIJE, WADIHA
; TITLE OF INVENTION: SMALL SEGMENTS OF DNA DETERMINE ANIMAL IDENTITY AND
; TITLE OF INVENTION: SOURCE
; FILE REFERENCE: 34579-97951
; CURRENT APPLICATION NUMBER: US/11/041,776
; CURRENT FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: 60/538,791
; PRIOR FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: 60/539,728
; PRIOR FILING DATE: 2004-01-26
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 79
; LENGTH: 1500
; TYPE: DNA
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1500)
; OTHER INFORMATION: nucleotides 1501-3000 of PRKAG_STS3
US-11-041-776-79

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Alignment Scores:
Pred. No.: 7.85e-10 Length: 1500
Score: 234.50 Matches: 97
Percent Similarity: 25.28% Conservative: 16
Best Local Similarity: 21.70% Mismatches: 46
Query Match: 9.76% Indels: 290
DB: 8 Gaps: 6

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US-10-070-794A-30 (1-464) x US-11-041-776-79 (1-1500)

```

Qy 84 ThrProProThrGlyTyrPheCysLeuProSerAspCysThrAlaSerAlaAlaGlySer 103
Db 71 ACACCTTGGAGTGTCTGGGAGGGGTACCTCAGYACCTCTGGCCACGACGCTTAGA 130

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Qy 104 SerThrAspAspValGluLeuAlaThrGluPheProAlaThrGlu-AlaTyrGluCysG1 123
Db 131 TCTGGAAACAATGTGACACAGATCTCTGTGAGGCGATGCCAGNAGCTGGGAGAGGCA 190
Qy 123 uLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGlnAlaPro-PheP 143
Db 191 GACAGCAGGCTCATGTAGAGGCGAGGCGCGG-----AGGCGCGCGGTGGA 235
Qy 143 roLysLeuGlyTyrAspAspGluLeuArgLysProGlyAlaGlnIleTyrMetArgPheM 163
Db 236 AGAACCTCTGCTGGCAGGCGGACCTCTGAGGCGCAGGGAACG---ATTACACCTCAA--- 288
Qy 163 etGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValIlePheAspT 183
Db 289 -----CTGTTCTCTC 298
Qy 183 hrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyValArgAlaAlap 203
Db 299 CGGCGCTCAG-ATCAAGAAGGCTCTTCTTGTGGTGGCCAACGGCTCCGAGCGGCAC 357
Qy 203 roLeuTyrAspSerLysLysGlnSerPheVal----- 213
Db 358 CTTTGTGGGACAGCAAGACAGAGCTTCGTGGGTGAGAGGGGCTCGGGAGGAGGAGGT 417
Qy 213 ----- 213
Db 418 GYGGGGAAGGAATAGGGGRACCTTGTGGGTGATTCTTAGGGCCGAGCTCTGACAYACC 477
Qy 213 ----- 213
Db 478 ACAGGCTTSAACCAAGCAGGCGCTCGCTTGGRRSCGGAGGAGCATVTGACCCCGGT 537
Qy 213 ----- 213
Db 538 CTCCYGTGGCCRCGTGGGAGATCTCAACTGTAGGAGAGCTGTGACCAGCTGACCCCTCC 597
Qy 213 ----- 213
Db 598 AGCTCTACTACCCCAAGTCCCTCTCGCAGGTGCTTAAGTAAGAGAGACAGCGGAGGA 657
Qy 213 ----- 213
Db 658 AGGAAGTCAGAAAANTAGAAGAAGCAGGCGCAGGAAGAGAGAGAAATCAACAGGGGAAGCATAA 717
Qy 213 ----- 213
Db 718 GAGGGACAACCCCATTTTTCAGGCACGCGGAGGGGCTGCCCTCTCTCTCTTTTGGCCAC 777
Qy 213 ----- 213
Db 778 CCTCAGTAAAGGATGTGGGCGAGGCTGGGGGAGGGGCGCGGCTGACCCCATTTGCTCC 837
Qy 214 -----GlyMetLeuThrIleThrAspPheIleLeuValLeuHisA 227
Db 838 CCCCYTTTGGCCCCSYACAGSGATGCTGACCATCACAGACTTCATCTTGTGTCTGCACC 897
Qy 227 rGlyTyrArgSerProLeu----- 233
Db 898 GCTATTACAGGTCCCGCCCT-GGTGAGGAGTGTCTTGGGGGTCTTGGGAACACCCATCTGGG 956
Qy 233 ----- 233
Db 957 CTGGGTGGAAGGAGTTTACAGGGGACCTCGCTGACTTTTGGGAGTTCCGTTGCTGCTTT 1016
Qy 234 --ValGlnIleTyrGluIleGluGlnHisLysIleGluThrTyrParg----- 248
Db 1017 AGGTCCAGATCTACGAGATTGAAGAAATAAGATTGAGACCTTGGAGGGGTGAGCAGGCGA 1076
Qy 248 ----- 248
Db 1077 GGGGACSGKGAAGGGGCTGAGGGGTGTGTGGGTGAGGTGTRGGCCAGCAAGACCTCAGGGAG 1136

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QY 248 ----- 248
Db 1137 AGCATGCCAGTGCAGGTTTCTCGAGGAAGCGGGAGGAGGTTGATCGGAGCCAGGG 1196
QY 248 ----- 248
Db 1197 ATCTAAGGAGGAGACAGTCTGGGTGGCCACCTGAGCGGGGTGGTGGCCCTTTG 1256
QY 249 -----
Db 1257 TGCTGATTCCTGCTCGACAGATCTACCTTCAAGGCTGCTTCAAGGCTCTGCT 1316
QY 261 erlleSerProAsnAsp 266
Db 1317 CCATCTCTCCCAATGAC 1333

RESULT 9
US-11-000-688-851
; Sequence 851, Application US/11000688
; Publication No. US20050287544A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, Francois
; APPLICANT: HOULGATTE, Remi
; APPLICANT: BIRNBAUM, Daniel
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS
; FILE REFERENCE: 1423-K-03
; CURRENT APPLICATION NUMBER: US/11/000,688
; CURRENT FILING DATE: 2004-12-01
; PRIOR APPLICATION NUMBER: US 60/525,987
; PRIOR FILING DATE: 2003-12-01
; NUMBER OF SEQ ID NOS: 1596
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 851
; LENGTH: 3439
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial sequences: primer
; NAME/KEY: misc feature
; LOCATION: (1)-(3439)
; OTHER INFORMATION: collagen, type vi, alpha 2(COL6A2) gene.
US-11-000-688-851

Alignment Scores:
Pred. No.: 50 Length: 3439
Score: 113.50 Matches: 44
Percent Similarity: 39.74% Conservative: 16
Best Local Similarity: 29.14% Mismatches: 52
Query Match: 4.72% Indels: 39
DB: 8 Gaps: 8

US-10-070-794A-30 (1-464) x US-11-000-688-851 (1-3439)
QY 14 SerProAlaValThrSerSerGluArgIleArgGlyLysArgAlaLysAlaLeu 33
Db 1128 GCCCCGACGGTTACCCGGGGAAGCAGGAGTCCAGGGAGCCAGGACCAAGGGCGCA 1187
QY 34 ArgTrpThrArgGlnLysSerValGluGluGlyProGlyGlnGlyGluGlyPro 53
Db 1188 AGGGGACC-----CTGGCCCGCCAGGACGAGGGCCCCCGGAGAAATCGGGGCCA 1241
QY 54 ArgSerArgProThrAlaGluSerThrGlyLeuGluAlaThrPheProLysThrPro 73
Db 1242 AGG-----GAAGCAAGGGGTATCAAGGCAACATGGAGCCCGAGGAATC 1286
QY 74 LeuAlaGlnAlaAspPro-----AlaGlyValGlyThrProThrGlyTrpAspCysLeu 92
Db 1287 CTGCTGTGAAGGAGGACCAAGGGGGCTGGGC----- 1319
QY 93 ProSerAspCysThrAlaSerAlaAlaGlySerThrAspValGlu----- 109
Db 1320 CCGGGGACCAAGGCGAGCGGGGCGCAGGGGAGACCCCGCACCAAGGGGAGCCCGCAG 1379
```

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QY 110 -----LeuAlaThrGluPheProAlaThrGlu 118
Db 1380 GCAGCGATGCCCCCAAGGGGGAAGAGGACCTGGCCCTGTAGGGCCCCCGCG----- 1433
QY 119 AlaTrpGluCysGluLeuGluGlyLeuLeuGluGluArgPro-----AlaLeuCys 135
Db 1434 GCCTGG-----CTGGAGAGGTTGGCAACAAGAGGACCAAGGAGACCGAGGCTTGC 1484
QY 136 LeuSerProGlnAlaProPheProLysLeuGly 146
Db 1485 CTGACCCAGAGGCCCCCAGGGAGCTCTTGGGG 1517

RESULT 10
US-10-995-561-464
; Sequence 464, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 464
; LENGTH: 3175
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-464

Alignment Scores:
Pred. No.: 80.2 Length: 3175
Score: 110.50 Matches: 44
Percent Similarity: 39.07% Conservative: 15
Best Local Similarity: 29.14% Mismatches: 53
Query Match: 4.60% Indels: 39
DB: 7 Gaps: 8

US-10-070-794A-30 (1-464) x US-10-995-561-464 (1-3175)
QY 14 SerProAlaValThrSerSerGluArgIleArgGlyLysArgAlaLysAlaLeu 33
Db 1159 GCCCCGACGGTTACCCGGGGAAGCAGGAGTCCAGGGAGCCAGGACCAAGGGCGCA 1218
QY 34 ArgTrpThrArgGlnLysSerValGluGluGlyGluProGlyGlnGlyGluGlyPro 53
Db 1219 AGGGGACC-----CTGGCCCGCCAGGACGAGGGCCCCCGGAGAAATCGGGGCCA 1272
QY 54 ArgSerArgProThrAlaGluSerThrGlyLeuGluAlaThrPheProLysThrPro 73
Db 1273 AGG-----GAAGCAAGGGGTATCAAGGCAACARTGGAGCCCGAGGAATC 1317
QY 74 LeuAlaGlnAlaAspPro-----AlaGlyValGlyThrProThrGlyTrpAspCysLeu 92
Db 1318 CTGCTGTGAAGGAGGACCAAGGGGGCTGGGC----- 1350
QY 93 ProSerAspCysThrAlaSerAlaAlaGlySerThrAspValGlu----- 109
Db 1351 CCGGAGACCAAGGCGAGCGGGGCGAGAGCCCGGAGGAGACCCCGCACCAAGGAGCCCGCAG 1410
QY 110 -----LeuAlaThrGluPheProAlaThrGlu 118
Db 1411 GCAGCGATGCCCCCAAGGGGGAAGAGGAGCCCTGGCCCTGTAGGGGGCCCCCGCG----- 1464
QY 119 AlaTrpGluCysGluLeuGluGlyLeuLeuGluGluArgPro-----AlaLeuCys 135
Db 1465 GCCTGG-----CTGGAGAGGTTGGCAACAAGGAGGACCAAGGAGGAGCGGAGGCTTGC 1515
QY 136 LeuSerProGlnAlaProPheProLysLeuGly 146
Db 136 LeuSerProGlnAlaProPheProLysLeuGly 146
```

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Db 1516 CTGGACCCAGAGGCCCCCAGGAGCTCTTGGG 1548
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 466
; LENGTH: 3468
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-995-561-466

Alignment Scores:
Pred. No.: 91 Length: 3468
Score: 110.50 Matches: 44
Percent Similarity: 39.07% Conservative: 15
Best Local Similarity: 29.14% Mismatches: 53
Query Match: 4.60% Indels: 39
DB: 7 Gaps: 8

US-10-070-794A-30 (1-464) x US-10-995-561-466 (1-3468)
Qy 14 SerProAlaValThrSerSerGluArgIleArgGlyLysArgAlaLysAlaLeu 33
Db 1159 GCCCGACGGTTACCCGGGGGAAGCAGGAGTCCAGGGGAGCGAGGAGCAAGCGCGCA 1218
Qy 34 ArgTrpThrArgGlnLysSerValGluGluGlyProProGlyGlnGlyGluGlyPro 53
Db 1219 AGGGGGACC-----CTGGCGCCCGCAGGAGCGAGGCGGCCCGGGAGAAATCGGGGCCA 1272
Qy 54 ArgSerArgProThrAlaGluSerThrGlyLeuGluAlaThrPheProLysThrPro 73
Db 1273 AGG-----GAAGCAAGGGGTATCAAGGCAACARTGGAGCCCGAGGAAGTC 1317
Qy 74 LeuAlaGlnAlaAspPro---AlaGlyValGlyThrProProThrGlyTrpAspCysLeu 92
Db 1318 CTGGTGTGAAGGAGCCAAAGCGCGGCTCTGGC----- 1350
Qy 93 ProSerAspCysThrAlaSerAlaAlaGlySerSerThrAspValGlu----- 109
Db 1351 CCCGYGACCCAAAGCGAGCGCGGCGCGAGAGACCCCGGACCAAGGGCAGCCAG 1410
Qy 110 -----LeuAlaThrGluPheProAlaThrGlu 118
Db 1411 GCAGCGATGCGCCCAAGGGGAGAGGGGACCTGGCCCTGAGGGGCCCGCG----- 1464
Qy 119 AlaTrpGluCysGluLeuGluGlyLeuLeuGluGluArgPro-----AlaLeuCys 135
Db 1465 GCCTGG-----CTGGAGAGGTGGCAACAAGAGGAGCCAAAGGAGACCGAGGCTTGC 1515
Qy 136 LeuSerProGlnAlaProPheProLysLeuGly 146
Db 1516 CTGGACCCAGAGGCCCCCAGGAGCTCTTGGG 1548

RESULT 13
US-11-075-185-38/c
; Sequence 38, Application US/11075185
; Publication No. US2005026434A1
; GENERAL INFORMATION:
; APPLICANT: REEVES, CHRISTOPHER D
; APPLICANT: JULIEN, BRYAN
; APPLICANT: REID, RALPH
; TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FOR AMBRUTICINS
; FILE REFERENCE: 010099.03
; CURRENT APPLICATION NUMBER: US/11/075,185
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/551,103
; PRIOR FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: US 60/568,290
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38
; LENGTH: 6594

Db 1516 CTGGACCCAGAGGCCCCCAGGAGCTCTTGGG 1548
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 465
; LENGTH: 3464
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-995-561-465

Alignment Scores:
Pred. No.: 90.8 Length: 3464
Score: 110.50 Matches: 44
Percent Similarity: 39.07% Conservative: 15
Best Local Similarity: 29.14% Mismatches: 53
Query Match: 4.60% Indels: 39
DB: 7 Gaps: 8

US-10-070-794A-30 (1-464) x US-10-995-561-465 (1-3464)
Qy 14 SerProAlaValThrSerSerGluArgIleArgGlyLysArgAlaLysAlaLeu 33
Db 1159 GCCCGACGGTTACCCGGGGGAAGCAGGAGTCCAGGGGAGCGAGGAGCAAGCGCGCA 1218
Qy 34 ArgTrpThrArgGlnLysSerValGluGluGlyProProGlyGlnGlyGluGlyPro 53
Db 1219 AGGGGGACC-----CTGGCGCCCGCAGGAGCGAGGCGGCCCGGGAGAAATCGGGGCCA 1272
Qy 54 ArgSerArgProThrAlaGluSerThrGlyLeuGluAlaThrPheProLysThrPro 73
Db 1273 AGG-----GAAGCAAGGGGTATCAAGGCAACARTGGAGCCCGAGGAAGTC 1317
Qy 74 LeuAlaGlnAlaAspPro---AlaGlyValGlyThrProProThrGlyTrpAspCysLeu 92
Db 1318 CTGGTGTGAAGGAGCCAAAGCGCGGCTCTGGC----- 1350
Qy 93 ProSerAspCysThrAlaSerAlaAlaGlySerSerThrAspValGlu----- 109
Db 1351 CCCGYGACCCAAAGCGAGCGCGGCGCGAGAGACCCCGGACCAAGGGCAGCCAG 1410
Qy 110 -----LeuAlaThrGluPheProAlaThrGlu 118
Db 1411 GCAGCGATGCGCCCAAGGGGAGAGGGGACCTGGCCCTGAGGGGCCCGCG----- 1464
Qy 119 AlaTrpGluCysGluLeuGluGlyLeuLeuGluGluArgPro-----AlaLeuCys 135
Db 1465 GCCTGG-----CTGGAGAGGTGGCAACAAGAGGAGCCAAAGGAGACCGAGGCTTGC 1515
Qy 136 LeuSerProGlnAlaProPheProLysLeuGly 146
Db 1516 CTGGACCCAGAGGCCCCCAGGAGCTCTTGGG 1548

RESULT 12
US-10-995-561-466
; Sequence 466, Application US/10995561
; Publication No. US2005027054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; DETECTION AND USES THEREOF
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TYPE: DNA
 ORGANISM: Sorangium cellulosum
 US-11-075-185-38

Alignment Scores:

Pred. No.: 277 Length: 6594
 Score: 109.50 Matches: 126
 Percent Similarity: 34.36% Conservative: 74
 Best Local Similarity: 21.65% Mismatches: 196
 Query Match: 4.56% Indels: 186
 DB: 8 Gaps: 29

US-10-070-794A-30 (1-464) x US-11-075-185-38 (1-6594)

Qy 7 GluAenSerSerSerpProAlaValThrSerSerSerGluArgileArgly 26
 Db 5845 GAACGCTCCGAGACACCCAGTCCGACTCGAGCGTCTCGAGCGAGCAATCCGAGT 5786
 Qy 27 LysArgArgAlaLysAlaLeuArg----- 34
 Db 5785 GGTCCGACGTTCGCTTCGAGCTCGCGCGCGCGCTTCGCCGAACGGAATCGACGG 5726
 Qy 35 -----TTPThrArgGlnLysSerValGluGluGluProProGlyGlnGlyGlu 51
 Db 5725 CGATCACCTTGGACACAGGCGAGCTCTCCAGCA-----GGGCTTCAGCGCGCGCGG 5672
 Qy 52 GlyProArgSerArgProThrAlaGluSerThr-----GlyLeu 64
 Db 5671 GCTCCGCGTTCGACACCAACGCCCGCGCGGTGAAGATGGGGCTCCCTTGAGGACGA 5612
 Qy 65 GluAlaThrPheProLysThrThrProLeuAlaGlnAlaPheProAlaGlyValGlyThr 84
 Db 5611 GCAGCGCGGAGCCCTCTCTCGCGCGAGCGAGCCCGAGCTTCACGCGG-----TCTCGA 5558
 Qy 85 ProProThr-GlyTrpAspCysLeuProSerAspCysThrAlaSerAlaLagLysSerSe 104
 Db 5557 CCGCGCTCGCGG-----GCCCGCGCGGGAAGA 5528
 Qy 104 rThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTrpGluCysGluLe 124
 Db 5527 CCGCGCGGAAGTCCGTCTCGCGCGGTATCGCGCG----- 5494
 Qy 124 uGluGlyLeuLeuGluArgProAlaLeuCysLeuSerProGlnAlaProPheProLys 144
 Db 5493 -----CTCAGATCCGCCAGTAGTC-----CCTCGTATGT 5462
 Qy 144 sLeuGlyTrpAspAspGluLeuArgLysProGlyValaGlnLileTrpMetArgPheMetG1 164
 Db 5461 CGTGGGTGCCAGGACCACTCGCGCATCTCGGAGCGCGGTGCGCCCTCGAAACGACCGCG 5402
 Qy 164 nGluHis-----ThrCysTrpAspAlaMe 172
 Db 5401 TCGTCACGAGGTACAGTTGATGACCCGCGCGAGCTTCGTCATCTCGTCTCATCTCAT 5342
 Qy 172 tAlaThrSerSerLysLeuValIlePheAspThrMetLeuGluLeuLysLysAlaPheP 192
 Db 5341 AGCCGCGTCCGCGCGTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 5290
 Qy 192 eAlaLeuValAlaasnGlyValArgAlaAlaProLeuTrpAspSerLysLysGlnSerPh 212
 Db 5289 -CGACTCCAGAGACACGGGGTTCATAGCTCCGCTCGGTCGCTCCGCGCGCGGTGAT 5231
 Qy 212 eValGlyMetLeuThrIleThrAspPheIleLeuValLeuHisArgTrpTrpArgSerPr 232
 Db 5230 CCAGCGCGATCCGCGCGAGGTTCGCGGTGTGTCTGTCACGACCGCGCGGATCGCC 5171
 Qy 232 oLeuValGlnLileTrpGluLeuGlnHisLysLysLysLysLysLysLysLysLysLys 252
 Db 5170 G-----CAGGATGTCTCTCCCTCAGCGGTGAGCGCGCGCGCGCGCGCGCGCGCG 5123
 Qy 252 uGlnGlyCysPheLysProLeuValSerLileSer---ProAsnAspSerLeuPheGluAl 271
 Db 5122 CCGGGACTCGCACCGCAACTCTCTCGCGGTGGCGCGTCCACACCGCGCTCTCATGGAAGC 5063

Qy 271 aValTyThr-----LeuLysAsn-- 278
 Db 5062 GCCGTATCGCGCACACGCCGAAACCGCAGCTCGAAACCGAGCGATCGCTCGTCGAGCACCA 5003
 Qy 279 -----ArgIleHisArgLeuProValLeuLeuAspProValSerGlyAsnValLeuHisI1 296
 Db 5002 CGACGTTCAGCGCTTCGAGCGCGAGCTTCGCCGAGACGAGCTCGCGGTTCGCGGTGACGT 4943
 Qy 296 eLeuThrHisLys-----ArgLeu----- 302
 Db 4942 CTCGAGCACGACACGATCCCGCGCGCGGCGACTCCGCGCGCGACCTCTCGAGGGTGG 4883
 Qy 303 -----LeuLysPheLeuHisIlePheGlySerLeuLeuProAr 315
 Db 4882 CGTCATCGCATCGGTGACGTACGCGCGCGCGAGCTCTCTCGCGCT---CTCGACGA 4826
 Qy 315 gProSerPheLeuTyArgThrIleGlnAspLeuGlyLileGlyThrPheArgAspLeuAl 335
 Db 4825 GCCGAGCAGCTCGCGGATTCGCCACAGATTCAGATCGGGGAAGCGCGCTCTCG 4766
 Qy 335 aValValLeuGluThrAlaProIleLeuThrAlaLeuAspIlePheValAspArg---Ar 354
 Db 4765 GGAGAACTCGAA---ATGCCGCGGAGAGCTCTCTCGGATCGAGACGAGCTCTTCG 4709
 Qy 354 gValSerAlaLeuPro-----ValValas 362
 Db 4708 CGTCGCGCGAGCCCTCGAGAGCTTTGCCGCGCGGTTCGAAACCGCAGCGCTCGTGA 4649
 Qy 362 n-----GluCysGlyGln-----ValValGlyLeuTySerArgPheAspVa 376
 Db 4648 CCGCTCGAGCGCGCGAGCATGAAGAAGCAGTGTGTAGGGGCTCTCGCGCGCTTC- 4594
 Qy 376 lIleHisLeuAlaGlnGlnThrTyAsnHisLeu----- 388
 Db 4593 -----CTGCTCGCTCAGGAGCGGTGAGCAATAGCCGACCTGACCCCGCAGCGGCG 4541
 Qy 389 -----AspMetSerValGlyGluAlaLeuArgGlnArgThrLeuCy 402
 Db 4540 AGGCTCCACCCCGAAGCATCTCTCTCTCCAGGTAGCTTTCAGCGCGCGAGCG 4481
 Qy 402 sLeuGluGlyValLeuSerCysGlnPro----- 411
 Db 4480 ACTCTGGCTCATCTTTCG---CAACCCACCGCGCGCGAGCGCTGACCGAGAGACC 4424
 Qy 412 -----HisGluSerLeuGlyGluValIleAspArgIleAl 423
 Db 4423 TCGCCGAGCGCTCTCTGCTCCCGAGCAGCAAGCATTCACAGGTG---GACCGAGCAGC 4367
 Qy 423 a-----ArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLe 439
 Db 4366 CACCGTGAGACAGCGCGAGGAAGTCCCGCG-----GCCCTCGACGATGTGGAGCGTCG 4313
 Qy 439 uLeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyI1 459
 Db 4312 CGTTGGATTTGGCGCG-----CGCAGGCGGTTCGCGGT 4280
 Qy 459 eAsp 460
 Db 4279 GGAT 4276

RESULT 14

US-11-075-185-1/c
 ; Sequence 1, Application US/11075185
 ; Publication No. US2005026643A1
 ; GENERAL INFORMATION:
 ; APPLICANT: REEVES, CHRISTOPHER D
 ; APPLICANT: JULIEN, BRYAN
 ; APPLICANT: REID, RALPH
 ; TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FOR AMBRUTICINS
 ; FILE REFERENCE: 010099.03
 ; CURRENT APPLICATION NUMBER: US/11/075,185
 ; CURRENT FILING DATE: 2005-03-07

; PRIOR APPLICATION NUMBER: US 60/551,103
; PRIOR FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: US 60/568,290
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 78869
; TYPE: DNA
; ORGANISM: Sorangium cellulosum
US-11-075-185-1

Alignment Scores:
Pred. No.: 9.57e+03 Length: 78869
Score: 109.50 Matches: 126
Percent Similarity: 34.36% Conservative: 74
Best Local Similarity: 21.65% Mismatches: 196
Query Match: 4.56% Indels: 186
DB: 8 Gaps: 29

US-10-070-794A-30 (1-464) x US-11-075-185-1 (1-78869)

Qy 7 GluAenSerSerSerTrpProSerProAlaValThrSerSerSerGluArgGly 26
Db 48271 GAACGCTCCGTAGACACCCAGTCCGACTCGACGGTCTCGAGCCAGCAATCCGAGT 48212
Qy 27 LysArgArgAlaLysAlaLeuArg----- 34
Db 48211 CGTCCGAGCTCAGCTTCGCTCGAGCTCGGGCGCGCCCTTCGCGAACGGATCGACGG 48152
Qy 35 -----TrpThrArgGlnLysSerValGluGluGluProProGlyGlnGlyGlu 51
Db 48151 CGATCACCTTGGACCAAGGCGAGCTCTCCACGA-----GGGCTTCAGCGCGGCGAGCGG 48098
Qy 52 GlyProArgSerArgProThrAlaGluSerThr-----GlyLeu 64
Db 48097 GCTCGCGGTGCGACCAACCGCCCGCGGTGAAGATGGGCTCCCTTGGAGCGA 48038
Qy 65 GluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAlaGlyValGlyThr 84
Db 48037 GCAGCGCGAGCCCTTCCTCGCGGCGAGCAGCGCGAGCTTCCAGCGCG-----TCTCGA 47984
Qy 85 ProProThr-GlyTrpAspCysLeuProSerAspCysThrAlaSerAlaLagLysSerSe 104
Db 47983 CGCGCGTCCGCGG-----GCGCCCGCGGGAAGA 47954
Qy 104 rThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTrpGluCysGluLe 124
Db 47953 CCGCGCGAAGTCTCGTTCGCGGCGTATGCGCG----- 47920
Qy 124 uGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGlnAlaProPheProLy 144
Db 47919 -----CTCGAGATCCGCCAGTAGTC-----CCTCGTGATGT 47888
Qy 144 sLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnLysLeuMetArgPheMetG1 164
Db 47887 CGTGGTCCCGAGGACCGACTGCGCATCTCGAGCGGTGTGCTCGAACAGACGCGC 47828
Qy 164 nGluHis-----ThrCysTrpAspAlaLeu 172
Db 47827 TCGTACAGGTTACAGTTGATGACCCGGCGGAGCTTCGTCATCTCGCTCATCTCAT 47768
Qy 172 tAlaThrSerSerLysLeuValLysPheAspThrMetLeuGluLysLysAlaPhePh 192
Db 47767 AGCCGCGTCCGTCGCGTTCGCGCGCGCGCGAGTTCGAGCGGTGTGCTCGAACCGCTGAG- 47716
Qy 192 eAlaLeuValAlaAsnGlyValArgAlaAlaProLeuTrpAspSerLysLysGlnSerPh 212
Db 47715 -CGATCCAGGACCGGGTTTCATAGTCCGCGGTCTCTCGTCCGCGCGCGGCGGATCGCC 47657
Qy 212 eValGlyMetLeuThrThrAspPheIleLeuValLeuHisArgTrpTrpArgSerPr 232
Db 47656 CCACGGCGATCCGCGCGAGGTTCCGCGGTGCTGCTGTCACGACGCGCGGGAATCGCC 47597

Qy 232 oLeuValGlnIleTyreGluIleGluGlnHisLysIleGluThrTrpArgGluIleTyLe 252
Db 47596 G-----CAGGATGTTTCTCCCTACAGCGGTACGCGGCGGCCGCCCATCGACC 47549
Qy 252 uGlnGlyCysPheLeuProLeuValSerIleSer---ProAsnAspSerLeuPheGluAl 271
Db 47548 CCGGGACTCGCACCGGAACTCTCTGGGCTGGCGGTCCACACGCGCTCTCTGGAAGC 47489
Qy 271 aValTyThr-----LeuIleLysAsn-- 278
Db 47488 GCGTATCGCGCACACGCCGACCGCAGCTCGAAACCCAGCGATGGCTCTCGAGCACCA 47429
Qy 279 -----ArgIleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisI 296
Db 47428 CGACGTGAGCTTCGAGCGCAGCTTCGCCGAGACGAGCTCGCGGTGTCTCGGTGCGAGCT 47369
Qy 296 eLeuThrHisLys-----ArgLeu----- 302
Db 47368 CTCGAGCACCGACACGATCCCGCGCGCGCACTCCGCGCGAGCGCTCTCGAGGCTGG 47309
Qy 303 -----LeuLysPheLeuHisIlePheGlySerLeuLeuProAr 315
Db 47308 CGTCATCGCATGCGTGTGACGTACGCGCGCGCGAGCTCTCTCGGCGCT---CTGCAGCA 47252
Qy 315 gProSerPheLeuTyArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAl 335
Db 47251 GCGGAGCAGCTCGCGCATTCGCCACAGAGATCAGATCGGGAAGAGCGCTCTCTGCG 47192
Qy 335 aValValLeuGluThrAlaProIleLeuThrAlaLeuAspIlePheValAspArg---Ar 354
Db 47191 GGAGGAACTCGAA---ATGCGCGGAGAGCTCCTCGGATCGAGGACGAGCTCTCG 47135
Qy 354 gValSerAlaLeuPro-----ValValAs 362
Db 47134 CGTCCGCGAGCCCTCGAGAGCTTTCGCCGAGCGCTTCGAAACCGAGCGCTCGCTCGA 47075
Qy 362 n-----GluCysGlyGln-----ValValGlyLeuTySerArgPheAspVa 376
Db 47074 CCGCTCGAGCGCGCGCGCATGAAGAAGCGTGTAGGGGCTCTCGGCGCTTC----- 47020
Qy 376 lIleHisLeuAlaAlaGlnGlnThrTyAsnHisLeu----- 388
Db 47019 -----CTGTCCCTCAGGAGCGGTGTGAGCAAAATAGCCGACCTGACCGCGCGGCG 46967
Qy 389 -----AspMetSerValGlyGluAlaLeuArgGlnArgThrLeuCy 402
Db 46966 AGGCCTCCACCCCGAAGCGATCTCTCCTCTCCAGTAGCTCTTTCAGCGCGCGGACCG 46907
Qy 402 sLeuGluGlyValLeuSerCysGlnPro----- 411
Db 46906 ACTCTGCTCATCTTGG-----CAACCCACCGCGCGGAGCGCTGACCGAGGAGACC 46850
Qy 412 -----HisGluSerLeuGlyGluValIleAspArgIleAl 423
Db 46849 TCGCGGAGCGGTCTCTGTCGCCGAGCAGAACCAATTCAAGGTTG---GACACGACGC 46793
Qy 423 a-----ArgGlnGlnValHisArgLeuValLeuValAspGluThrGlnHisLe 439
Db 46792 CACCGTGAGACAGCGCGAGGAAGTCCCGC-----GCCCTCGACGATGTGGAGCGTGC 46739
Qy 439 uLeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyI 459
Db 46738 CGTTGGGATTCGCG-----CCGAGCGCTTCTCGGCT 46706
Qy 459 eAsp 460
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RESULT 15
US-10-821-234-55/c
; Sequence 55, Application US/10821234
; Publication No. US20050255114A1

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; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821.234
; PRIOR FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 55
; LENGTH: 2736
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-55

Alignment Scores:
Pred. NO.: 106 Length: 2736
Score: 108.00 Matches: 48
Percent Similarity: 38.51% Conservative: 19
Best Local Similarity: 27.59% Mismatches: 60
Query Match: 4.49% Indels: 47
DB: 7 Gaps: 10

US-10-070-794A-30 (1-464) x US-10-821-234-55 (1-2736)

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Db 2411 TCCTGGCCACCGCCGCCACCTCGGGCCCTCATCCCTGCGGCTCACTGCGCGCTCCGCC 2352
Qy 22 -----GluArgIleArgGlyLysArgArgAlaLysAla 32
Db 2351 CGTTTGTGCTCGCGGTACGGTACAGTCCCGGTCCCGGCCGCGCTCGCGCTCG 2292
Qy 33 LeuArgTrpThrArgGlnLysSerValGluGlyGluPro----- 46
Db 2291 CTCGGTGGTTCGCGCGTCCGCTCCGCTCAGATCCCGGCCCTTTTCTCTGGACCGTCA 2232
Qy 47 -----ProGlyGlnGlyGluGlyProArgSer----- 59
Db 2231 GGGCGGTACGGCCCGAGCTCCCTCGAGGCCCATCATCAGGGGGCGGTCACCGCGCTCG 2172
Qy 60 GluSerThrGlyLeuGluAlaThrPheProLysThrThr-ProLeuAlaGlnAlaAspPr 79
Db 2171 GAGGCTCCGCCATGTCCGCCACCGCCCGCCAGCTCTCTGTGCGCTCCCGCT---CC 2115
Qy 79 oAlaGlyValGlyThrProProThrGlyTrpAspCysLeu-----ProSerAs 95
Db 2114 CGCGGG--CCCGCTCCCGACTCCGGC-----TGCTTCGCGCTTCGGTCCCGGTCC 2064
Qy 95 pCysThrAlaSerAlaAlaGlySerSerThr-----AspAspValGluLe 110
Db 2063 TTGTCTTGTCTCCGCTCCCTCGAGCGCTCGCTCTCTCTGTGCGACTCCGTTGAGC-- 2006
Qy 110 uAlaThrGluPheProAlaThrGluAlaTrpGluCysGluLeuGluGlyLeuGluGlu 130
Db 2005 -GCCTCCGCGGTCCCGGAGCGGAGC---GTCGCGGTTCCTGCTCTTGTCTCGTCC 1950
Qy 130 uArgProAlaLeuCysLeuSerProGlnAlaProPhePro 143
Db 1949 CGGCTCCGCTCTTGGCTCCCGCTCCCGCTCAGGTCGCGGTCCC 1910
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Job time : 1122.05 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 25, 2006, 22:06:06 ; Search time 7342.54 Seconds
(without alignments)
3494.061 Million cell updates/sec

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Perfect score: 2403
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Searched: 79147668 seqs, 27645789525 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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59: /cgn2_6/ptodata/1/pna/US107E_COMB.seq:
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62: /cgn2_6/ptodata/1/pna/US108_COMB.seq:
63: /cgn2_6/ptodata/1/pna/US109A_COMB.seq:
64: /cgn2_6/ptodata/1/pna/US109B_COMB.seq:
65: /cgn2_6/ptodata/1/pna/US109C_COMB.seq:
66: /cgn2_6/ptodata/1/pna/US110A_COMB.seq:
67: /cgn2_6/ptodata/1/pna/US110B_COMB.seq:
68: /cgn2_6/ptodata/1/pna/US110C_COMB.seq:
69: /cgn2_6/ptodata/1/pna/US110D_COMB.seq:
70: /cgn2_6/ptodata/1/pna/US111A_COMB.seq:
71: /cgn2_6/ptodata/1/pna/US111B_COMB.seq:
72: /cgn2_6/ptodata/1/pna/US112_COMB.seq:
73: /cgn2_6/ptodata/1/pna/US117_COMB.seq:
74: /cgn2_6/ptodata/1/pna/US600_COMB.seq:
75: /cgn2_6/ptodata/1/pna/US601_COMB.seq:
76: /cgn2_6/ptodata/1/pna/US602A_COMB.seq:
77: /cgn2_6/ptodata/1/pna/US602B_COMB.seq:
78: /cgn2_6/ptodata/1/pna/US603_COMB.seq:
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80: /cgn2_6/ptodata/1/pna/US604B_COMB.seq:
81: /cgn2_6/ptodata/1/pna/US605_COMB.seq:
82: /cgn2_6/ptodata/1/pna/US606_COMB.seq:
83: /cgn2_6/ptodata/1/pna/US607_COMB.seq:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description
1	2403	100.0	1470	52	US-10-503-175-1			Sequence 1, Appli
2	2403	100.0	2115	40	US-10-070-794A-29			Sequence 29, Appli
3	2398	99.8	1647	1	PCT-US03-34114A-73			Sequence 73, Appli
4	2398	99.8	1647	33	US-09-826-581-5			Sequence 5, Appli
5	2398	99.8	1647	54	US-10-695-614A-73			Sequence 73, Appli
6	2398	99.8	1647	55	US-10-705-137-5			Sequence 5, Appli
7	2398	99.8	2301	42	US-10-170-235-24862			Sequence 24862, A
8	2398	99.8	2781	1	PCT-US02-10818-30			Sequence 30, Appli

9	2398	99.8	2781	51	US-10-473-670-30	Sequence 30, Appl
10	2394	99.6	2109	40	US-10-070-794A-3	Sequence 3, Appl
11	2391	99.5	2314	1	PCT-US01-27760-386	Sequence 386, App
12	2391	99.5	2314	1	PCT-US01-27760A-386	Sequence 386, App
13	2391	99.5	2314	29	US-09-687-527-420	Sequence 420, App
14	2391	99.5	2314	50	US-10-399-103-386	Sequence 386, App
15	2391	99.5	2314	50	US-10-399-103A-386	Sequence 386, App
16	2374	98.8	2301	79	US-60-452-680-32	Sequence 32, Appl
17	2374	98.8	2522	63	US-10-932-349-6	Sequence 6, Appl
18	2374	98.8	2522	81	US-60-500-337-7	Sequence 6, Appl
19	2374	98.8	2612	63	US-10-932-349-7	Sequence 7, Appl
20	2374	98.8	2612	81	US-60-500-337-7	Sequence 7, Appl
21	2372	98.7	2290	1	PCT-US03-34114A-75	Sequence 75, Appl
22	2372	98.7	2290	3	PCT-US03-02638-4	Sequence 4, Appl
23	2372	98.7	2290	37	US-09-949-003C-782	Sequence 782, App
24	2372	98.7	2290	54	US-10-695-614A-75	Sequence 75, Appl
25	2372	98.7	2290	61	US-10-756-149-1235	Sequence 1235, Ap
26	2013	83.8	1873	66	US-11-075-134-3	Sequence 3, Appl
27	2011	83.7	1873	40	US-10-070-794A-27	Sequence 27, Appl
28	2011	83.7	1873	66	US-11-075-134-1	Sequence 1, Appl
29	2011	83.7	2022	40	US-10-070-794A-31	Sequence 31, Appl
30	2010	83.6	1873	66	US-11-075-134-7	Sequence 7, Appl
31	2007	83.5	1873	66	US-11-075-134-9	Sequence 9, Appl
32	2005	83.4	1873	66	US-11-075-134-5	Sequence 5, Appl
33	2002	83.3	1867	40	US-10-070-794A-1	Sequence 1, Appl
34	2000	83.2	1518	52	US-10-503-175-3	Sequence 3, Appl
35	1835	76.4	2612	42	US-10-144-771-21737	Sequence 21737, A
36	1835	76.4	2612	78	US-60-360-207-21737	Sequence 21737, A
37	1298.5	54.0	13413	37	US-09-949-003C-4472	Sequence 4472, Ap
38	1278.5	53.2	21722	63	US-10-932-349-18998	Sequence 18998, A
39	1278.5	53.2	21722	81	US-60-500-337-18998	Sequence 18998, A
40	1276	53.1	9100	52	US-10-503-175-5	Sequence 5, Appl
41	1276	53.1	26000	52	US-10-503-039-1	Sequence 1, Appl
42	1099	45.7	2297	77	US-60-278-232-699	Sequence 699, App
43	1098.5	45.7	2205	75	US-60-172-373-4233	Sequence 4233, Ap
44	1094	45.5	2223	1	PCT-US02-01048-13	Sequence 13, Appl
45	1094	45.5	2223	1	PCT-US03-34114A-67	Sequence 67, Appl

ALIGNMENTS

RESULT 1

US-10-503-175-1

Sequence 1, Application US/10503175

GENERAL INFORMATION:

APPLICANT: Andersson, Leif

APPLICANT: Marklund, Stefan

TITLE OF INVENTION: Transgenic animals expressing prkag3

FILE REFERENCE: 11145-020DS1

CURRENT APPLICATION NUMBER: US/10/503,175

PRIOR FILING DATE: 2004-07-30

PRIOR APPLICATION NUMBER: PCT/IB03/00912

PRIOR FILING DATE: 2003-01-31

PRIOR APPLICATION NUMBER: US 60/353,430

PRIOR FILING DATE: 2002-02-01

NUMBER OF SEQ ID NOS: 12

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1

LENGTH: 1470

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (1)..(1470)

OTHER INFORMATION:

US-10-503-175-1

Alignment Scores:

Pred. No.: 4,43e-306

Length: 1470

Score: 2403.00

Matches: 464

Percent Similarity: 100.00%

Conservative: 0

Best Local Similarity: 100.00%

Mismatches: 0

Query Match: 100.00%

Indels: 0

DB:	52	Gaps:	0
US-10-070-794A-30 (1-464) x US-10-503-175-1 (1-1470)			
Qy	1	MetSerPheLeuGluGlnGluAenSerSerTrpProSerProAlaValThrSerSer	20
Db	76	ATGAGCTTCCTAGAGCAAGAAAAACAGCAGCTCATGGCCATCACCCAGCTGTGACCAAGC	135
Qy	21	SerGluArgLleArgGlyLysArgArgAlaLysAlaLeuArgTrpThrArgGlnLysSer	40
Db	136	TCAGAAAGATCCGTGGGAAACGAGGGCCAAACCTTGAGATGGCAACGACGAAGTCG	195
Qy	41	ValGluGluGluProGlyGlnGluGlyProArgSerArgProThrAlaGlu	60
Db	196	GTGAGGAGGAGGAGCCACAGGTACAGGGGAGAGTCCCGGTCCAGGCCACTGCTGAG	255
Qy	61	SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla	80
Db	256	TCCACCGGGCTGGAGGCCACATTCGCCAAGACACACACCTTGGCTCAAGCTGATCTGCC	315
Qy	81	GlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSerAla	100
Db	316	GGGTGGGCACTCCACCAACAGGGTGGGACTGCCCTCCCTCTGACTGTACAGCTCAGCT	375
Qy	101	AlaGlySerSerThrAspValGluLeuAlaThrGluPheProAlaThrGluAlaTrp	120
Db	376	GCAGGCTCCAGACACAGATGATGGAGCTGGCCACGAGTTCCAGCCACAGAGGCTGG	435
Qy	121	GluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGlnAla	140
Db	436	GAGTGTGAGCTAGAAAGCCCTGCTGGAAGAGAGGCTGCCCTGTGCTGCCCTCCAGGCC	495
Qy	141	ProPheProLysLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnLysMet	160
Db	496	CCATTTCACAGCTGGGCTGGGATGACGAACTGCGGAAACCCCGGCCACGATCTACATG	555
Qy	161	ArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValile	180
Db	556	CGTTTCATGAGGAGCACACCTGCTACGATGCCATGGCACTAGCTCCAGCTAGTCATC	615
Qy	181	PheAspThrMetLeuGluLleLysLysAlaPhePheAlaLeuValAlaAsnGlyValArg	200
Db	616	TTGACACCATGCTGGAGATCAAGAGGCCCTTCTTGTCTGTGGTGGCCACCGTGTGGCG	675
Qy	201	AlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrLleThrAsp	220
Db	676	GCAGCCCCCTCTATGGGACAGCAAGCAGAGCTTTTGTGGGGATGCTGACCATCCTGAC	735
Qy	221	PheLleLeuValLeuHisArgTyrTrpArgSerProLeuValGlnLleTyrGluLleGlu	240
Db	736	TTGATCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	795
Qy	241	GlnHisLysLleGluThrTrpArgGluLleTyrLeuGlnGlyCysPheLysProLeuVal	260
Db	796	CAACATAAGATTGAGACCTGAGGAGGAGATCTACCTGCAAGGCTGCTTCAAGCCTCTGTC	855
Qy	261	SerLysSerProAsnAspSerLeuPheGluAlaValTyrThrLeuLysLysAsnArgLle	280
Db	856	TCCATCTCTCTTAATGATAGCTGTTTGAAGCTGTCTACACCTCATCAAGAACCGGATC	915
Qy	281	HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisLleLeuThrHisLys	300
Db	916	CATGCCCTGCTGCTTCTTGTACCCGGTGTGAGGCAACGTTACTCCACATCTCCACACAAA	975
Qy	301	ArgLeuLeuLysPheLeuHisLlePheGlySerLeuLeuProArgProSerPheLeuTyr	320
Db	976	CGCCTGCTCAAGTTCCTGCACATCTTGTGTTCCCTGCTGCCCGGCCCTCTCTCTCTAC	1035
Qy	321	ArgThrLleGlnAspLeuGlyLleGlyThrPheArgAspLeuAlaValValLeuGluThr	340
Db	1036	CGCACTATCCCAAGATTTGGGCATCGGCACATTCGAGACCTTGGCTGTGTGTGTGAGACA	1095
Qy	341	AlaProLleLeuThrAlaLeuAspilePheValAspArgArgValSerAlaLeuProVal	360


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Db 1081 GTCAACGAATGTGGTCAGGTCGTGGGCTCTATTCCCGCTTTGATGTGATTACCTGGCT 1140
Qy 381 AlaGlnGlnThrTyrAenHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr 400
Db 1141 GCCCAGCAAACTTACACCACTGGACATGAGTGTGGGAGAACCTTGGAGCAGAGACA 1200
Qy 401 LeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValLeuAsp 420
Db 1201 CTATGTCTGGAGGAGTCTTCTTCTGTCAGCCACAGAGCTTGGGGGAAGTGTATCGAC 1260
Qy 421 ArgLeuAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeu 440
Db 1261 AGGATTCTCTGGAGCAGGTATACACAGGCTGGTGTGTAGTGACGAGACCCAGCATCTCTTG 1320
Qy 441 GlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAsp 460
Db 1321 GGCTGTGTCTCCCTCTCCGACATCTTTCAGGCACTGTGTGCTCAGCCCTGTGGCATCGAT 1380
Qy 461 AlaLeuGlyAla 464
Db 1381 GCCCTCGGGCC 1392

RESULT 3
PCT-US03-34114A-73
; Sequence 73, Application PC/TUS0334114A
; GENERAL INFORMATION:
; APPLICANT: Curagen Corporation at al.
; TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT MODULATE PROTEIN ACTIVITY
; FILE REFERENCE: Cura 951 [PCT]
; CURRENT APPLICATION NUMBER: PCT/US03/34114A
; CURRENT FILING DATE: 2003-10-27
; NUMBER OF SEQ ID NOS: 151
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 73
; LENGTH: 1647
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (20)..(1486)
PCT-US03-34114A-73

Alignment Scores:
Pred. No.: 2,6e-305 Length: 1647
Score: 2398.00 Matches: 463
Percent Similarity: 99.78% Conservative: 0
Best Local Similarity: 99.78% Mismatches: 1
Query Match: 99.79% Indels: 0
DB: 1 Gaps: 0

US-10-070-794A-30 (1-464) x PCT-US03-34114A-73 (1-1647)
Qy 1 MetSerPheLeuGluGlnGluAsnSerSerTyrProSerProAlaValThrSerSer 20
Db 95 ATGAGCTCTCCCTAGACAGAAACAGCAGCTCATGGCCATCACCGCTGTGACACGAGC 154
Qy 21 SerGluArgIleArgGlyLysArgArgAlaLysAlaLeuArgTyrThrArgGlnLysSer 40
Db 155 TCAGAAAGATCCGTGGGAACCGGAGGCGCAAGCGCTTGTAGATGACAAAGCAGAGTCG 214
Qy 41 ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60
Db 215 GTGGAGGAAGGGAGCCACAGGTGAGGGGGAAGGTCCCGGTCCAGGCCAGCTCTGAG 274
Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla 80
Db 275 TCCACGGGCTGGAGGCCACATTCGCCAAGACCAACCCCTTGGCTCAAGCTGATCTCTGCC 334
Qy 81 GlyValGlyThrProProThrGlyTyrAspCysLeuProSerAspCysThrAlaSerAla 100
Db 335 GGGGTGGGCACTCCCAACAGGGTGGGAGTGCCTCCCTCTGAGCTGTACAGCCCTCAGCT 394
Qy 101 AlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTrp 120
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Db 395 GCAGGCTCCAGCACACATGATGTGGAGCTGGCCACGAGTTCCAGCCACAGAGCCCTGG 454
Qy 121 GluCysGluLeuGluGlyLeuLeuGluArgProAlaLeuCysLeuSerProGlnAla 140
Db 455 GAGTGTGAGCTAGAGGCTGTCTGGAGAGAGAGGCTGCTGCTGTGCTGTGCTGCTGCTGCTG 514
Qy 141 ProPheProLysLeuGlyTyrAspAspGluLeuArgLysProGlyAlaGlnIleTyrMet 160
Db 515 CCATTTCCTCCAGCTGGGCTGGGATGACAACTCGGAAACCCCGCGCCGAGATCTCATG 574
Qy 161 ArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerTysLeuValIle 180
Db 575 CGCTTCATGACGAGGACACCTCTACGATGCCATGSCAACTAGTCCAAAGTAGTCATC 634
Qy 181 PheAspThrMetLeuGluLeuLysLysAlaPhePheAlaLeuValAlaAsnGlyValArg 200
Db 635 TTCGACACCATGCTGGAGATCAAGAAGGCTCTCTTTGCTGTGGTGGCAACGGGTGTCGG 694
Qy 201 AlaAlaProLeuThrAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAsp 220
Db 695 GCAGCCCTCTATGGGACAGCAAGAGCAGAGCTTTGTGGGATGCTGACCATCCTGAC 754
Qy 221 PheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGlu 240
Db 755 TTCTCTCTGTGTGCTGCTACTACAGTCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 814
Qy 241 GlnHisLysIleGluThrTyrArgGluLeuLysLysLysLysLysLysLysLysLysLys 260
Db 815 CAACATAAGATTGAGACCTGGAGGAGATCTACCTGCAAGGCTGCTTCAAGGCTCTGCTGCT 874
Qy 261 SerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIle 280
Db 875 TCCATCTCTCTAATGATAGCTGTTTGAAGCTGTCTACACCTCATCAAGAACCGGATC 934
Qy 281 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 300
Db 935 CATGCCCTGCTGCTTCTTGACCCGCTGTCAGGCAACGCTACTCCACATCTCCACACAAA 994
Qy 301 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 320
Db 995 CGCCTGCTCAAGTTCTCTGTCACATCTTTGGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1054
Qy 321 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGluThr 340
Db 1055 CGCACTATCCAAAGATTGGGGCATTCGACACATTCGAGACTTGGCTGTGCTGCTGCTGCTGCTG 1114
Qy 341 AlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProVal 360
Db 1115 GCACCCATCTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1174
Qy 361 ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeuAla 380
Db 1175 GTCAACGAATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1234
Qy 381 AlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr 400
Db 1235 GCCCAGCAAACTTACACCACTGGACATGAGTGTGGGAGAACCTTGGAGCAGAGACA 1294
Qy 401 LeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAsp 420
Db 1295 CTATGTCTGGAGGAGTCTTCTTCTGTCAGCCACGAGAGCTTGGGGGAAGTGTATCGAC 1354
Qy 421 ArgLeuAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeu 440
Db 1355 AGGATTGTCTGGAGCAGGTATACACAGGCTGTGCTGTAGTGGACGAGACCCAGCATCTCTTG 1414
Qy 441 GlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAsp 460
Db 1415 GCGGTGGTCTCCCTCTCCGACATCTTTCAGGCACTGGTGTGCTCAGCCCTGCTGGCATCGAT 1474
Qy 461 AlaLeuGlyAla 464
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Db 1475 GCCCTCGGGCC 1486

RESULT 4

US-09-826-581-5

; Sequence 5, Application US/09826581

; GENERAL INFORMATION:

; APPLICANT: Andersson, Leif

; APPLICANT: Luthman, L. Holger

; APPLICANT: Marklund, Stefan

; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNIT

; FILE REFERENCE: 11145-007001

; CURRENT APPLICATION NUMBER: US/09/826.581

; CURRENT FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: US 60/195,665

; PRIOR FILING DATE: 2000-04-07

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 5

; LENGTH: 1647

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (20)...(1486)

US-09-826-581-5

Alignment Scores:

Pred. No.:	2,66-305	Length:	1647
Score:	2398.00	Matches:	463
Percent Similarity:	99.78%	Conservative:	0
Best Local Similarity:	99.78%	Mismatches:	1
Query Match:	99.79%	Indels:	0
DB:	33	Gaps:	0

US-10-070-794A-30 (1-464) x US-09-826-581-5 (1-1647)

Qy 1 MetSerPheLeuGluGlnGluAsnSerSerSerTrpProSerProAlaValThrSerSer 20

Db 95 ATGAGCTTCTTAGAGCAAGAAACAGCAGCTCATGGCCATCACCAGCTGTGACCAGCAGC 154

Qy 21 SerGluArgLeuArgGlyLysArgArgAlaLysAlaLeuArgTrpThrArgGlnLysSer 40

Db 155 TCAGAAAGATCCCTGGAAACGAGAGGCCAAAGCCTTGAGATGGAACAGCAGAGCTG 214

Qy 41 ValGluGluGluProProGlyGlnGlyGlnGlyProArgSerArgProThrAlaGlu 60

Db 215 GTGAGGAAAGGGAGCCAGCAGCTCAGGGGAGAGTCCCGGTCCAGCCAGCTGTGAG 274

Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla 80

Db 275 TCCACCGGGCTGGAGGGCCACATTCGCCAAGACCAACACCTTGGCTCAAGCTGATCTCTGCC 334

Qy 81 GlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSerAla 100

Db 335 GGGGTGGGCACTCCACCAACAGGTGGAGTGCCTCCCTCTGACTGTACAGCTCAGCT 394

Qy 101 AlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTrp 120

Db 395 GCAGGCTCCAGCAGATGATGTGAGCTGCGCCAGCAGGTCCAGCCACAGAGGCTGG 454

Qy 121 GluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGlnAla 140

Db 455 GAGTGTGAGCTAGAAAGGCTGCTGGAAGAGAGGCTGCCCTGTGCTGTGCTCCCGCAGGCC 514

Qy 141 ProPheProLysLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnLysMet 160

Db 515 CCATTTCCCAAGCTGGGCTGGATGAGCAATCTGGGAACCCGGGCCAGATCTCATG 574

Qy 161 ArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValLe 180

Db 575 CGCTTCATGAGGAGCACACCTGCTACGATGCCATGCACTAGCTCCAGCTAGTCATC 634

Qy 181 PheAspThrMetLeuGluLeuLysLysAlaPhePheAlaLeuValAlaAsnGlyValArg 200

Db 635 TTCACACCATGCTGGAGATCAAGAGGCTTCTTTGCTCTGGTGGCAACGGTGTGGG 694

Qy 201 AlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAsp 220

Db 695 GCAGCCCTCTTAGGGACCAAGACAGAGCTTTGTGGGATGCTGACCATCCTGAC 754

Qy 221 PheIleLeuValLeuHisArgTyrTrpArgSerProLeuValGlnLysTyrGluIleGlu 240

Db 755 TTCATCTGCTGCTGATCGTCTACTACAGGTCCCTCTGGTCCAGATCTATGAGATTGAA 814

Qy 241 GlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeuVal 260

Db 815 CAACATAAGATTGAGACCTGGAGGAGATCTACCTGCAAGGCTCTTCAAGCCCTCTGCTC 874

Qy 261 SerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuLysLysAsnArgIle 280

Db 875 TCCATCTCTCTAATGATGACCTGTTGAAGCTGTCTACACCTCATCAAGACCGGATC 934

Qy 281 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 300

Db 935 CATCGCTGCTGCTGTTCTTGACCCGGTGTGAGGCAACGTACTCCACATCTCTCACACAAA 994

Qy 301 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 320

Db 995 CGCTGCTCAAGTTCTCTGACATCTTTGGTTCCCTGCTGCCCGGCCCTCTCTCTCTAC 1054

Qy 321 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGluThr 340

Db 1055 CGCATATCCAGATTTGGGATCGGCATTCGAGATTTGGCTGTGGTGTGGAGACA 1114

Qy 341 AlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProVal 360

Db 1115 GCACCATCTGACTGCTGACATCTTTGTGACCGGCTGTGTGCACTGCTGCTGTG 1174

Qy 361 ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeuAla 380

Db 1175 GTCAACGAATGTGCTGAGTGTGGGCTCTATTTCGGCTTTGATGTGATTTACCTGGCT 1234

Qy 381 AlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr 400

Db 1235 GCCAGCAACCTTACAAACCTTGGACCTGGACNTGAGTGTGGAGAACCTTGGAGCAGGACA 1294

Qy 401 LeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAsp 420

Db 1295 CTATGCTGAGGAGAGTCTTTCTTCCAGCCCGCCAGAGAGCTTGGGGAAGTGTGAC 1354

Qy 421 ArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeu 440

Db 1355 AGGATTTGCTCGGAGCAGGTACACAGGCTGTGTAGTGGACGAGACCCAGCATCTCTTG 1414

Qy 441 GlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAsp 460

Db 1415 GGGTGTGCTCTCCCTCTCCGACATCTTTCAGGCACTGTGTGCTGAGCCCTGTGTCATCGAT 1474

Qy 461 AlaLeuGlyAla 464

Db 1475 GCCCTCGGGCC 1486

RESULT 5

US-10-695-614A-73

; Sequence 73, Application US/10695614A

; GENERAL INFORMATION:

; APPLICANT: Berghs, Constance

; APPLICANT: Catterton, Elina

; APPLICANT: Ellerman, Karen E.

; APPLICANT: Ort, Tatiana A.

; APPLICANT: Rieger, Daniel K.

; TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT MODULATE PROTEIN ACTIVITY

; FILE REFERENCE: Cura 951 [PCT]

; CURRENT APPLICATION NUMBER: US/10/695,614A

; CURRENT FILING DATE: 2003-10-27

; NUMBER OF SEQ ID NOS: 151

; SOFTWARE: CurSeqList version 0.1
; SEQ ID NO 73
; LENGTH: 1647
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (20) .. (1486)
US-10-695-614A-73

Alignment Scores:
Pred. No.: 2,66-305 Length: 1647
Score: 2398.00 Matches: 463
Percent Similarity: 99.78% Conservativity: 0
Best Local Similarity: 99.78% Mismatches: 1
Query Match: 99.79% Indels: 0
DB: 54 Gaps: 0

US-10-070-794A-30 (1-464) x US-10-695-614A-73 (1-1647)

Qy 1 MetSerPheLeuGluGlnGluAsnSerSerTrpProSerProAlaValThrSerSer 20
Db 95 ATGAGCTTCTTAGAGCAAGAAACAGCAGCTCATGGCCATCACCAGCTGTGACCAAGCAGC 154
Qy 21 SerGluArgIleArgGlyIleArgAlaIleArgAlaIleArgAlaIleArgAlaIleArg 40
Db 155 TCAGAAAGAAATCCGTGGGAAACGAGGGCCAAAGCCTTGAGATGCAAGGCAAGATCG 214
Qy 41 ValGluGluGlyGluProGlyGlnGlyProGlyGlyProGlyGlyProGlyGlyProGly 60
Db 215 GTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 274
Qy 61 SerThrGlyLeuGluAlaThrPheProIleThrThrProLeuAlaGlnAlaAspProAla 80
Db 275 TCCACCGGGCTGGAGGCCACATTCCTCCCAAGACACACACCTTGGCTCAAGCTGATCTGCC 334
Qy 81 GlyValGlyThrProProThrGlyThrAspCysLeuProSerAspCysThrAlaSerAla 100
Db 335 GGGGTGGGCACCTCCACCAACAGGGTGGGACTGCCCTCTGACTGTGACAGCCTCAGCT 394
Qy 101 AlaGlySerSerThrAspValGluLeuAlaThrGluPheProAlaThrGluAlaTrp 120
Db 395 CGAGCTCCAGCAGCAGATGATGGAGCTGGCCAGGAGTTCACAGCCACAGAGGCGCTGG 454
Qy 121 GluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGlnAla 140
Db 455 GAGTGTGAGCTAGAAGGCTGCTGGAAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 514
Qy 141 PropheProIleLeuGlyThrAspAspGluLeuArgIleProGlyAlaGlnIleTyMet 160
Db 515 CCATTTCCTCAAGCTGGGCTGGGATGACCACTGCGGAAACCGGGCCAGATCTACATG 574
Qy 161 ArgPheMetGlnGluHisThrCysTytrAspAlaMetAlaThrSerSerIleLeuValIle 180
Db 575 CGCTTCATCAGGAGCAGCAGCTGCTACGATGCCATGGCACTAGCTCCAGCTAGTCATC 634
Qy 181 PheAspThrMetLeuGluIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 200
Db 635 TTCGACACCATGCTGGAGATCAAGAAGGCTTCTTTGCTGCTGCTGCTGCTGCTGCTGCTG 694
Qy 201 AlaAlaProLeuTrpAspSerIleIleIleIleIleIleIleIleIleIleIleIleIleIle 220
Db 695 CGAGCCCTCTATGGGACGACGAAGCAGAGCTTTGTGGGATGCTGACCACTACTGAC 754
Qy 221 PheIleLeuValLeuHisArgTytrArgSerProLeuValGlnIleTytrGluIleGlu 240
Db 755 TTCACTCTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 814
Qy 241 GlnHisIleIleGluThrTrpArgGluIleTytrLeuGlnGlyCysPheIleIleIleIleIle 260
Db 815 CAACATAAGATTGAGACCTGGAGGAGATCTACCTGCAAGGCTGCTTCAAGCCTCTGGTC 874
Qy 261 SerIleSerProAsnAspSerLeuPheGluAlaValThrLeuIleIleIleIleIleIleIle 280

Db 875 TCCATCTCTCTAATGATACCTGTTTGAAGCTGTCTACACCTCATCAAGAACCGGATC 934
Qy 281 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisIle 300
Db 935 CATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 994
Qy 301 ArgLeuLeuIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 320
Db 995 CGCTGCTCAAGTTCCTGACATCTTTGGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1054
Qy 321 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGluThr 340
Db 1055 CGCACTATCCAGATTTGGGCATCGGCACATTCGAGACTTGGCTGCTGCTGCTGCTGCTG 1114
Qy 341 AlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProVal 360
Db 1115 GCACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1174
Qy 361 ValAsnGluCysGlyGlnValValGlyLeuTytrSerArgPheAspValIleHisLeuAla 380
Db 1175 GTCAACCAATGTGCTAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1234
Qy 381 AlaGlnGlnThrTytrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr 400
Db 1235 GCCCAGCAACCTACACCACTGGACATGATGTTGGGAGGAGGCTTGGGGGAGGATCGAT 1294
Qy 401 LeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAsp 420
Db 1295 CTATGCTGGAGGAGTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1354
Qy 421 ArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeu 440
Db 1355 AGGATGCTCGGAGCAGGTACACAGGCTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 1414
Qy 441 GlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAsp 460
Db 1415 GGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1474
Qy 461 AlaLeuGlyAla 464
Db 1475 GCCCTCGGGGCC 1486

RESULT 6

US-10-705-137-5
; Sequence 5, Application US/10705137
; GENERAL INFORMATION:
; APPLICANT: Andersson, Leif
; APPLICANT: Luthman, L. Holger
; APPLICANT: Marklund, Stefan
; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNIT
; FILE REFERENCE: 11145-007002
; CURRENT APPLICATION NUMBER: US/10705,137
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: US 09/826,581
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 60/195,665
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1647
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (20) ... (1486)
US-10-705-137-5

Alignment Scores:
Pred. No.: 2,66-305 Length: 1647
Score: 2398.00 Matches: 463
Percent Similarity: 99.78% Conservativity: 0

Best Local Similarity:	99.78%	Mismatches:	1
Query Match:	99.79%	Indels:	0
DB:	55	Gaps:	0
US-10-070-794A-30 (1-464) x US-10-705-137-5 (1-1647)			
Qy	1	MetSerPheLeuGluGlnGluAnsSerSerSerTrpProSerProAlaValThrSerSer	20
Db	95	ATGAGCTTCTTAGAGCAAGAAAAAGAGAGCTCATGGCCATCACCAGCTGTGACCAGCAGC	154
Qy	21	SerGluArgIleArgGlyLysArgArgAlaLysAlaLeuArgTrpThrArgGlnLysSer	40
Db	155	TCAGAAGAATCCGTGGGNAACGAGGGCCAAAGCCTTGAGATGGCAAGGAGGAAGTCG	214
Qy	41	ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu	60
Db	215	GTGAGGAAGGGGAGCCACAGGTCAGGGGAAGTCCCGGTCCAGGCCAGCTGCTGAG	274
Qy	61	SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla	80
Db	275	TCCACCGGGCTGGAGGCCACATTCCCAAGACCACACCTTTGGCTCAAGCTGATCTCTGCC	334
Qy	81	GlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSerAla	100
Db	335	GGGGTGGGCACTCCACCAACAGGGTGGGACTGCGCTCCCTCTGACTGTACAGCCTCAGCT	394
Qy	101	AlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTrp	120
Db	395	GCAGCTCCAGCACAGATGATGTGGAGCTGGCCACGGAGTTCCAGCCACAGAGGCCCTGG	454
Qy	121	GluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGlnAla	140
Db	455	GAGTGTGAGCTAGAAAGGCCTCTCGAAAGAGAGGCGTGCCTGTGCTGTCCCGCAGGCC	514
Qy	141	ProPheProLysLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnIleTyMet	160
Db	515	CCATTTCCCAAGCTGGGCTGGGATGAGCAATGCGGAAACCCGGCGCCACATCTACATG	574
Qy	161	ArgPheMetGlnGluHisThrCysTyAspAlaMetAlaThrSerSerLysLeuValIle	180
Db	575	CGCTTCATGCAGGAGCACACTGTCAGATGCCATGGCACTAGCTCCAGCTAGTCATC	634
Qy	181	PheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyValArg	200
Db	635	TTGCACACCATGCTGGAGATCAAGAAAGGCCCTTCTTTGCTGTGTGGCCACACGGTGGCG	694
Qy	201	AlaAlaProLeuTrpAspSerLysGlnSerPheValGlyMetLeuThrIleThrAsp	220
Db	695	GCAGCCCTCTATGGGACAGCAAGACAGAGCTTTGTGGGGATGCTGACCATCAGCTGAC	754
Qy	221	PheIleLeuValLeuHisArgTyTyArgSerProLeuValGlnIleTyGluIleGlu	240
Db	755	TTCACTCTGTGTGCATCGCTACTACAGGTCCCCCTGGTCCAGATCTATGAGATTGAA	814
Qy	241	GlnHisLysIleGluThrTrpArgGluIleTyLeuGlnGlyCysPheLysProLeuVal	260
Db	815	CAACATAAGATTGAGACTGGAGGGAGATCTACTCGCAAGGCTGCTTCAAGSCCTCTGGTC	874
Qy	261	SerIleSerProAnAspSerLeuPheGluAlaValTyThrLeuIleLysAsnArgIle	280
Db	875	TCCATCTCTCTATATGATAGCTGTTTGAAGCTGTCTACACCCCTCATCAAGAACCGGATC	934
Qy	281	HisArgLeuProValLeuAspProValSerGlyValLeuHisIleLeuThrHisLys	300
Db	935	CATCGCTCTGCTTCTTGAGCCCGGTGTGAGCAACGCTACTCCACATCTCTCACACACAA	994
Qy	301	ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTy	320
Db	995	CGCTGTCTCAAGTTCCTGCACATCTTTGTTCCTGTGTCGCCCGGCCCTCTCTCTCTAC	1054
Qy	321	ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGluThr	340
Db	1055	CGCACTATCAAGATTGGGCAATCGGCACATCTCGAGACTTGGCTGTGCTCGGACACA	1114

Qy	341	AlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProVal	360
Db	1115	GCACCCATCCTGACTGCACCTGGACATCTTTGTGGACCGCGGTGTCTGCACCTGCCTGTG	1174
Qy	361	ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeuAla	380
Db	1175	GTCAACGAATGGTCAGTCTGGGCGCTCTATTCCCGCTTTGATGTGATTCACCTGGCT	1234
Qy	381	AlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr	400
Db	1235	GCCAGCAAAACCTPACAAACACCACTGGACATGAGTGTGGGAGAAGCCCTGAGGCGAGAGCA	1294
Qy	401	LeuCysLeuGluGlyValLeuLeuSerCysGlnProHisGluSerLeuGlyGluValIleAsp	420
Db	1295	CTATGTCTGGAGGAGTCCCTTTCTCCACGCCCCACGAGAGCTTGGGGGAAGTATCGAC	1354
Qy	421	ArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeu	440
Db	1355	AGGATTGCTCGGAGCAGGTACACAGGCTGTGTAGTGGACGAGNCCCAGCATCTCTTG	1411
Qy	441	GlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAsp	460
Db	1415	GGCGTGTGTCTCCCTCTCCGACATCCCTTCAGGCACTGGTCTCAGGCCCTGTCGCATCGAT	1474
Qy	461	AlaLeuGlyAla 464	
Db	1475	GCCTTCGGGGCC 1486	
RESULT 7			
US-10-170-235-24862			
; Sequence 24862, Application US/10170235			
; GENERAL INFORMATION:			
; APPLICANT: VENTER, J. Craig			
; TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY			
; TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THE			
; FILE REFERENCE: CL001380			
; CURRENT APPLICATION NUMBER: US/10/170,235			
; CURRENT FILING DATE: 2003-03-17			
; NUMBER OF SEQ ID NOS: 42514			
; SEQ ID NO 24862			
; LENGTH: 2301			
; TYPE: DNA			
; ORGANISM: HUMAN			
US-10-170-235-24862			
Alignment Scores:			
Pred. No.: 5,24e-305 Length: 2301			
Score: 2398.00 Matches: 463			
Percent Similarity: 99.78% Conservative: 0			
Best Local Similarity: 99.78% Mismatches: 1			
Query Match: 99.79% Indels: 0			
DB: 42 Gaps: 0			
US-10-070-794A-30 (1-464) x US-10-170-235-24862 (1-2301)			
Qy	1	MetSerPheLeuGluGlnGluAsnSerSerTyrProSerProAlaValThrSerSer	20
Db	95	ATGAGCTTCTAGCAAGAAACACGACGCTCATGGCCATCACAGCTGTGTGACCAGCAGC	154
Qy	21	SerGluArgIleArgGlyLysArgArgAlaLysAlaLeuArgTyrThrArgGlnLysSer	40
Db	155	TCAGAAAGAATCCGTGGGAACGAGGGCCAAAGCCTTGAGATGGACAGCCAGAGTCG	214
Qy	41	ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu	60
Db	215	GTGAGCAAGGGAGGCCACCAAGTTCAGGGGGAAGTCCCGGTCCAGGCCAGCTGCTGAG	274
Qy	61	SerThrGlyLeuGluAlaThrPheProTyrLysThrThrProLeuAlaGlnAlaAspProAla	80
Db	275	TCCACCGGGCTGGAGGCCACATTCGCCAAGACCACACCCCTTGGCTCAAGCTGATCCTGCC	334
Qy	81	GlyValGlyThrProProThrGlyTyrAspCysLeuProSerAspCysThrAlaSerAla	100

335 GGGTGGGCACTCACCAAGGAGTGGGACTGCTCCCTCTGACTGTACAGCTCAGCT 394
 101 AlaGlySerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTyr 120
 395 GCAGGCTCCAGCACAGATGATGGAGCTGGCCACGAGTTCACGACACAGAGGCGCTGG 454
 121 GluCysGlnLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGlnAla 140
 455 GAGTGTGAGCTAGAAGGCTGCTGGAAGAGAGGCTGCTGCTGTGCTGCTGCTGCTGCTG 514
 141 ProPheProLysLeuGlyTyrAspAspGluLeuArgLysProGlyAlaGlnIleTyrMet 160
 515 CCATTTCCCAAGCTGGGCTGGGATGACAACTGGGAACCCGGCGCCAGATCTACATG 574
 161 ArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValIle 180
 575 CGCTTCATGACGAGACACCTGCTACGATGCCATGCACTAGCTCCAAAGTATGTCATC 634
 181 PheAspThrMetLeuGluIleLysAlaPheAlaLeuValAlaAsnGlyValArg 200
 635 TTCGACACCATGCTGGAGATCAAGAAGGCTTCTTGTCTGTGGTGGCCAAAGTGTGGG 694
 201 AlaAlaProLeuTyrAspSerLysGlnSerPheValGlyMetLeuThrIleThrAsp 220
 695 GCAGCCCTCTATGGGACAGCAAGACAGAGCTTTGTGGGATGCTGACCATCACATGAC 754
 221 PheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGlu 240
 755 TTCAATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 814
 241 GlnHisLysIleGluThrTyrArgGluIleTyrLeuGlnGlyCysPheLysProLeuVal 260
 815 CAACATAAGATTGAGACCTGGAGGAGATCTACCTGCAAGGCTGCTTCAAGCCCTCTGCTC 874
 261 SerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIle 280
 875 TCCATCTCTCAATGATGAGCTGTTTGAAGCTGTACACCCCTCATCAGAACCGGATC 934
 281 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 300
 935 CATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 994
 301 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 320
 995 CGCTGCTCAAGTTCTCTGACATCTTTGGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTG 1054
 321 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGluThr 340
 1055 CGCACTATCCAAGATTTGGGCAATCGGCATCTCCGAGACTTGGCTGTGCTGTGGAGACA 1114
 341 AlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProVal 360
 1115 GCACCATCTCTGACTGCACTGGACATCTTTGGGACCGGCTGTGCTGTGCACTGCTGTG 1174
 361 ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeuAla 380
 1175 GTCAACGAATGTGGTCAAGTCTGCTGGGCTCTATTTCCTGCTTGTGATTCACCTGCTG 1234
 381 AlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr 400
 1235 GCCCAGCAAACTCAACCACTGAGCATGATGTTGGGAGAGAGCCCTGAGGACAGAGACA 1294
 401 LeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAsp 420
 1295 CTATGCTGGAGGAGTCTTTCTGCTGCCAGCCCAAGAGAGCTTGGGGAAGTATGATGAC 1354
 421 ArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeu 440
 1355 AGGATTGCTCGGAGCAGGTACACAGGCTGTGCTGTGAGTGGAGAGACCCAGCATCTCTTG 1414
 441 GlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAsp 460

Db 1415 GGGTGGTCTCTCCCTCCGACATCTTTCAGGCACTGGTGTCTGAGCCCTGCTGGCATCGAT 1474
 Qy 461 AlaLeuGlyAla 464
 Db 1475 GCCCTCGGGGCC 1486
 RESULT 8
 PCT-US02-10818-30
 ; Sequence 30, Application PC/TUS0210818
 ; GENERAL INFORMATION:
 ; APPLICANT: INCYTE GENOMICS, INC.
 ; APPLICANT: Recipon, Shirley A.
 ; APPLICANT: Burrill, John D.
 ; APPLICANT: Marcus, Gregory A.
 ; APPLICANT: Zingler, Kurt A.
 ; APPLICANT: Tang, Y. Tom
 ; APPLICANT: Thornton, Michael
 ; APPLICANT: Borowsky, Mark L.
 ; APPLICANT: Baughn, Mariah R.
 ; APPLICANT: Burford, Neil
 ; APPLICANT: Lee, Soo Yeun
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Hafalia, April J.A.
 ; APPLICANT: Yao, Monique G.
 ; APPLICANT: Ramkumar, Jayalaxmi
 ; APPLICANT: Walia, Narinder K.
 ; APPLICANT: Lu, Dyung Aina M.
 ; APPLICANT: Arvizu, Chandra S.
 ; APPLICANT: Ison, Craig H.
 ; APPLICANT: Ding, Li
 ; APPLICANT: Lu, Yan
 ; APPLICANT: Gururajan, Rajagopal
 ; APPLICANT: Walsh, Roderick T.
 ; APPLICANT: Gandhi, Ameena R.
 ; APPLICANT: Swarnakar, Anita
 ; APPLICANT: Forsythe, Ian J.
 ; APPLICANT: Yue, Henry
 ; APPLICANT: Au-Young, Janice K.
 ; APPLICANT: Elliott, Vicki S.
 ; APPLICANT: Lee, Sally
 ; TITLE OF INVENTION: KINASES AND PHOSPHATASES
 ; FILE REFERENCE: PI-0398 PCT
 ; CURRENT APPLICATION NUMBER: PCT/US02/10818
 ; CURRENT FILING DATE: 2002-04-05
 ; PRIOR APPLICATION NUMBER: 60/282,119; 60/283,588; 60/283,759; 60/285,589; 60/287,037;
 ; 60/287,036; 60/288,608; 60/288,712; 60/289,909; 60/292,246
 ; PRIOR FILING DATE: 2001-04-06; 2001-04-13; 2001-04-13; 2001-04-20; 2001-04-27;
 ; 2001-04-27; 2001-05-04; 2001-05-04; 2001-05-09; 2001-05-17
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 30
 ; LENGTH: 2781
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No: 7474666CB1
 PCT-US02-10818-30
 Alignment Scores:
 Pred. No.: 7,8e-305 Length: 2781
 Score: 2398.00 Matches: 463
 Percent Similarity: 99.78% Conservative: 0
 Best Local Similarity: 99.78% Mismatches: 1
 Query Match: 99.79% Indels: 0
 DB: 1 Gaps: 0
 US-10-070-794A-30 (1-464) x PCT-US02-10818-30 (1-2781)
 Qy 1 MetSerPheLeuGluGlnGluAsnSerSerSerTyrProSerProAlaValThrSerSer 20
 Db 96 ATGAGCTCTTAGAGCAAGAAACAGCAGCTCATGGCCATCATCCAGCTGTGTGACGACG 155

Qy 21 SerGluArgIleArgGlyLysArgAlaLysAlaLeuArgThrThrArgGlnLysSer 40
Db 156 TCAGAAAGATCCGTGGGAAACGAGGCGCCAAAGCCTTGAGATGGACAAAGCAGAGTCG 215
Qy 41 ValGluGluGlyGluProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60
Db 216 GTGAGGAGAGGGAGGACCAACAGGTTCAGGGGAGAGTCCCGGTCCAGCCAGCTGCTGAG 275
Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla 80
Db 276 TCCACCGGCTGGAGGCCACATTCCTCCCAAGACACACCTTTGGCTCAAGCTGATCTCTGCC 335
Qy 81 GlyValGlyThrProProThrGlyThrAspCysLeuProSerAspCysThrAlaSerAla 100
Db 336 GGGGTGGGCATCTCCACCAACAGGGTGGAGCTGCCCTCTCCCTCTGAGCTGTACAGCCTCAGCT 395
Qy 101 AlaGlySerSerThrAspValGluLeuAlaThrGluPheProAlaThrGluAlaTrp 120
Db 396 GCAGGCTCCAGCACAGATGATGTGGAGCTGGCCACGAGGTTCCTCCAGCCACAGAGGCTGG 455
Qy 121 GluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGlnAla 140
Db 456 GAGTGTGAGCTAGAGGCTGCTGGAAGAGAGGCTGCCCTGTGCTGCTGCCCGCAGGCC 515
Qy 141 ProPheProLysLeuGlyThrAspAspCysLeuArgLysProGlyAlaGlnIleTyrMet 160
Db 516 CCATTTCCCAAGCTGGGCTGGGATGAGCAACTGGCGAAACCCGCGCGCCAGATCTACATG 575
Qy 161 ArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValIle 180
Db 576 CGCTTCATGAGGAGCACACTGCTAGATGCCATGCACTAGCTCCAGCTAGTATC 635
Qy 181 PheAspThrMetLeuGluIleLysLysAlaPheAlaLeuValAlaAsnGlyValArg 200
Db 636 TCGACACCATCTGGAGATCAGAAGGCTCTCTTCTGCTGGTGGCCACGGTGTGGCG 695
Qy 201 AlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAsp 220
Db 696 GCAGCCCTCTATGGGACAGCAAGACAGAGCTTTGTGGGATGCTGACCATCACTGAC 755
Qy 221 PheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGlu 240
Db 756 TTCTATCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 815
Qy 241 GlnHisLysIleGluThrTrpArgGluIleLysLeuGlnGlyCysPheLysProLeuVal 260
Db 816 CAACATAAGATTGAGACCTGGAGGAGATCTACCTGCAAGGCTGCTTCAAGCCTCTGCTC 875
Qy 261 SerIleSerProLeuAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIle 280
Db 876 TCCATCTCTCTAATGATAGCTGTTTGAAGCTGTCTACACCTCTCATCAAGAACCGGATC 935
Qy 281 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 300
Db 936 CATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 995
Qy 301 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 320
Db 996 CGCTGCTCAAGTCTCTGACATCTTTGGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1055
Qy 321 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGluThr 340
Db 1056 CGCACTATCAAGATTTGGGCGATCGGCACATTCGAGACTTGGCTGTGGTGTGGAGACA 1115
Qy 341 AlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProVal 360
Db 1116 GCACCCATCTGATGCTGACATCTTTGTGACCGGCTGTGTCTGACCTGCTGCTGCTGCTGCT 1175
Qy 361 ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeuAla 380
Db 1176 GTCAACGAATGTGGTCAAGTGTGGGCTCTATTCGCGCTTTGATGTGATTCACCTGGCT 1235
Qy 381 AlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr 400

Db 1236 GCCCAGCAAACTTACACCACTGGACATGATGTGGGAGAACCTTGGAGCAGGACACA 1295
Qy 401 LeuCysLeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValIleAsp 420
Db 1296 CTATGTCTGGAGGAGTCTTCTTCTCCAGCCACGAGAGCTTGGGGGAAGTGTATCGAC 1355
Qy 421 ArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeu 440
Db 1356 AGGATTGCTCGGAGCAGGTACACAGGCTGGTGTAGTGGACGAGACCCAGCATCTCTTG 1415
Qy 441 GlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAsp 460
Db 1416 GGGGTGTCTCTCCCTCTCCGACATCTTTCAGGCACTGTGTGTGTGTGTGTGTGTGTGTGT 1475
Qy 461 AlaLeuGlyAla 464
Db 1476 GCCCTCGGGGCC 1487

RESULT 9
US-10-473-670-30
; Sequence 30. Application US/10473670
; GENERAL INFORMATION:
; APPLICANT: RECIPON, Shirley A.; BURRILL, John D.;
; APPLICANT: MARCUS, Gregory A.; ZINGLER, Kurt A.;
; APPLICANT: TANG, Y. Tom; THORNTON, Michael;
; APPLICANT: BOROWSKY, Mark L.; BAUGHN, Mariah R.;
; APPLICANT: BURFORD, Neil; LEE, Soo Yeun;
; APPLICANT: BANDMAN, Olga; HAPALIA, April J.A.;
; APPLICANT: YAO, Monique G.; RAMKUMAR, Jayalaxmi;
; APPLICANT: CHAWLA, Nandinder K.; LU, Byung Aina M.;
; APPLICANT: ARVIZU, Chandra S.; ISON, Craig H.;
; APPLICANT: DING, Li; LU, Yan;
; APPLICANT: GURURAJAN, Rajagopal; WALSH, Roderick T.;
; APPLICANT: GANDHI, Ameena R.; SWARNAKAR, Anita;
; APPLICANT: FORSYTHE, Ian J.; YUE, Henry;
; APPLICANT: AD-YOUNG, Janice K.; ELLIOTT, Vicki S.;
; APPLICANT: LEE, Sally
; TITLE OF INVENTION: KINASES AND PHOSPHATASES
; FILE REFERENCE: PI-0398 USN
; CURRENT APPLICATION NUMBER: US/10/473,670
; CURRENT FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: PCT/US02/10818
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 60/282,119
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/283,588
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/283,759
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/285,589
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: US 60/287,037
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/287,036
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/288,608
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/288,712
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/289,909
; PRIOR FILING DATE: 2001-05-09
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PERL Program
; SEQ ID NO 30
; LENGTH: 2781
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7474666CBI
; US-10-473-670-30

Alignment Scores:

Pred. No.: 7,8e-305 Length: 2781
Score: 2398.00 Matches: 463
Percent Similarity: 99.78% Conservative: 0
Best Local Similarity: 99.78% Mismatches: 1
Query Match: 99.79% Indels: 0
DB: 51 Gaps: 0

US-10-070-794A-30 (1-464) x US-10-473-670-30 (1-2781)

Qy 1 MetSerPheLeuGluGlnGluAsnSerSerSerTrpProSerProAlaValThrSerSer 20
Db 96 ATGAGCTCTCCCTAGAGCAGAAACAGCAGCTCAATGGCCATCACCAGCTGTGACCAAGCAGC 155
Qy 21 SerGluArgIleArgGlyLysArgAlaLysAlaLeuArgTrpThrArgGlnLysSer 40
Db 156 TCAGAAAGATCCCTGGGAAACGGAGGCCCAAGCCCTTGAGATGGACAGCAGAGCTG 215
Qy 41 ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60
Db 216 GTGGAGGAAGGGAGGCCACCAAGGTCCAGGGGAAAGGTCCCGGTCCAGGCCAGCTGCTGAG 275
Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla 80
Db 276 TCCACCGGGCTGGAGGCCACATTCCTCCAGACACACCTTGGCTCAAGCTGATCTCTGCC 335
Qy 81 GlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSerAla 100
Db 336 GGGGTGGGCATCTCCACCAACAGGGTGGGACTGCTCCCTCTGACTGTATACAGCTCAGCT 395
Qy 101 AlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTrp 120
Db 396 GCAGGCTCCAGCAGACAGATGATGTGGAGCTGGCCACGGAGTTCCAGGCCACAGAGGCTGG 455
Qy 121 GluCysGluLeuGluGlyLeuLeuGluArgProAlaLeuCysLeuSerProGlnAla 140
Db 456 GAGTGTAGCTAGAAAGGCTCTGGAAGAGAGGCTGCGCTGTGCTGCCCGCAGGCC 515
Qy 141 ProPheProLysLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnIleTrpMet 160
Db 516 CCATTTCCAAAGCTGGGCTGGGATGACGAACCTGGCGAAACCGCGGCCAGATCTACATG 575
Qy 161 ArgPheMetGlnGluHisThrCysTrpAspAlaMetAlaThrSerSerLysLeuValIle 180
Db 576 CGCTTCATGAGGAGCACACCTGTCTACATGCCATGGCAACTAGCTCCAAAGCTAGTCATC 635
Qy 181 PheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyValArg 200
Db 636 TTCGACACATGCTGGAGATCAAGAAAGCCCTCTTTGCTGTGGGCCCAACGGTGTGGGG 695
Qy 201 AlaAlaProLeuTrpAspSerLysGlnSerPheValGlyMetLeuThrIleThrAsp 220
Db 696 GCAGCCCTCTATGGACAGCAAGAGCAGAGCTTTGTGGGATGCTGACCATCACTGAC 755
Qy 221 PheIleLeuValLeuHisArgTrpTrpArgSerProLeuValGlnIleTrpGluLeuGlu 240
Db 756 TTCACTCTGGTGTGCTCATGCTACTACAGGTCCCTGGTCCAGATCTATGAGATTGAA 815
Qy 241 GlnHisLysIleGluThrTrpArgGluIleTrpLeuGlnGlyCysPheLysProLeuVal 260
Db 816 CACATATAGATTGACACTGGAGGAGATCTACTCTGCAAGGCTGTTCAAGCTCTGGTC 875
Qy 261 SerIleSerProAsnAspSerLeuPheGluAlaValThrLeuIleLysAsnArgIle 280
Db 876 TCCATCTCTCTTAATGATAGCTGTTTGAAGCTGTCTACACCTCATCAAGAACCGGATC 935
Qy 281 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 300
Db 936 CATCGCTCTGCTGCTTTGACCCGGTGTGAGCAACGCTACTCCATCTCTCACACAAA 995
Qy 301 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTrp 320

Db 996 CGCCTGCTCAAGTTCTCTGCACATCTTTGGTTCCCTGCTGCCCGCCCTCTCTCTCTAC 1055
Qy 321 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGluThr 340
Db 1056 CGCAGCTATCCAAAGATTGGGCAATCGGCATCGGCATCTCGAGACTGGCTGGTGGAGACA 1115
Qy 341 AlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProVal 360
Db 1116 GCACCATCTCTGACTGCATCGACATCTTTGTGGACCGCGCTGTCTGCACCTGCTGTG 1175
Qy 361 ValAsnGluCysGlyGlnValValGlyLeuTrpSerArgPheAspValIleHisLeuAla 380
Db 1176 GTCAACGAATGTGCTCAGGTCTGGGCTCTATTTCGCGCTTGTATGTGATTCACCTGGCT 1235
Qy 381 AlaGlnGlnThrTrpAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr 400
Db 1236 GCCCAGCAAACTTACACCACTGGACATGAGTGTGGGAAGCCCTTGAGCAGAGACA 1295
Qy 401 LeuCysLeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValIleAsp 420
Db 1296 CTATGCTCGAGGGAGTCTCTTCTGCGACGCCCCAGAGCTTGGGGGAAGTGCATCGAC 1355
Qy 421 ArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeu 440
Db 1356 AGGATTCTCGGGAGCAGGTACACAGGCTGTGTCTAGTGGACGAGACCCAGCATCTCTTG 1415
Qy 441 GlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyLeuAsp 460
Db 1416 GCGTGTGTCTCTCTCTCCGACATCTTTCAGGACATGCTGTGCTCAGCCCTGCTGGCATCGAT 1475
Qy 461 AlaLeuGlyAla 464
Db 1476 GCCCTCGGGGCC 1487

RESULT 10

US-10-070-794A-3
; Sequence 3, Application US/10070794A
; GENERAL INFORMATION:
; APPLICANT: ANDERSSON, Leif
; APPLICANT: LOOFT, Christian
; APPLICANT: KALM, Ernst
; APPLICANT: MILAN, Denis
; APPLICANT: ROBIC, Annie
; APPLICANT: ROGEL-GAILLARD, Claire
; APPLICANT: IANNUCCELLI, Nathalie
; APPLICANT: GELIN, Joel
; APPLICANT: LE ROY, Pascale
; APPLICANT: CHARDON, Patrick
; TITLE OF INVENTION: VARIANTS OF THE GAMMA CHAIN OF AMPK, DNA SEQUENCES ENCODING
; TITLE OF INVENTION: THE SAME, AND USES THEREOF
; FILE REFERENCE: 11145-023US1
; CURRENT APPLICATION NUMBER: US/10/070,794A
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/EP00/09896
; PRIOR FILING DATE: 2000-09-11
; PRIOR APPLICATION NUMBER: EP 00401388.4
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: EP 99402236.3
; PRIOR FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 42
; SEQ ID NO 3
; LENGTH: 2109
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (472) .. (1389)
US-10-070-794A-3
Alignment Scores: 1.48e-304 Length: 2109
Pred. No.: 2394.00 Matches: 462
Score: 99.78% Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.63% Indels: 0
DB: 40 Gaps: 0

US-10-070-794A-30 (1-464) x US-10-070-794A-3 (1-2109)

Qy 3 PheLeuGluGlnGluAenSerSerSerTrpProSerProAlaValThrSerSerSerGlu 22
Db 1 TTCTAGAGCAGAGAAACAGAGCTCATGGCCATCACCAGCTGTGACAGCAGCTCAGAA 60

Qy 23 ArgIleArgGlyLysArgAlaLysAlaLeuArgTrpThrArgGlnLysSerValGlu 42
Db 61 AGATTCCTGGGAAACGAGAGGCGCCAGCCCTTGATGAGACAGAGAGAGCTCGGTGAG 120

Qy 43 GluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGluSerThr 62
Db 121 GAAGGGAGCCACAGAGTCAGGGGAGGTCCCGGTCCAGGCCAATGCTGAGTCCACC 180

Qy 63 GlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAaspProAlaGlyVal 82
Db 181 GGGCTGGAGGCCACATTCCTCCCAAGACCAACACCTTGGCTCAAGCTGATCTCTGCCGGGTG 240

Qy 83 GlyThrProProThrGlyTrpAaspCysLeuProSerAaspCysThrAlaSerAlaAagly 102
Db 241 GGCATTCACACAGAGGTGGAGCTGCTCCCTCTGACTGTACAGCTCAGCTGACGGC 300

Qy 103 SerSerThrAaspAaspValGluLeuAlaThrGluPheProAlaThrGluAlaTrpGluCys 122
Db 301 TCCAGCAGATGATGGAGCTGGCCAGGAGTTCAGGCCACAGAGGCTGGGAGTGT 360

Qy 123 GluLeuGluGlyLeuLeuGluGluAargProAlaLeuCysLeuSerProGlnAlaProPhe 142
Db 361 GAGCTAGAAGCCCTGTCTGAGAGAGAGGCTGCCCTGTGCTGTCTCCCGCAGGCCCATTT 420

Qy 143 ProLysLeuGlyTrpAaspAaspGluLeuArgLysProGlyAlaGlnIleTyrMetArgPhe 162
Db 421 CCCAAGCTGGCTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 480

Qy 163 MetGlnGluHisThrCysTrpAaspAlaMetAlaThrSerSerLysLeuValIlePheAasp 182
Db 481 ATGCAGGAGCACACCTGCTAGATGCCATGATGCCATGATGCCATGATGCCATGATGCC 540

Qy 183 ThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAenGlyValArgAlaAla 202
Db 541 ACCATGTGGAGATCAAGAGGCCCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600

Qy 203 ProLeuTrpAaspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAaspPhe 222
Db 601 CCTCTATGGGACAGACAGAGCAGAGCTTTGTGGGAGTGTGACCATCATCTGATCTTCATC 660

Qy 223 LeuValLeuHisArgTyrTrpArgSerProLeuValGlnIleTyrGluLeuGlnHis 242
Db 661 CTGGTGTGATCTGCTACTACAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720

Qy 243 LysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeuValSerIle 262
Db 721 AAGATTGAGACCTGGAGGAGATCTACCTGCAAGGCTGCTTCAAGCCTCTGCTGCTCCTC 780

Qy 263 SerProAaspSerLeuPheGluAlaValTyrThrLeuIleLysAenArgIleHisArg 282
Db 781 TCTCTAATGATAGCTGTTGAGAGTGTGTACACCTCATCAAGAACCGGATCCATCGC 840

Qy 283 LeuProValLeuAaspProValSerGlyAenValLeuHisIleLeuThrHisLysArgLeu 302
Db 841 CTGGCTGTTCTTGACCCCGGTGTGAGGCAAGTACTTCCACATCTCCACACACAAACGCTG 900

Qy 303 LeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyrArgThr 322
Db 901 CTCAAGTCTCTGACATCTTTGGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960

Qy 323 IleGlnAaspLeuGlyIleGlyThrPheArgAaspLeuAlaValValLeuGluThrAlaPro 342
Db 961 ATCAAGATTGGGCATCGGCACATTCGAGACTTGGCTGTGGTGTGGTGTGGTGTGGTGTGG 1020

Qy 343 IleLeuThrAlaLeuAaspIlePheValAaspArgValSerAlaLeuProValValAen 362
Db 1021 ATCTGACTGACTGGACATCTTTGTGACCGGGTGTGTCTGACTGCTGCTGCTGCTGCTG 1080

Qy 363 GluCysGlyGlnValValGlyLeuTyrSerArgPheAaspValIleHisLeuAlaGln 382
Db 1081 GAATGTGTGTGAGTGTGGGCTCTATTCGGCTTTGATGTGATTCACCTGGCTGCTGCTG 1140

Qy 383 GlnThrTyrAenHisLeuAaspMetSerValGlyGluAlaLeuArgGlnArgThrLeuCys 402
Db 1141 CAACCTTACACCACTTGGACATGAGTGTGGAGAGCCCTTGAGGACAGACTATGT 1200

Qy 403 LeuGluGlyValLeuSerCysGlnProHisSerLeuGlyGluValIleAaspArgIle 422
Db 1201 CTGGAGGAGTCTCTTCTTCCAGGCCACAGAGAGCTTGGGGAAGTGTATCGACAGATT 1260

Qy 423 AlaArgGluGlnValHisArgLeuValLeuValAaspGluThrGlnHisLeuLeuGlyVal 442
Db 1261 GCTCGGAGCAGGAGTACACAGGCTGTGTAGTGGAGCAGACCCAGCATCTCTTGGGCTG 1320

Qy 443 ValSerLeuSerAaspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAaspAlaLeu 462
Db 1321 GTCTCCCTCTCCGACATCTTTCAGGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380

Qy 463 GlyAla 464
Db 1381 GGGGCC 1386

RESULT 11
PCT-US01-27760-386
; Sequence 386, Application PC/TUS0127760
; GENERAL INFORMATION:
; APPLICANT: Hysseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCES: 21272-115/785
; CURRENT APPLICATION NUMBER: PCT/US01/27760
; CURRENT FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: 09/687,527
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 892
; SOFTWARE: Custom
; SEQ ID NO 386
; LENGTH: 2314
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (22)..(1491)
PCT-US01-27760-386

Alignment Scores:
Pred. No.: 4,52e-304 Length: 2314
Score: 2391.00 Matches: 461
Percent Similarity: 99.78% Conservative: 2
Best Local Similarity: 99.35% Mismatches: 1
Query Match: 99.50% Indels: 0
DB: 1 Gaps: 0

US-10-070-794A-30 (1-464) x PCT-US01-27760-386 (1-2314)

Qy 1 MetSerPheLeuGluGlnGluAenSerSerSerTrpProSerProAlaValThrSerSer 20
Db 97 ATGAGCTTCTAGAGCAAGAAACAGAGCTCATGGCCATCAGCAGCTGTGACAGCAGC 156

Qy 21 SerGluArgIleArgGlyLysArgArgAlaLysAlaLeuArgTrpThrArgGlnLysSer 40
Db 157 TCAGAAAGAAATCCGTGGGAAACGAGAGGCCAAAGCCCTTGAGATGGACAGGACAGAGTCG 216

Qy 41 ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60
Db 217 GTGAGGAAGGGGAGGCCACAGGCTCAGGGGGAAGGTCCCGGCTCAGGCCAGCTGCTGAG 276

QY 61 SerThrGlyLeuGluAlaThrPheProIysThrThrProLeuAlaGlnAlaAspProAla 80
 DB 277 TCCACCGGGCTGGAGGCCACATATCCCAAGACCACACCTTGGCTCAAGCTGATCTCTGCC 336
 QY 81 GlyValGlyThrProProThrGlyTyrAspCysLeuProSerAspCysThrAlaSerAla 100
 DB 337 GGGGTGGGCATCTCCACCAACAGGTGGGACATGCTCTCTGACTGTACAGCTCAGCT 396
 QY 101 AlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTyr 120
 DB 397 GCAGGCTCCAGCACAGATGATGGAGCTGGCCACGGAGTTCCACGACACAGAGGCGCTGG 456
 QY 121 GluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGlnAla 140
 DB 457 GAGTGTGAGCTAGAGGCTCTGGAAGAGAGGCTGCTCTGCTGGTCCCTGCTGCTCCCGCAGGCC 516
 QY 141 ProPheProIysLeuGlyTyrAspAspGluLeuArgLysProGlyValAlaGlnIleTyrMet 160
 DB 517 CCATTTCCAAAGCTGGGCTGGGATGACGAACCTGGGAAACCCGGCGGCCAGATCTACATG 576
 QY 161 ArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValIle 180
 DB 577 CGCTTTCAGAGGAGCACACCTGCTACGATGCCATGCACTAGCTCAAGCTAGTCAATC 636
 QY 181 PheAspThrMetLeuGluIleLysLysAlaPheAlaLeuValAlaAsnGlyValArg 200
 DB 637 TTCACACCATGCTGGAGATCAAGAGGCTTCTTGTCTGGTGGCCAAACGGTGTGGCG 696
 QY 201 AlaAlaProLeuTyrAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAsp 220
 DB 697 GCAGCCCTCTATGGGACAGCAGACGACGAGCTTTGTGGGATGCTGACCATCACTGAC 756
 QY 221 PheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGlu 240
 DB 757 TTCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 816
 QY 241 GlnHisLysIleGluThrTyrArgGluIleTyrLeuGlnGlyCysPheLysProLeuVal 260
 DB 817 CAACATAGATTTGAGACCTGGAGGAGATCTACCTGCAAGGCTGCTTCAAGCCCTCTGCTC 876
 QY 261 SerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIle 280
 DB 877 TCCATCTCTCTATGATAGCTGTTTGAAGCTGTCTACACCTCATCAAGACCGGATC 936
 QY 281 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 300
 DB 937 CATGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 996
 QY 301 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 320
 DB 997 GCCTGCTCAAGTTCTCTGACATCTTGGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1056
 QY 321 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGluThr 340
 DB 1057 GCACATATCCAAAGTTGGGCTGCGCATCTCCAGACTTGGCTGTGCTGCTGAGACA 1116
 QY 341 AlaProfileLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProVal 360
 DB 1117 GCACCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1176
 QY 361 ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeuAla 380
 DB 1177 GTCAACGAATGTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1236
 QY 381 AlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr 400
 DB 1237 GCCCAGCAACCTACCAACCTGACATGATGTGGGAGAGCCCTGAGGACAGGACA 1296
 QY 401 LeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAsp 420
 DB 1297 CTATGCTGGAGGAGTCTTTCTCTGCCACCCACGAGCTTGGGGAAGTGTATCGAC 1356
 QY 421 ArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeu 440

DB 1357 AGATTGCTCGGAGCAGGTACACAGCTGCTGTAGTGACGAGACCCAGCATCTCTTG 1416
 QY 441 GlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAsp 460
 DB 1417 GGGGTGGTCTCCCTCTCCGACATCTTTCAGGCACTGGTGTCTCAGCCCTGTGGCATCGAT 1476
 QY 461 AlaLeuGlyAla 464
 DB 1477 GCCTTCGGGGCC 1488
 RESULT 12
 PCT-US01-27760A-386
 ; Sequence 386, Application PC/TUS0127760A
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq, Inc
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
 ; FILE REFERENCE: 21272-115/ 785
 ; CURRENT APPLICATION NUMBER: PCT/US01/27760A
 ; CURRENT FILING DATE: 2001-10-11
 ; PRIOR APPLICATION NUMBER: 09/687,527
 ; PRIOR FILING DATE: 2000-10-12
 ; NUMBER OF SEQ ID NOS: 892
 ; SOFTWARE: Custom
 ; SEQ ID NO 386
 ; LENGTH: 2314
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (22)..(1491)
 PCT-US01-27760A-386
 Alignment Scores:
 Pred. No.: 4,52e-304 Length: 2314
 Score: 2391.00 Matches: 461
 Percent Similarity: 99.78% Conservative: 2
 Best Local Similarity: 99.35% Mismatches: 1
 Query Match: 99.50% Indels: 0
 DB: 1 Gaps: 0
 US-10-070-794A-30 (1-464) x PCT-US01-27760A-386 (1-2314)
 QY 1 MetSerPheLeuGluGlnGluAsnSerSerSerTrpProSerProAlaValThrSerSer 20
 DB 97 ATGAGCTTCTTAGAGCAAGAAACAGCAGCTCATGGCCATCCAGCTGTGACCCAGCAGC 156
 QY 21 SerGluArgIleArgGlyLysArgArgAlaLysAlaLeuArgTrpThrArgGlnLysSer 40
 DB 157 TCAGAAAGATCCGTGGGAAACGGAGGCCAAAGCTTTGAGATGGACAAGGCAAGATCG 216
 QY 41 ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60
 DB 217 GTGGAGGAAGGGAGGCCACCAAGGTTCAGGGGGAAGGTCCTCCCGTCCAGGCCAGCTGCTGAG 276
 QY 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla 80
 DB 277 TCCACCGGCTGGAGGCCACATTTCCCAAGACCAACACCTTGGCTCAGCTGATCTGCTGCC 336
 QY 81 GlyValGlyThrProProThrGlyTyrAspCysLeuProSerAspCysThrAlaSerAla 100
 DB 337 GGGGTGGGCACTCCACCAACAGGGTGGGACTGCTCTCTCTGACTGTACAGCTCAGCT 396
 QY 101 AlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTyr 120
 DB 397 GCAGGCTCCAGCACAGATGATGGAGCTGGCCACGGAGTTCCCGCAGGCCACAGAGGCGCTGG 456
 QY 121 GluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGlnAla 140
 DB 457 GAGTGTGAGCTAGAGGCTGCTGGAAGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 516
 QY 141 ProPheProLysLeuGlyTyrAspAspGluLeuArgLysProGlyValAlaGlnIleTyrMet 160

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Db 517 CCATTTCCTCCAGCTGGGCTGGGATGACGAACTCGGGAACCCCGCGGCCAGATCTCATG 576
Qy 161 ArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValile 180
Db 577 GCGTTTCATCGAGGAGCACACCTGTACGATGCCATGCACTAGCTCCAGCTAGTCTCATC 636
Qy 181 PheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyValArg 200
Db 637 TTCGACACCATGCTGGGAGATCAAGAAGCCCTTCTTGTCTGTGGTGGCAACGGTGTGGG 696
Qy 201 AlaAlaProLeuTyrAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAsp 220
Db 697 GCACCCCTCTATGGGACAGCAGCAGAGCAGCTTTTGGGGATGCTGACCATCAGTAC 756
Qy 221 PheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGlu 240
Db 757 TTCATCTCTGGTGTGCTGCTACTACAGGTCTCCCTGCTGGTCCAGATCTATGAGATTGAA 816
Qy 241 GlnHisLysIleGluThrTyrArgGluIleTyrLeuGlnGlyCysPheLysProLeuVal 260
Db 817 CAACATAGATTGAGACCTGGAGGGAGATCTACCTGCAAGGCTGCTTCAAGCCCTCTGGTC 876
Qy 261 SerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIle 280
Db 877 TCCATCTCTCTAATGATAGCTCTTTGAAGCTGTCTACACCTCATCAAGAACCGGATC 936
Qy 281 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 300
Db 937 CATCGCTGCTGCTTCTTGACCCGGTGTGAGGCAAGTACTCCACATCTCTCACACAAA 996
Qy 301 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 320
Db 997 CGCCTGTCTCAAGTCTCTGCACATCTTTGGTTCCTGCTGCCCGCGCTCTCTCTCTAC 1056
Qy 321 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGluThr 340
Db 1057 CGCACTATCAAGATTGGGATCGGCATCGGCACATTCGAGACTGGCTGTGGTGTGGAGACA 1116
Qy 341 AlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProVal 360
Db 1117 GCACCCATCTGACTGCACTGGACATCTTTGTGACCGGGCTGTCTGTGACTGCTGTG 1176
Qy 361 ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeuAla 380
Db 1177 GTCAACAAATGTGTCAAGTGTGGGCTCTATTCGGCTTTGATGTGATTCACCTGGCT 1236
Qy 381 AlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr 400
Db 1237 GCCCAGCAACCTTACAAACCACTGGACATGATGTGGGGAAGCCCTGAGGAGAGACCA 1296
Qy 401 LeuCysLeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValIleAsp 420
Db 1297 CTATGCTGGAGGAGTCTTCTTCTGCGAGCCCAAGAGCTTGGGGAGTATGATCGAC 1356
Qy 421 ArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeu 440
Db 1357 AGGATTGCTGGGAGCAGGTACACAGGCTGGTGTGTAGTACGACGAGACCCAGCATCTCTG 1416
Qy 441 GlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAsp 460
Db 1417 GGCCTGTCTCCCTCTCCGACATCTTTCAGGCATCTGTGTGCTCAGCCCTGTGTGGCATCAT 1476
Qy 461 AlaLeuGlyAla 464
Db 1477 GCCCTCGGGGCC 1488
```

RESULT 13

US-09-687-527-420

; Sequence 420, Application US/09687527

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

; APPLICANT: Liu, Chenghua

; APPLICANT: Zhou, Ping

```
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE REFERENCE: 795
; CURRENT APPLICATION NUMBER: US/09/687,527
; CURRENT FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 482
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 420
; LENGTH: 2314
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (22)..(1491)
US-09-687-527-420
```

```
Alignment Scores:
Pred. No.: 4,52e-304 Length: 2314
Score: 2391.00 Matches: 461
Percent Similarity: 99.78% Conservative: 2
Best Local Similarity: 99.35% Mismatches: 1
Query Match: 99.50% Indels: 0
DB: 29 Gaps: 0
```

US-10-070-794A-30 (1-464) x US-09-687-527-420 (1-2314)

```
Qy 1 MetSerPheLeuGlnGlnGlnAAsnSerSerSerTrpProSerProAlaValThrSerSer 20
Db 97 ATGAGCTTCTTAGAGCAAGAAAAACAGCAGCTCATGGCCATCACACGCTGTGACGAGC 156
Qy 21 SerGluArgIleArgGlyLysArgAlaLysAlaLeuArgTrpThrArgGlnLysSer 40
Db 157 TCAGAAAGATTCGTGGGAAACGGAGGGCCAAAGCCTTGAGATGACACAGGACAGAGTCG 216
Qy 41 ValGluGluGlyGluProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60
Db 217 GTGGAGGAGGAGGAGCACCAGGTCAGGGGGAAGTCCCGGTCAGGCCAGCTGCTCAG 276
Qy 61 SerThrClyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla 80
Db 277 TCCACCGGGCTGGAGGCCACATTTCCCAAGACCAACACCTTGGGCTCAAGCTGATCTCTGCC 336
Qy 81 GlyValGlyThrProProThrGlyTyrAspCysLeuProSerAspCysThrAlaSerAla 100
Db 337 GGGGTGGGCACTCCACACAGGGTGGGACTGGCTCCCTCTGACTGTACAGCTCAGCT 396
Qy 101 AlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTrp 120
Db 397 GCAGGCTCCAGCACAGATGATGTGGAGTGGCCAGGAGTTCCAGGCCACAGAGGCTGG 456
Qy 121 GlnCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGlnAla 140
Db 457 GAGTGTGAGCTAGAAGCCCTGCTGGAGAGAGGCTGCTCCCTGTGTGCTGTCTCCCGCAGGCC 516
Qy 141 ProPheProLysLeuGlyTyrAspAspGluLeuArgLysProGlyAlaGlnIleTyrMet 160
Db 517 CCATTTCCCAAGCTGGGCTGGGATGACAACTGGGAAACCCGGCGCCAGATCTACATG 576
Qy 161 ArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValile 180
Db 577 CGCTTTCATCGAGGAGCACACCTGCTACGATGCCATGCGCAACTAGCTCCAAGTAGTCAATC 636
Qy 181 PheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyValArg 200
Db 637 TTCGACACCATGCTGGAGATCAAGAAGCCCTTCTTGTCTGTGGTGGCAACGGTGTGGG 696
```

```
Qy 201 AlaAlaProLeuTrpAspSerLysGlnSerPheValGlyMetLeuThrIleThrAsp 220
Db 697 GCAGCCCTCTATGGGACAGCAAGACAGAGCTTTGTGGGATGCTGACCATCACTGAC 756
Qy 221 PheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGlu 240
Db 757 TTCATCTCTGGTGGCTGCATCGCTACTACAGGTCCCTCGGTCCAGATCTATGAGATTGAA 816
Qy 241 GlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeuVal 260
Db 817 CAACATAAGATTGAGACCTGGAGGAGATCTACCTGCAAGGCTCTTCAAGCCTCTGTC 876
Qy 261 SerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIle 280
Db 877 TCCATCTCTCTAATGATAGCTGCTTTGAAGCTGTCTACACCTCATCAAGAACCGGATC 936
Qy 281 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 300
Db 937 CATCGCCTGCTGCTTCTTGAACCCGGTGTACGGCAACGTACTCCACATCCTCACACAAA 996
Qy 301 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 320
Db 997 CGCTGTCTCAAGTCTCTGACATCTTTGGTTCCTGTGCTGCCCGCCTCTCTCTAC 1056
Qy 321 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGluThr 340
Db 1057 CGCACTATCAAGATTTGGGCATCGGCACATTCGAGACTTGGCTGTGTGCTGGAGACA 1116
Qy 341 AlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuProVal 360
Db 1117 GCACCCATCTGACTGCACTGGACATCTTTGTGACCGCGGTGTGTGCACTGCCTGTG 1176
Qy 361 ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeuAla 380
Db 1177 GTCAAGANTGTGTGCTGAGTGTGGGCTCTATTCCCGCTTTGATGTGATCACTGGCT 1236
Qy 381 AlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr 400
Db 1237 GCCCAGCAAACTCAACACCTGACATGATGATGTGGGAGAGCCCTGAGGCAGAGACA 1296
Qy 401 LeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAsp 420
Db 1297 CTATGTCTGGAGGGAGTCTTCTTCCCGCAGCCACAGAGCTTGGGGAAAGTGAATGAC 1356
Qy 421 ArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeu 440
Db 1357 AGGATTGCTCGGAGCAGGTACACAGGCTGGTGTAGTGGACGAGACCCAGCATCTCTTG 1416
Qy 441 GlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAsp 460
Db 1417 GCGTGGTCTCCCTCTCGACATCTTTCAGGCACTGTGTGCTCAGCCCTGCTGGCATCGAT 1476
Qy 461 AlaLeuGlyAla 464
Db 1477 GCGCTCGGGGCC 1488
```

RESULT 14

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US-10-399-103-386
; Sequence 386, Application US/10399103
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-115/ 785
; CURRENT APPLICATION NUMBER: US/10/399,103
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 09/687,527
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 892
; SOFTWARE: Custom
; SEQ ID NO 386
; LENGTH: 2314
; TYPE: DNA
```

```
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (22)..(1491)
US-10-399-103-386
```

```
Alignment Scores:
Pred. No.: 4,52e-304 Length: 2314
Score: 2391.00 Matches: 461
Percent Similarity: 99.78% Conservative: 2
Best Local Similarity: 99.35% Mismatches: 1
Query Match: 99.50% Indels: 0
DB: 0 Gaps: 0
```

US-10-070-794a-30 (1-464) x US-10-399-103-386 (1-2314)

```
Qy 1 MetSerPheLeuGluGlnGluAsnSerSerTrpProSerProAlaValThrSerSer 20
Db 97 ATGAGCTTCTAGAGCAAGAAAACAGCAGCTCATGGCCATCACCCAGCTGTGACCCAGCAG 156
Qy 21 SerGluArgIleArgGlyLysArgArgAlaLysAlaLeuArgTrpThrArgGlnLysSer 40
Db 157 TCAGAAAGAATCCGTGGGAAACCGAGGGCCAAAGCCTTGAGATGGACAAAGCGCAAGATCG 216
Qy 41 ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60
Db 217 GTGAGGAAGGGAGGCCAGCAGGTACAGGGGAAGGTCCCGGTCCAGGCCAGCTGCTGAG 276
Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla 80
Db 277 TCCACCGGGCTGGAGGCCACATTCCTCCCAAGACCACACCTTGGCTCAAGCTGATCTGCC 336
Qy 81 GlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSerAla 100
Db 337 GGGTGGGCACTCCACCAACAGGGTGGGACTGCCCTCCCTCTGACTGTACAGCTCAGCT 396
Qy 101 AlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTrp 120
Db 397 GCAGGCTCCAGACACAGATGATGTGAGCTGGCCACGAGGTTCACGAGCCAGGCTGG 456
Qy 121 GluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGlnAla 140
Db 457 GAGTGTGAGCTAGAAAGCCCTGCTGGAAGAGAGAGGCTGCCCTGTGCTGTCTCCCGCAGGCC 516
Qy 141 ProPheProLysLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnIleTyrMet 160
Db 517 CCATTTCCCAAGCTGGGCTGGGATGACGAACTCGGAAACCCCGGCGCCAGACTACATG 576
Qy 161 ArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValIle 180
Db 577 CGCTTCATCGAGGAGCACACCTGTACATGCCATGGCACTAGCTCCAAGCTAGTCATC 636
Qy 181 PheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyValArg 200
Db 637 TTCGACACCATGCTGGAGATCAAGAAGCCCTTCTTGTCTGTGTGGCCAAACGGGTGTGGCG 696
Qy 201 AlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAsp 220
Db 697 GCAGCCCTCTATGGGACAGCAAGACAGAGCTTTGTGGGGATGCTGACCATCACTGAC 756
Qy 221 PheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGlu 240
Db 757 TTCATCTCTGGTGGCTGCATCGCTACTACAGGTCCCTCGGTCCAGATCTATGAGATTGAA 816
Qy 241 GlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeuVal 260
Db 817 CAACATAAGATTGAGACCTGGAGGAGATCTACCTGCAAGGCTGCTTCAAGCCTCTGTC 876
Qy 261 SerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIle 280
Db 877 TCCATCTCTCTAATGATAGCTGCTTTGAAGCTGTCTACACCTCATCAAGAACCGGATC 936
Qy 281 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 300
```

```

Db 937 CATGCCCTGCTGTTCTTGACCCGGGTGTCAGGCAACGTAATCCATCCTCCACACAAA 996
Qy 301 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 320
Db 997 CGCTGCTCAAGTTCCTGCACATCTTGGTTCCTGCTGCCCGCCCTCTTCTCTAC 1056
Qy 321 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGluThr 340
Db 1057 CGCACTATCCAAAGATTGGGCATCGGCACATTCGGAGACTTGGCTGTGGTCTGGAGACA 1116
Qy 341 AlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProVal 360
Db 1117 GCACCCATCTCTGACTGACATCTTGTGGACCGCGGTGTCTGCACTGCCCTGTG 1176
Qy 361 ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeuAla 380
Db 1177 GTCAACGAATGTGCTAGGTGCTGGCTCTATTCCCGCTTGTATGTGATTCACCTGGCT 1236
Qy 381 AlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr 400
Db 1237 GCCCAGCAAACTACAAACCACTGGACATGATGTGGGAGAACCCCTGAGGACAGGACA 1296
Qy 401 LeuCysLeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValIleAsp 420
Db 1297 CTATGCTGTGAGGAGTCTCTTCTGCGACGCCCCACGAGACTTGGGGGAAGTATCGAC 1356
Qy 421 ArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeu 440
Db 1357 AGGATGCTCGGAGACAGGTACACAGCTGGTGTGTAGTGACGAGACCCAGCATCTCTTG 1416
Qy 441 GlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAsp 460
Db 1417 GCGGTGCTCTCCCTCTCCGACATCTTCAGGCACTGGTGTCTGAGCCCTGCTGGCATCGAT 1476
Qy 461 AlaLeuGlyAla 464
Db 1477 GCCCTCGGGGCC 1488

```

RESULT 15

```

US-10-399-103A-386
; Sequence 386, Application US/10399103A
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-115/ 785
; CURRENT APPLICATION NUMBER: US/10/399,103A
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: PCT/US01/27760
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: US 09/687,527
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 892
; SOFTWARE: Custom
; SEQ ID NO 386
; LENGTH: 2314
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (22)..(1491)
US-10-399-103A-386

```

Alignment Scores:

```

Pred. No.: 4,52e-304 Length: 2314
Score: 2391.00 Matches: 461
Percent Similarity: 99.78% Conserved: 2
Best Local Similarity: 99.35% Mismatches: 1
Query Match: 99.50% Indels: 0
DB: 50 Gaps: 0

```

US-10-070-794A-30 (1-464) x US-10-399-103A-386 (1-2314)

```

Qy 1 MetSerPheLeuGluGlnGluAsnSerSerSerTyrProSerProAlaValThrSerSer 20
Db 97 ATGAGCTTCTTAGAGCAAGAAAAACAGCAGCTCATGGCCATCACCAGCTGTGACGACGAG 156
Qy 21 SerGluArgIleArgGlyIysArgAlaValAlaLeuArgTyrThrArgGlnLysSer 40
Db 157 TCAGAAAGAAATCCGTGGGAAACCGAGGGCCAAAGCCCTTGAGATGGACAAAGCAAGTCG 216
Qy 41 ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60
Db 217 GTGGAGGAAGGGAGGCCACAGCTCAGGGGGAAGGTCCCGGTCCAGGCCAGCTGCTGAG 276
Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla 80
Db 277 TCCACCGGGCTGGAGGCCACATTCGCCACAGACCAACCCCTTGGCTCAAGCTGATCTGCC 336
Qy 81 GlyValGlyThrProProThrGlyTyrAspCysLeuProSerAspCysThrAlaSerAla 100
Db 337 GGGGTGGGCACTCCACCAACAGGGTGGGACTGCTCCCTCTGACTGTACAGCCTCAGCT 396
Qy 101 AlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTyr 120
Db 397 GCAGGCTCCAGCACACATGATGTGGAGCTGCCACCGAGTTCCAGGCCACAGAGCCCTGG 456
Qy 121 GluCysGluLeuGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGlnAla 140
Db 457 GAGTGTGAGCTAGAAAGCCCTGCTGGAAGAGAGGCGCTGCCCTGTGCTGCTGCCGCGGCC 516
Qy 141 ProPheProLysLeuGlyTyrAspAspGluLeuArgLysProGlyAlaGlnIleTyrMet 160
Db 517 CCATTTCCTCCAGCTGGGCTGGGATGACAACTCGGAAACCCCGGCCCTCAGATCTCATG 576
Qy 161 ArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValIle 180
Db 577 CGCTTCATCGAGAGGACACCTCTGCTAGCATGCCATGSCAACTAGCTCCAGCTAGTCAATC 636
Qy 181 PheAspThrMetLeuGluLeuLysLysAlaPhePheAlaLeuValAlaAsnGlyValArg 200
Db 637 TTCGACACCATGCTGGAGATCAAGAAGGCCCTCTTTGCTCTGGTGGCCAAACGGTGTGGG 696
Qy 201 AlaAlaProLeuTyrAspSerLysGlnSerPheValGlyMetLeuThrIleThrAsp 220
Db 697 GCAGCCCTCTATGGGACAGCAAGAGCAGAGCTTTGTGGGATGCTGACCATCAGCTGAC 756
Qy 221 PheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGlu 240
Db 757 TTCATCTCTGCTGTGATCTGCTACTACAGTCCCTCTGCTGCTGATCTATGATTTGAA 816
Qy 241 GlnHisLysIleGluThrTyrArgGluIleTyrLeuGlnGlyCysPheLysProLeuVal 260
Db 817 CAACATAAGATTGAGACCTGGAGGAGATCTACTCTGCAAGGCTGCTTCAAGCCTCTGGTC 876
Qy 261 SerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIle 280
Db 877 TCCATCTCTCTAATGATAGCTGTGTTGAGCTGTCTACACCTCTCATCAAGAACCCGATC 936
Qy 281 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 300
Db 937 CATCGCTCTGCTGTTCTTGACCCCGGTGTGAGGCAACGCTACTCCACATCTCCACACAAA 996
Qy 301 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 320
Db 997 CGCCTGCTCAAAGTTCCTGACATCTTGGTTCCTGCTGCCCGGCCCTCTCTCTCTAC 1056
Qy 321 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGluThr 340
Db 1057 CGCACTATCCAAAGATTGGGCATTCGGACATTCGGAGCTTGGCTGTGGTGGGAGACA 1116
Qy 341 AlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProVal 360
Db 1117 GCACCCATCTGACTGACTGGACATCTTGTGGACCGGGCTGTGTGCTGACCTGCTGTG 1176
Qy 361 ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeuAla 380

```

Db		1177	GTCAACGAATGTGTGTCAGTGGGCTCTATTCCCGCTTTGATGTGATTCACCTGGCT	1236
Qy		381	AlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr	400
Db		1237	GCCCAGCAACCTACACCACTGACATGAGTGTGGGAGAGCCCTGAGGCAGAGGACA	1296
Qy		401	LeuCysLeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValIleAsp	420
Db		1297	CTATGCTCTGGAGGAGTCCCTTCTCTGCCAGCCCCACGAGAGCTTGGGGGAAGTGATCGAC	1356
Qy		421	ArgIlealaargGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeu	440
Db		1357	AGGATTGCTCGGGAGCGAGGTACACAGGCTGGTGTGTAGTGACGAGACCCAGCATCTCTTG	1416
Qy		441	GlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAsp	460
Db		1417	GGCGTGTCTCCCTCTCCGACATCTTCAGGCACCTGGTGCTCAGCCCTGCTGGCATCGAT	1476
Qy		461	AlaLeuGlyAla	464
Db		1477	GCCCTCGGGGC	1488

Search completed: January 26, 2006, 06:57:49
Job time : 7377.54 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 24, 2006, 22:01:17 ; Search time 136.967 Seconds
(without alignments)
2390.094 Million cell updates/sec

Title: US-10-070-794a-30
Perfect score: 2403
Sequence: 1 MSFLEQNSSWPSPAVTSS.....LSDIQLVLSPAGIDALGA 464

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2403	100.0	464	1	AAGK3_HUMAN
2	2398	99.8	489	2	Q4V779_HUMAN
3	2390	99.5	489	2	Q4Q0G8_HUMAN
4	2011	83.7	464	2	Q532T5_PIG
5	2011	83.7	514	1	AAKG1_PIG
6	2010	83.6	464	2	Q8C34I_MOUSE
7	2010	83.6	489	2	Q8BGW7_MOUSE
8	2001.5	83.3	490	2	Q80WK8_MOUSE
9	1988.5	82.8	465	2	Q4G3U3_BOVIN
10	1920	79.9	447	2	Q6TEH8_HORSE
11	1888	78.6	440	2	Q6U7S1_HORSE
12	1280	53.3	363	2	Q4JK38_CHICK
13	1280	53.3	382	2	Q4JK39_CHICK
14	1213.5	50.5	337	2	Q7ZY12_XENLA
15	1100.5	45.8	443	2	Q8BIQ9_MOUSE
16	1093.5	45.5	524	2	Q5R4S0_PONPY
17	1093	45.5	525	2	Q6NU10_HUMAN
18	1093	45.5	569	1	AAKG2_HUMAN
19	1092.5	45.5	558	2	Q6P6G0_XENLA
20	1091.5	45.4	343	2	Q4RVG2_TETNG
21	1084.5	45.1	328	2	Q5ZK07_CHICK
22	1084.5	45.1	566	2	Q91NG5_MOUSE
23	1082.5	45.0	448	2	Q4QRB9_FAT
24	1080.5	45.0	328	2	Q53X07_HUMAN
25	1078	44.9	326	2	Q6V7V4_FAT
26	1078	44.9	326	2	Q6V7V5_MOUSE
27	1050	43.7	297	2	Q4RTT1_TETNG
28	1040	43.3	330	2	Q6PCS7_BRARE
29	1028	42.8	330	1	AAKG1_FAT
30	1028	42.8	330	2	Q4QQW6_FAT
31	1027	42.7	323	2	Q4RXW4_TETNG

32	1019	42.4	333	2	Q4S129_TETNG
33	1018	42.4	330	2	Q5PRE8_MOUSE
34	1017	42.3	330	2	Q6X275_PIG
35	1017	42.3	331	1	AAKG1_HUMAN
36	1013	42.2	330	1	AAKG1_BOVIN
37	1003	41.7	299	2	Q4RSP4_MACFA
38	1002.5	41.7	340	2	Q8N7V9_HUMAN
39	1000	41.6	287	2	Q6U7I6_RAT
40	1000	41.6	334	2	Q6GN94_XENLA
41	997	41.5	330	1	AAKG1_MOUSE
42	960	40.0	329	2	Q4RY44_TETNG
43	899	37.4	267	2	Q8EM63_MOUSE
44	874.5	36.4	718	2	Q810K6_DROME
45	874.5	36.4	814	2	Q810A1_DROME

ALIGNMENTS

RESULT 1
ID AAKG3_HUMAN STANDARD; PRT; 464 AA.
AC Q8UG19; Q9NEL1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE 5'-AMP-activated protein kinase, gamma-3 subunit (AMPK gamma-3 chain)
DE (AMPK gamma3).
GN Name=PRKAG3; Synonyms=AMPKG3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20164049; PubMed=10698692; DOI=10.1042/0364-6021:3460659;
RA Cheung P.C.F., Salt I.P., Davies S.P., Hardie D.G., Carling D.;
RT "Characterization of AMP-activated protein kinase gamma-subunit
RT isoforms and their role in AMP binding.";
RL Biochem. J. 346:659-669(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skeletal muscle;
RX MEDLINE=20280150; PubMed=10818001; DOI=10.1126/science.288.5469.1248;
RA Milan D., Jeon J.-T., Looft C., Amarger V., Robic A., Thelander M.,
RA Rogel-Gaillard C., Paul S., Iannuccelli N., Rask L., Ronne H.,
RA Lundstroem K., Reinsch N., Gellin J., Kalm B., Le Roy P., Chardon P.,
RA Andersson L.;
RT "A mutation in PRKAG3 associated with excess glycogen content in pig
RT skeletal muscle.";
RL Science 288:1248-1251(2000).
CC -I- FUNCTION: AMPK is responsible for the regulation of fatty acid
CC synthesis by phosphorylation of acetyl-CoA carboxylase. Also
CC regulates cholesterol synthesis via phosphorylation and
CC inactivation of hydroxymethylglutaryl-CoA reductase and hormone-
CC sensitive lipase. This is a regulatory subunit. It may play a role
CC in the regulation of energy metabolism in skeletal muscle.
CC -I- SUBUNIT: Heterotrimer of an alpha catalytic subunit, a beta and a
CC gamma non-catalytic regulatory subunits.
CC -I- TISSUE SPECIFICITY: Skeletal muscle, with weak expression in heart
CC and pancreas.
CC -I- SIMILARITY: Belongs to the 5'-AMP-activated protein kinase gamma
CC subunit family.
CC -I- SIMILARITY: Contains 4 CBS domains.

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the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.

EMBL; AJ249977; CAB65117.1; ALT_INIT; mRNA.

DR EMBL; AF214519; AAF73987.1; -; mRNA.
 DR Ensembl; ENSG00000115592; Homo sapiens.
 DR HGNC; HGNC:9387; PRKAG3.
 DR MIM; 604976; -.
 DR GO; GO:0004679; P:AMP-activated protein kinase activity; TAS.
 DR GO; GO:0007243; P:protein kinase cascade; TAS.
 DR InterPro; IPR000644; CBS.
 DR Pfam; PF00571; CBS; 2.
 DR SMART; SM00116; CBS; 4.
 KW CBS domain; Fatty acid biosynthesis; Lipid synthesis; Repeat.
 FT DOMAIN 147 201 CBS 1.
 FT DOMAIN 228 282 CBS 2.
 FT DOMAIN 303 356 CBS 3.
 FT DOMAIN 375 428 CBS 4.
 FT CONFLICT 58 58 T -> A (in Ref. 1).
 FT CONFLICT 163 164 MQ -> IE (in Ref. 1).
 FT CONFLICT 398 398 Q -> K (in Ref. 1).
 FT CONFLICT 461 464 ALGA -> PSGPEKI (in Ref. 1).
 SQ SEQUENCE 464 AA; 51514 MW; 53985C2C77003A63 CRC64;
 Query Match 100.0%; Score 2403; DB 1; Length 464;
 Best Local Similarity 100.0%; Pred. No. 3.1e-174;
 Matches 464; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MSFLEQNSSWSPSPAVTSSSIRGRKRAKALRWTRQKSVSEGEPPGQEGPGRSPRTAE 60
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 Db 121 ECELEGLLEERPALCLSPQAPFPKLGWDDLELRKFGAQIYMRFMQEHCTCYDAMATSSKLVI 180
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 Db 181 FDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMGLTITDFILVHLHYRSPVLQIYEIE 240
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 Db 241 QHKIETWREIYLCQCFKPLVSI SPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHK 300
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 Qy 361 VNECGQVGLYSRFDVHLAAQQTYNHLDMSVGEALRQRTLCLEGLVSCQPHESLGEVID 420
 Db 361 VNECGQVGLYSRFDVHLAAQQTYNHLDMSVGEALRQRTLCLEGLVSCQPHESLGEVID 420
 Qy 421 RIAREQVHRLVLDVETQHLGVLSLSDILQALVLSPPAGIDALGA 464
 Db 421 RIAREQVHRLVLDVETQHLGVLSLSDILQALVLSPPAGIDALGA 464
 RESULT 2
 Q4V779 HUMAN
 ID Q4V779_HUMAN PRELIMINARY; PRT; 489 AA.
 AC Q4V779;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE AMP-activated protein kinase, non-catalytic gamma-3 subunit.
 GN Name=PRKAG3;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RC TISSUE=PCR rescued clones;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=PCR rescued clones;
 RG NIH MC Project;
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC098102; AAH98102.1; -; mRNA.
 DR EMBL; BC098277; AAH98277.1; -; mRNA.
 KW Kinase.
 SQ SEQUENCE 489 AA; 54258 MW; 0E93E2B5117B328D CRC64;
 Query Match 99.8%; Score 2398; DB 2; Length 489;
 Best Local Similarity 99.8%; Pred. No. 7.9e-174;
 Matches 463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 MSFLEQNSSWSPSPAVTSSSIRGRKRAKALRWTRQKSVSEGEPPGQEGPGRSPRTAE 60
 Db 26 MSFLEQNSSWSPSPAVTSSSIRGRKRAKALRWTRQKSVSEGEPPGQEGPGRSPAEE 85
 Qy 61 STGLEATFPKTTPLAQADPAGVGTPTGWDCLPSDCTASAGSSTDVDELATEPPATEAW 120
 Db 86 STGLEATFPKTTPLAQADPAGVGTPTGWDCLPSDCTASAGSSTDVDELATEPPATEAW 145
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 Db 146 ECELEGLLEERPALCLSPQAPFPKLGWDDLELRKFGAQIYMRFMQEHCTCYDAMATSSKLVI 205
 Qy 181 FDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMGLTITDFILVHLHYRSPVLQIYEIE 240
 Db 206 FDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMGLTITDFILVHLHYRSPVLQIYEIE 265
 Qy 241 QHKIETWREIYLCQCFKPLVSI SPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHK 300
 Db 266 QHKIETWREIYLCQCFKPLVSI SPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHK 325
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 Db 326 RLLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLETPILTALDIFVDRRVSPALPV 385
 Qy 361 VNECGQVGLYSRFDVHLAAQQTYNHLDMSVGEALRQRTLCLEGLVSCQPHESLGEVID 420
 Db 386 VNECGQVGLYSRFDVHLAAQQTYNHLDMSVGEALRQRTLCLEGLVSCQPHESLGEVID 445
 Qy 421 RIAREQVHRLVLDVETQHLGVLSLSDILQALVLSPPAGIDALGA 464
 Db 446 RIAREQVHRLVLDVETQHLGVLSLSDILQALVLSPPAGIDALGA 489
 RESULT 3
 Q4QOG8 HUMAN
 ID Q4QOG8_HUMAN PRELIMINARY; PRT; 489 AA.
 AC Q4QOG8;

DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE AMP-activated protein kinase, non-catalytic gamma-3 subunit.
 GN Name=PRKAG3;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=PCR rescued clones;
 RA MDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RX Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaudo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ugin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fanev J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smalhus D.E.,
 RA Schnurch A., Schein J.B., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=PCR rescued clones;
 RG NIH MGC Project;
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC098306; AAH98306.1; -; mRNA.
 DR EMBL; BC098255; AAH98255.1; -; mRNA.
 KW Kinase.
 SQ SEQUENCE 489 AA; 54232 MW; A67D9DEAB76BFC9 CRC64;
 Query Match 99.5%; Score 2390; DB 2; Length 489;
 Best Local Similarity 99.6%; Pred. No. 3.2e-173;
 Matches 462; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MSFLEQENSSSWPSPAVTSSSRIRGKRRAKALRWTRQKSVGEPPGQGGPRSPRTAE 60
 DB 26 MSFLEQENSSSWPSPAVTSSSRIRGKRRAKALRWTRQKSVGEAPGQGGPRSPAAE 85
 QY 61 STGLEATFPKTTPLAQADPAGVTPPTGWDCPLSDCTASAGSSTDDVELATEFPATEAW 120
 DB 86 STGLEATFPKTTPLAQADPAGVTPPTGWDCPLSDCTASAGSSTDDVELATEFPATEAW 145
 QY 121 ECEGLELEERPALCLSPQAPFFKLGWDDDELKPGQAIYMRFMQEHCTCYDAMATSSKLVI 180
 DB 146 ECEGLELEERPALCLSPQAPFFKLGWDDDELKPGQAIYMRFMQEHCTCYDAMATSSKLVI 205
 QY 181 FDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMLTITDFFILVHRYRSPVLQIYEI 240
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 DB 326 RLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSAALPV 385
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 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE AMP-activated protein kinase, non-catalytic gamma-3 subunit.
 GN Name=PRKAG3;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=PCR rescued clones;
 RA MDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RX Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaudo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ugin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fanev J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smalhus D.E.,
 RA Schnurch A., Schein J.B., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=PCR rescued clones;
 RG NIH MGC Project;
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC098306; AAH98306.1; -; mRNA.
 DR EMBL; BC098255; AAH98255.1; -; mRNA.
 KW Kinase.
 SQ SEQUENCE 489 AA; 54232 MW; A67D9DEAB76BFC9 CRC64;
 Query Match 99.5%; Score 2390; DB 2; Length 489;
 Best Local Similarity 99.6%; Pred. No. 3.2e-173;
 Matches 462; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MSFLEQENSSSWPSPAVTSSSRIRGKRRAKALRWTRQKSVGEPPGQGGPRSPRTAE 60
 DB 26 MSFLEQENSSSWPSPAVTSSSRIRGKRRAKALRWTRQKSVGEAPGQGGPRSPAAE 85
 QY 61 STGLEATFPKTTPLAQADPAGVTPPTGWDCPLSDCTASAGSSTDDVELATEFPATEA 119
 DB 86 STGLEATFPKTTPLAQADPAGVTPPTGWDCPLSDCTASAGSSTDDVELATEFPATEA 120
 QY 120 WECEGLELEERPALCLSPQAPPPKLGWDDDELKPGQAIYMRFMQEHCTCYDAMATSKLV 179
 DB 121 SGDEL-GLVEEKPAFCPSPEVLLPRLGWDDDELKPGQAIYMRFMQEHCTCYDAMATSKLV 179
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 DB 180 IFDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMLTITDFFILVHRYRSPVLQIYEI 239
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 QY 420 DRIARQVHRLVLDVSTQHLGVVSLDILQALVLSFAGIDALGA 464
 DB 420 DRIARQVHRLVLDVSTQHLGVVSLDILQALVLSFAGIDALGA 464
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE AMP-activated protein kinase, non-catalytic gamma-3 subunit.
 GN Name=PRKAG3;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
 OC Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC PubMed=14970697; DOI=10.1159/000075743;
 RX Anarger V., Erlansson R., Pielberg G., Jeon J.T., Andersson L.;
 RA "Comparative sequence analysis of the PRKAG3 region between human and
 RT pig: evolution of repetitive sequences and potential new exons."
 RL Cytogenet. Genome Res. 102:163-172(2003).
 DR EMBL; AY264345; AAP12533.1; -; mRNA.
 KW Kinase.
 SQ SEQUENCE 464 AA; 51308 MW; 17638CB12A2BA9DF CRC64;
 Query Match 83.7%; Score 2011; DB 2; Length 464;
 Best Local Similarity 86.0%; Pred. No. 2.1e-144;
 Matches 400; Conservative 19; Mismatches 44; Indels 2; Gaps 2;
 QY 1 MSFLEQENSSSWPSPAVTSSSRIRGKRRAKALRWTRQKSVGEPPGQGGPRSPRTAE 60
 DB 1 MSFLEQENSSSWPSPAVTSSSRIRGKRRAKALRWTRQKSVGEPPGQGGPRSPRTAE 60
 QY 61 STGLEATFPKTTPLAQADPAGVTPPTGWDCPLSDCTASAGSSTDDVELATEFPATEA 119
 DB 61 STGLEATFPKTTPLAQADPAGVTPPTGWDCPLSDCTASAGSSTDDVELATEFPATEA 120
 QY 120 WECEGLELEERPALCLSPQAPPPKLGWDDDELKPGQAIYMRFMQEHCTCYDAMATSKLV 179
 DB 121 SGDEL-GLVEEKPAFCPSPEVLLPRLGWDDDELKPGQAIYMRFMQEHCTCYDAMATSKLV 179
 QY 180 IFDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMLTITDFFILVHRYRSPVLQIYEI 239
 DB 180 IFDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMLTITDFFILVHRYRSPVLQIYEI 239
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 DB 360 VNECGQVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQRTLCLEGLVSCQPHESLGEVI 419
 QY 420 DRIARQVHRLVLDVSTQHLGVVSLDILQALVLSFAGIDALGA 464
 DB 420 DRIARQVHRLVLDVSTQHLGVVSLDILQALVLSFAGIDALGA 464
 RESULT 5
 AAKG3_PIG STANDARD; PRT; 514 AA.

RC	STRAIN=C57BL/6J; TISSUE=Bone;	
RX	MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;	
RA	Shibata K., Itoh M., Aizawa K., Nagakawa S., Sasaki N., Carninci P.,	
RA	Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,	
RA	Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,	
RA	Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,	
RA	Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,	
RA	Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,	
RA	Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;	
RT	"RIKEN integrated sequence analysis (RISA) system-384-format	
RT	sequencing pipeline with 384 multicapillary sequencer.";	
RL	Genome Res. 10:1757-1771(2000).	
RN	[7]	
RP	NUCLEOTIDE SEQUENCE.	
RC	STRAIN=C57BL/6J; TISSUE=Bone;	
RA	Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,	
RA	Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,	
RA	Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,	
RA	Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,	
RA	Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,	
RA	Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,	
RA	Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,	
RA	Saito K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,	
RA	Sasaki D., Shibata K., Shinagawa A., Shiraki T., Soabe Y., Tagami M.,	
RA	Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,	
RA	Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;	
RL	Submitted (JUL-2001) to the ENBL/GenBank/DBJ databases.	
DR	ENBL; AF525500; AAN47137.1; -; mRNA.	
DR	ENBL; AK036585; BAC29492.1; -; mRNA.	
DR	Ensembl; ENSMUSG0000006542; Mus musculus.	
DR	MGI; MGI:1891343; Prkg3.	
DR	GO; GO:0016301; P:kinase activity; IEA.	
DR	GO; GO:0006633; P:fatty acid biosynthesis; IEA.	
DR	InterPro; IPR006644; CBS.	
DR	Pfam; PF00571; CBS; 2.	
DR	SMART; SM00116; CBS; 4.	
KW	Kinase.	
SQ	SEQUENCE 489 AA; 53848 MW; 85C9F71DBBDDA5D CRC64;	
Query Match 83.6%; Score 2010; DB 2; Length 489;		
Best Local Similarity 85.8%; Pred. No. 2.7e-144;		
Matches 399; Conservative 16; Mismatches 48; Indels 2; Gaps 2;		
Qy	1 MSFLEQENSSWPSPAVTSSSIRGKRRAKALRWTRQKSVVEEGEPGQEGPSRPTAE 60	
Db	26 MDFLEQ-GENSWPSPAVTSSSIRGKRRAKALRWTRQEAEEAEPPGLGEGAQSRPAE 84	
Qy	61 STGLEATFPKTTPLAQADP-AGVGTPTGWDCLPSCDTASAAGSSTDDELATEFPATEA 119	
Db	85 STQREATFPKATPLAQAVPLAEAEPTSPTGWDLLLPDCAASAGSGSTGDELTIEFPAP 144	
Qy	120 WECELEGLEERPALCLSPQAPFPKLGWDDLRKPGAQIYMRFMQEHCTCYDAMATSSKLV 179	
Db	145 WDCELEGIGKDRPRPGSPQAPLGLSWDDLEQEGAQVYMHFMQEHCTCYDAMATSSKLV 204	
Qy	180 IFDTMLEIKKFAFFALVANGVRAAPLWDSKKQSFVGMGLTITDFILVHRYRSPVLQIYEI 239	
Db	205 IFDTTLEIKKFAFFANVANGVRAAPLWDSKKQSFVGMGLTITDFILVHRYRSPVLQIYEI 264	
Qy	240 EQHKIETWREIYLOQCFKPLVSIISPNDSLFEAVYTLIKNRHRLPVLDPVSGNVHLIHTH 299	
Db	265 EEHKIETWREIYLOQCFKPLVSIISPNDSLFEAVYALIKNRHRLPVLDPVSGTVLYILTH 324	
Qy	300 KRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRVRSALP 359	
Db	325 KRLKFLHIFGALLPRPSFLCRTIQDLGIGTFRDLAVVLETAPVLTALDIFVDRVRSALP 384	
Qy	360 VVNECGQVVGYSRFDVTHLAAQQTYNHLDMSVGEALQRQTLCLGVLSCQPHESLGEVI 419	
Db	385 VVNEGSQVVGYSRFDVTHLAAQQTYNHLDMSVGEALQRQTLCLGVLSCQPHESLGEVI 444	
Qy	420 DRIAREQVHRLVLDVETQHLGVVSLSDILQALVLSFAGIDALGA 464	


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RA Sandberg K., Anderson L.;
RT "Molecular characterization and mutational screening of the PRKAG3
RL gene in the horse.";
RL Cytogenet. Genome Res. 102:211-216(2003).
DR EMBL; AY376689; AA083583.1; -; mRNA.
DR GO; GO:0016301; P:kinase activity; IEA.
DR InterPro; IPR000644; CBS.
DR Pfam; PF00571; CBS; 2.
DR SMART; SM00116; CBS; 3.
KW Kinase.
FT NON TER 440 440
SQ SEQUENCE 440 AA; 48561 MW; CB6C706D98E4A66A CRC64;

Query Match 78.6%; Score 1888; DB 2; Length 440;
Best Local Similarity 84.4%; Pred. No. 4.5e-135;
Matches 372; Conservative 25; Mismatches 42; Indels 2; Gaps 2;

Qy 1 MSFLEQENSSWPSPAVTSSSIRGRKRAKALRWTRQKSVEEGEPGQEGPGRSPRTAE 60
Dy |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MSFLEQGDSSWPSPAVTASSERSHGTPGPPALSWTKQKAVEAELSGPEGPSRPAE 60
Qy 61 STGLEATFPKTTPLAQADP-AGVGTPTPTGMDCLPSCDCTASAGSSTDDELATEFPATEA 119
Dy |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 STGLEATFPKTTPLAQADPAGVDTPPPERGILPSCDSSSTGSDTDLGLIEFSATAG 120
Qy 120 WECSLEGLLERRPALCISQAPFPKLGWDDLRKPGAIYRFRMQEHTCYDAMATSKLV 179
Dy |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
121 WGCEL-GLVETTPARYSPRALLPRLGWDDLRKPGAIYRFRMQEHTCYDAMATSKLV 179
Qy 180 IFDFTMLETKKAFALVANGVRAAPLWDSKKOSFVGMLTITDILVLRHYRSPVQIYEI 239
Dy |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
180 IFDFTMLETKKAFALVANGVRAAPLWDSKKOSFVGMLTITDILVLRHYRSPVQIYEI 239
Qy 240 EQHKIETWREIYLGCCFKPLVSI SPNDSLF EAVYTLIKNRIHRLPVLDPVSGNVHLH 299
Dy |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
240 EHKIETWREIYLGCCFKPLVSI SPNDSLF EAVYTLIKNRIHRLPVLDPVSGNVHLH 299
Qy 300 KRLKLFHIFGSLPRSPFLYRTODLGIGTFRDLAVVLETAFLTALDIFVDRVSALP 359
Dy |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
300 KRLKLFHIFGSLPRSPFLYRTODLGIGTFRDLAVVLETAFLTALDIFVDRVSALP 359
Qy 360 VVNEGQVVGYSRFDVTHLAAQTYNHLDMSVGEALRQRTLCLEGVLSQCPHESLGEVI 419
Dy |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
360 VVNEGQVVGYSRFDVTHLAAQTYNHLDMSVGEALRQRTLCLEGVLSQCPHESLGEVI 419
Qy 420 DRIAREQVHRLVLDVDETOHLL 440
Dy |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
420 DRIAREQVHRLVLDVDETOHLL 440

RESULT 12
Q4JK38 CHICK
ID Q4JK38 CHICK PRELIMINARY; PRT; 363 AA.
AC Q4JK38
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE 5'-AMP-activated protein kinase gamma-3 non-catalytic subunit short
DE form.
GN Name=PRKAG3;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Skeletal muscle;
RA Proszkowiec-Weglarz M., Richards M.P., Poch S.M.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; DQ079815; AAY86042.1; -; mRNA.
KW Kinase.
SQ SEQUENCE 363 AA; 41151 MW; 06FCD094FCC3AEDC CRC64;
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Query Match 53.3%; Score 1280; DB 2; Length 363;
Best Local Similarity 75.7%; Pred. No. 6.7e-89;
Matches 240; Conservative 43; Mismatches 34; Indels 0; Gaps 0;

Qy 148 DDELKRPQAIYMRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFALVANGVRAAPLWDS 207
Dy |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
47 DNNFQSPDAEVYMHFMRSHCCYDAVPTSKLVVDFDTLEIKKAFALVANGVRAAPLWDS 106
Qy 208 KKQSFVGMLTITDILVLRHYRSPVQIYEI EHQKIETWREIYLGCCFKPLVSI SPNDS 267
Dy |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
107 KKQSFVGMLTITDILVLRHYRSPVQIYEI EHQKIETWREIYLGCCFKPLVSI SPNDS 166
Qy 268 LFEAVYTLIKNRIHRLPVLDPVSGNVHLHILTHKRLKFLHIFGSLPRSPFLYRTIQDLG 327
Dy |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
167 LFDVAVSLIKKHILHRLPVIEPISGNVHLHILTHKRLKFLHIFGSLPRSPFLYRTIQDLG 226
Qy 328 IGTFRDLAVVLETAFLTALDIFVDRVSALPVVNEGQVVGYSRFDVTHLAAQTYNH 387
Dy |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
227 VGTFRDVAVVPENAPVYAALEIFVDRVSALPVVNEGQVVGYSRFDVTHLAAQTYNH 286
Qy 388 LDMSVGEALRQRTLCLEGVLSQCPHESLGEVIDRIAREQVHRLVLDVDETOHLLGVVLSLD 447
Dy |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
287 LDISVREALRQRTVCLEGVLTCTYPHETMEDIIDRIAREQVHRLVLDVDETOHLLGVVLSLD 346
Qy 448 ILQALVLSVAGIDALGA 464
Dy |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
347 ILQALVLSVAGIDALGA 363

RESULT 13
Q4JK39 CHICK
ID Q4JK39 CHICK PRELIMINARY; PRT; 382 AA.
AC Q4JK39
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE 5'-AMP-activated protein kinase gamma-3 non-catalytic subunit long
DE form.
GN Name=PRKAG3;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Skeletal muscle;
RA Proszkowiec-Weglarz M., Richards M.P., Poch S.M.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; DQ079814; AAY86041.1; -; mRNA.
KW Kinase.
SQ SEQUENCE 382 AA; 42960 MW; 7098BFF1A2C77A59 CRC64;

Query Match 53.3%; Score 1280; DB 2; Length 382;
Best Local Similarity 75.7%; Pred. No. 7.2e-89;
Matches 240; Conservative 43; Mismatches 34; Indels 0; Gaps 0;

Qy 148 DDELKRPQAIYMRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFALVANGVRAAPLWDS 207
Dy |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
66 DNNFQSPDAEVYMHFMRSHCCYDAVPTSKLVVDFDTLEIKKAFALVANGVRAAPLWDS 125
Qy 208 KKQSFVGMLTITDILVLRHYRSPVQIYEI EHQKIETWREIYLGCCFKPLVSI SPNDS 267
Dy |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
126 KKQSFVGMLTITDILVLRHYRSPVQIYEI EHQKIETWREIYLGCCFKPLVSI SPNDS 185
Qy 268 LFEAVYTLIKNRIHRLPVLDPVSGNVHLHILTHKRLKFLHIFGSLPRSPFLYRTIQDLG 327
Dy |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
186 LFDVAVSLIKKHILHRLPVIEPISGNVHLHILTHKRLKFLHIFGSLPRSPFLYRTIQDLG 245
Qy 328 IGTFRDLAVVLETAFLTALDIFVDRVSALPVVNEGQVVGYSRFDVTHLAAQTYNH 387
Dy |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
246 VGTFRDVAVVPENAPVYAALEIFVDRVSALPVVNEGQVVGYSRFDVTHLAAQTYNH 305
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Qy 388 LDMVGBALRORTLCLEGVLSQPHESLGEVIDRIAREQVHRLVLDVETQHLGLVSLSD 447
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 306 LDIVREALRORTVCLGVLTCTPHETMEDIIDRTTEQVHRLVLDVENDRYPRGIVSLSD 365
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 448 ILQALVSPAGIDALGA 464
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 366 ILQALVLTTPAGIDALNS 382
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 14
Q7ZYL2_XENLA
ID Q7ZYL2_XENLA PRELIMINARY; PRT; 337 AA.
AC Q7ZYL2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Prkag1-prov protein.
OS Xenopus laevis (African Clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Fellings E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
initiative.";
RL Dev. Dyn. 225:384-391 (2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX Klein S., Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC043738; AA043738.1; -, mRNA.
DR InPro; IPR000644; CBS.
DR Pfam; PF00571; CBS; 2.
DR SMART; SM00116; CBS; 4.
SQ SEQUENCE 337 AA; 3825 MW; EFF4AE102D6F1DC4 CRC64;

Query Match 50.5%; Score 1213.5; DB 2; Length 337;
Best Local Similarity 73.3%; Pred. No. 7e-84;
Matches 233; Conservative 40; Mismatches 38; Indels 7; Gaps 1;

Qy 143 PKLGDWDELKPKGAIYNRFMQETCYDAMATSKLVIFDTMLKIKAFALVANGVRAA 202
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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Db 23 PDIGED-----ASLYMEFMKNCNNAIPTSCKL VVFTTTLQIKKAFALVANGVRAA 75
Qy 203 PLWDSKKQSFVGMILTITDFILVLRHYRSPLVQIYEIEQHKIETWRIYIQLGQCFKPLVSI 262
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 76 PLWDSKKQSFVGMILTITDFINILHRYKAPLVQIYEIEEHKIETWRDVLQSSFKPLIYI 135
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 263 SPNDSLPEAVYTLIKRIHRLPVLDPVSGNVHLHILTHKRLKFLHI FGSLLPRSPFLYRT 322
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 136 SPADSLFQAVYSLTKNRIHRLPVMDSVSGNLIHLTHKRLKFLHFLGDTLPRPQFLQKT 195
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 323 IQDLGIGTFRDLAVLTETAPILTALDIFVDRRYVALPVNVECGOVGLYSRFDVHLAAQ 382
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 196 ILELGIGTFRDIAVQVDTSSVNALEIFVRRYSALPVNVECGOVGLYSRFDVHLAAQ 255
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 383 QTYNHLDMVSVEALRQRTLCLEGVLSQPHESLGEVIDRIAREQVHRLVLDVETQHLGLV 442
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 256 KIYNLDISVLDAIRLSLCIEGVLMCYPHESLVEVDIVREQIHLVLDVEERRPLGI 315
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 443 VLSLDILQALVLTSPAGID 460
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 316 VLSLDILQALVLTSPAGID 333
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 15
Q8BIQ9_MOUSE
ID Q8BIQ9_MOUSE PRELIMINARY; PRT; 443 AA.
AC Q8BIQ9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Mus musculus adult male olfactory brain cDNA, RIKEN full-length
enriched library, clone:6430509K05 product:similar to AMP ACTIVATED
PROTEIN KINASE GAMMA 1.
DE NAME=Prkag2;
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;

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OM protein - protein search, using sw model

Run on: January 24, 2006, 22:04:33 ; Search time 38.6164 Seconds
(without alignments)
993.400 Million cell updates/sec

Title: US-10-070-794A-30
Perfect score: 2403
Sequence: 1 MSFLEQNSSSWSPAVTSS.....LSDIQLVLSPAGIDALGA 464

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2013	83.8	464	2	US-09-950-022A-4
2	2011	83.7	464	2	US-09-950-022A-2
3	2010	83.6	464	2	US-09-950-022A-8
4	2007	83.5	464	2	US-09-950-022A-10
5	2005	83.4	464	2	US-09-950-022A-6
6	1088.5	45.3	413	2	US-09-949-016-8261
7	1080.5	45.0	328	1	US-08-878-989-7
8	1080.5	45.0	328	2	US-09-272-796-7
9	1028	42.8	330	2	US-09-359-161-6
10	1017	42.3	331	1	US-08-878-989-21
11	1017	42.3	331	2	US-09-101-146-64
12	1017	42.3	331	2	US-09-272-796-21
13	1017	42.3	331	2	US-09-538-092-1211
14	1017	42.3	336	2	US-09-949-016-10881
15	457	19.0	322	2	US-09-359-161-7
16	457	19.0	322	2	US-09-538-092-297
17	312	13.0	101	2	US-09-513-999C-5736
18	258	10.7	254	2	US-09-248-796A-18872
19	214	8.9	379	2	US-09-359-161-5
20	205.5	8.6	629	2	US-09-248-796A-14535
21	190	7.9	373	2	US-09-359-161-3
22	117	4.9	776	2	US-09-252-991A-30380
23	114.5	4.8	490	2	US-09-252-991A-30355
24	106.5	4.4	272	2	US-09-252-991A-18313
25	104.5	4.3	375	2	US-09-328-352-6078
26	101	4.2	187	2	US-09-199-637A-287
27	101	4.2	187	2	US-09-252-991A-21454

28	100.5	4.2	622	2	US-09-605-703B-2098	Sequence 2098, Ap
29	100	4.2	419	2	US-09-270-767-46031	Sequence 46031, A
30	100	4.2	2766	2	US-09-964-956-62	Sequence 62, Appl
31	99.5	4.1	701	2	US-10-052-092-12	Sequence 12, Appl
32	99	4.1	676	2	US-09-248-796A-14898	Sequence 14898, A
33	98.5	4.1	375	2	US-09-634-238-260	Sequence 260, App
34	98.5	4.1	680	2	US-09-949-016-10770	Sequence 10770, A
35	97.5	4.1	510	2	US-09-489-039A-11778	Sequence 11778, A
36	97	4.0	752	2	US-09-919-039-235	Sequence 235, App
37	97	4.0	852	1	US-09-070-060-3	Sequence 3, Appli
38	97	4.0	852	2	US-09-357-746-3	Sequence 3, Appli
39	96.5	4.0	435	2	US-09-583-110-3768	Sequence 3768, Ap
40	96.5	4.0	481	2	US-09-252-991A-31708	Sequence 31708, A
41	96.5	4.0	736	2	US-09-949-016-8855	Sequence 8855, Ap
42	96	4.0	405	2	US-09-198-452A-301	Sequence 301, App
43	96	4.0	405	2	US-09-438-185A-290	Sequence 290, App
44	95.5	4.0	180	2	US-09-252-991A-18269	Sequence 18269, A
45	95.5	4.0	307	2	US-09-949-016-8453	Sequence 8453, Ap

ALIGNMENTS

RESULT 1
US-09-950-022A-4
; Sequence 4, Application US/09950022A
; Patent No. 6919177

; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Clobanul, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: No. 6919177el PRKAG3 Alleles and Use fo the Same as Genetic Mark.
; TITLE OF INVENTION: Reproductive
; TITLE OF INVENTION: and Meat Quality Traits
; FILE REFERENCE: P04668U3
; CURRENT APPLICATION NUMBER: US/09/950,022A
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-950-022A-4

Query Match	83.8%;	Score	2013;	DB	2;	Length	464;		
Best Local Similarity	86.0%;	Pred.	No. 8.1e-218;						
Mismatches	400;	Conservative	19;	Mismatches	44;	Indels	2;	Gaps	2;
QY	1	MSFLEQENSSSWPSAVTSSSRIRGKRAKALRWTRQKSVVEEGPPGQCGEPRSRPTAE	60						
Db	1	MSFLEQESRSWPSRAVTTSSSRSHGDQGTGKASRWTRQEDVEEGPPGREGPQSRPVAE	60						
QY	61	STGLEATFPKTTPLAQADP-AGVGTPTTGWDCPLSPDCTASAAGSSTDDVELATEFPATEA	119						
Db	61	STGQEAFTPKATPLAQAAPLAEVDNPFPTERDILPSDCAASASDNTDHLDLGIEFSASAA	120						
QY	120	WECELEGLLEERPALCLSPQAPFPKLGWDDELKPCAQIYMRFMQEHCTCYDAMATSSKLV	179						
Db	121	SGDEL-GLVEEKAPCFSPFVLLPRLGWDELQKPCAQVYMHFMQEHCTCYDAMATSSKLV	179						
QY	180	IFDTMLEIKKAPFALVANGRAAPLWDSKKQSPVGMLTITDFTILVLHRYRSPVLOIYEI	239						
Db	180	IFDTMLEIKKAPFALVANGRAAPLWDSKKQSPVGMLTITDFTILVLHRYRSPVLOIYEI	239						
QY	240	EQHKIETWREIYLGQCFKPLVSI SPNDSLFEAVYTLIKRIHRLPVLDPVSGNVLHILTH	299						

Db 240 EEHKIETWREIYLGCCFKPLVSI SPNDLSLFEAVYALIKNRIHRLPVLDPVSGAVLHILTH 299
Qy 300 KRLKFLHIFGSLPRPSFLYRTIQDGLIGTFRDLAVVLETAPILTALDIFVDRRVSAIP 359
Db 300 KRLKFLHIFGTLPRPSFLYRTIQDGLIGTFRDLAVVLETAPILTALDIFVDRRVSAIP 359
Qy 360 VVNECGVGLYSRFDVIHLAAQOTYNHLDMSVGEALRQRTLCLGVLSCOPHESLGEVI 419
Db 360 VVNETGVVGLYSRFDVIHLAAQOTYNHLDMSVGEALRQRTLCLGVLSCOPHETLGEVI 419
Qy 420 DRIAREQVHRLVLDVETQHLGGVVSLSLILQALVLSIPAGIDALGA 464
Db 420 DRIAREQVHRLVLDVETQHLGGVVSLSLILQALVLSIPAGIDALGA 464

RESULT 2

US-09-950-022A-2
; Sequence 2, Application US/09950022A
; Patent No. 6919177
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: No. 6919177el PRKAG3 Alleles and Use fo the Same as Genetic Mark
; TITLE OF INVENTION: Reproductive
; TITLE OF INVENTION: and Meat Quality Traits
; FILE REFERENCE: P04668US3
; CURRENT APPLICATION NUMBER: US/09/950,022A
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-950-022A-2

Query Match 83.7%; Score 2011; DB 2; Length 464;
Best Local Similarity 86.0%; Pred. No. 1.4e-217;
Matches 400; Conservative 19; Mismatches 44; Indels 2; Gaps 2;
Qy 1 MSFLEQENSSWSPSAVTSSEIRIRGKRRAKALRWTRQKSVVEEGEPGPGQSGPRSPRTAE 60
Db 1 MSFLEQESRSWSPSAVTSSEIRIRGKRRAKALRWTRQKSVVEEGEPGPGQSGPRSPVAE 60
Qy 61 STGLEATFPKTTPLAQADP-AGVGTPTGMDCLPSDCTASAGSSTDDELATFPATEA 119
Db 61 STGQEAATFPKATPLAQAPLAELVDNPPTERDILPDSCAASDSNTDHLDLGIEFSAA 120
Qy 120 WECELEGLEERPALCLSPQAPFPKLGWDDDELKPKGAQIYMRFMQHTCYDAMATSSKLV 179
Db 121 SGDEL-GLVEEKPAFCPSPEVLLPRLGWDDDELQKGAQVYMHFMQHTCYDAMATSSKLV 179
Qy 180 IFDPTMLEIKKAPFALVANGRAAPLWDSKKQSFVGMILTITDILVHLHYRSPVLQIYEI 239
Db 180 IFDPTMLEIKKAPFALVANGRAAPLWDSKKQSFVGMILTITDILVHLHYRSPVLQIYEI 239
Qy 240 EHKIETWREIYLGCCFKPLVSI SPNDLSLFEAVYALIKNRIHRLPVLDPVSGAVLHILTH 299
Db 240 EHKIETWREIYLGCCFKPLVSI SPNDLSLFEAVYALIKNRIHRLPVLDPVSGAVLHILTH 299
Qy 300 KRLKFLHIFGSLPRPSFLYRTIQDGLIGTFRDLAVVLETAPILTALDIFVDRRVSAIP 359
Db 300 KRLKFLHIFGTLPRPSFLYRTIQDGLIGTFRDLAVVLETAPILTALDIFVDRRVSAIP 359

Qy 360 VVNECGVGLYSRFDVIHLAAQOTYNHLDMSVGEALRQRTLCLGVLSCOPHESLGEVI 419
Db 360 VVNETGVVGLYSRFDVIHLAAQOTYNHLDMSVGEALRQRTLCLGVLSCOPHETLGEVI 419
Qy 420 DRIAREQVHRLVLDVETQHLGGVVSLSLILQALVLSIPAGIDALGA 464
Db 420 DRIAREQVHRLVLDVETQHLGGVVSLSLILQALVLSIPAGIDALGA 464
RESULT 3
US-09-950-022A-8
; Sequence 8, Application US/09950022A
; Patent No. 6919177
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: No. 6919177el PRKAG3 Alleles and Use fo the Same as Genetic Mark
; TITLE OF INVENTION: Reproductive
; TITLE OF INVENTION: and Meat Quality Traits
; FILE REFERENCE: P04668US3
; CURRENT APPLICATION NUMBER: US/09/950,022A
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-950-022A-8

Query Match 83.6%; Score 2010; DB 2; Length 464;
Best Local Similarity 85.8%; Pred. No. 1.8e-217;
Matches 399; Conservative 20; Mismatches 44; Indels 2; Gaps 2;
Qy 1 MSFLEQENSSWSPSAVTSSEIRIRGKRRAKALRWTRQKSVVEEGEPGPGQSGPRSPRTAE 60
Db 1 MSFLEQESRSWSPSAVTSSEIRIRGKRRAKALRWTRQKSVVEEGEPGPGQSGPRSPVAE 60
Qy 61 STGLEATFPKTTPLAQADP-AGVGTPTGMDCLPSDCTASAGSSTDDELATFPATEA 119
Db 61 STGQEAATFPKATPLAQAPLAELVDNPPTERDILPDSCAASDSNTDHLDLGIEFSAA 120
Qy 120 WECELEGLEERPALCLSPQAPFPKLGWDDDELKPKGAQIYMRFMQHTCYDAMATSSKLV 179
Db 121 SGDEL-GLVEEKPAFCPSPEVLLPRLGWDDDELQKGAQVYMHFMQHTCYDAMATSSKLV 179
Qy 180 IFDPTMLEIKKAPFALVANGRAAPLWDSKKQSFVGMILTITDILVHLHYRSPVLQIYEI 239
Db 180 IFDPTMLEIKKAPFALVANGRAAPLWDSKKQSFVGMILTITDILVHLHYRSPVLQIYEI 239
Qy 240 EHKIETWREIYLGCCFKPLVSI SPNDLSLFEAVYALIKNRIHRLPVLDPVSGAVLHILTH 299
Db 240 EHKIETWREIYLGCCFKPLVSI SPNDLSLFEAVYALIKNRIHRLPVLDPVSGAVLHILTH 299
Qy 300 KRLKFLHIFGSLPRPSFLYRTIQDGLIGTFRDLAVVLETAPILTALDIFVDRRVSAIP 359
Db 300 KRLKFLHIFGTLPRPSFLYRTIQDGLIGTFRDLAVVLETAPILTALDIFVDRRVSAIP 359
Qy 360 VVNECGVGLYSRFDVIHLAAQOTYNHLDMSVGEALRQRTLCLGVLSCOPHESLGEVI 419
Db 360 VVNETGVVGLYSRFDVIHLAAQOTYNHLDMSVGEALRQRTLCLGVLSCOPHETLGEVI 419
Qy 420 DRIAREQVHRLVLDVETQHLGGVVSLSLILQALVLSIPAGIDALGA 464
Db 420 DRIAREQVHRLVLDVETQHLGGVVSLSLILQALVLSIPAGIDALGA 464

RESULT 4

US-09-950-022A-10
; Sequence 10, Application US/09950022A

; Patent No. 6919177

; GENERAL INFORMATION:

; APPLICANT: Rothschild, Max

; APPLICANT: Ciobanu, Dan

; APPLICANT: Malek, Massoud

; APPLICANT: Plastow, Graham

; TITLE OF INVENTION: No. 6919177el PRKAG3 Alleles and Use fo the Same as Genetic Mark

; TITLE OF INVENTION: Reproductive

; TITLE OF INVENTION: and Meat Quality Traits

; FILE REFERENCE: P04668US3

; CURRENT APPLICATION NUMBER: US/09/950,022A

; PRIOR FILING DATE: 2001-09-10

; PRIOR APPLICATION NUMBER: 60/231045

; PRIOR FILING DATE: 2000-09-08

; PRIOR APPLICATION NUMBER: 60/260,239

; PRIOR FILING DATE: 2001-01-08

; PRIOR APPLICATION NUMBER: 60/299,111

; PRIOR FILING DATE: 2001-06-18

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 10

; LENGTH: 464

; TYPE: PR

; ORGANISM: Sus scrofa

US-09-950-022A-10

Query Match

Best Local Similarity 83.5%; Score 2007; DB 2; Length 464;

Mismatches 399; Conservative 20; Mismatches 44; Indels 2; Gaps 2;

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Db 1 MSFLEQENSSWPSPATVSSSRIRGKRRAKALRWTKSVSEGEPPGQCGEGRSRPTAE 60
Qy 61 STGLEATFPKTTPLAQADP-AGVGTPTPTGMDCLPSCDTASAAGSSTDVDELATFPATEA 119
Db 61 STGLEATFPKTTPLAQADP-AGVGTPTPTGMDCLPSCDTASAAGSSTDVDELATFPATEA 119
Qy 120 WECELEGLLEERPALCLSPQAPFPKLGWDDDELKPKGAQIYMRFMQEHCTYDAMATSSKLV 179
Db 120 WECELEGLLEERPALCLSPQAPFPKLGWDDDELKPKGAQIYMRFMQEHCTYDAMATSSKLV 179
Qy 121 SGDEL-GLVEEKAPCPSPVLLPRLGWDDDELQKPGAVYMHFMQEHCTYDAMATSSKLV 179
Db 121 SGDEL-GLVEEKAPCPSPVLLPRLGWDDDELQKPGAVYMHFMQEHCTYDAMATSSKLV 179
Qy 180 IFDTMLEIKKAPFALVANGVRAAPLWDSKQSFVGMLTITDFFILVLRHYRSPVQIYEI 239
Db 180 IFDTMLEIKKAPFALVANGVRAAPLWDSKQSFVGMLTITDFFILVLRHYRSPVQIYEI 239
Qy 240 EHKIETWREIYLGQCFKPLVSI SPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVHLHILTH 299
Db 240 EHKIETWREIYLGQCFKPLVSI SPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVHLHILTH 299
Qy 300 KRLLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLETPALITLALDIFVDRRVSAALP 359
Db 300 KRLLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLETPALITLALDIFVDRRVSAALP 359
Qy 360 VVNECGVGLYSRFDVIHLAAQOQTYNHLDMVGEALRQRTLCLEGLVSCOPHESLGEVI 419
Db 360 VVNECGVGLYSRFDVIHLAAQOQTYNHLDMVGEALRQRTLCLEGLVSCOPHESLGEVI 419
Qy 420 DRIAREQVHRLVLDVETQHLGLGVVSLSDIILQALVLSFAGIDALGA 464
Db 420 DRIAREQVHRLVLDVETQHLGLGVVSLSDIILQALVLSFAGIDALGA 464
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RESULT 5

US-09-950-022A-6

; Sequence 6, Application US/09950022A

; Patent No. 6919177

; GENERAL INFORMATION:

; APPLICANT: Rothschild, Max

; APPLICANT: Ciobanu, Dan

; APPLICANT: Malek, Massoud

; APPLICANT: Plastow, Graham

; TITLE OF INVENTION: No. 6919177el PRKAG3 Alleles and Use fo the Same as Genetic Mark

; TITLE OF INVENTION: Reproductive

; TITLE OF INVENTION: and Meat Quality Traits

; FILE REFERENCE: P04668US3

; CURRENT APPLICATION NUMBER: US/09/950,022A

; PRIOR FILING DATE: 2001-09-10

; PRIOR APPLICATION NUMBER: 60/231045

; PRIOR FILING DATE: 2000-09-08

; PRIOR APPLICATION NUMBER: 60/260,239

; PRIOR FILING DATE: 2001-01-08

; PRIOR APPLICATION NUMBER: 60/299,111

; PRIOR FILING DATE: 2001-06-18

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 6

; LENGTH: 464

; TYPE: PR

; ORGANISM: Sus scrofa

US-09-950-022A-6

Query Match

Best Local Similarity 83.4%; Score 2005; DB 2; Length 464;

Mismatches 399; Conservative 19; Mismatches 45; Indels 2; Gaps 2;

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Qy 1 MSFLEQENSSWPSPATVSSSRIRGKRRAKALRWTKSVSEGEPPGQCGEGRSRPTAE 60
Db 1 MSFLEQENSSWPSPATVSSSRIRGKRRAKALRWTKSVSEGEPPGQCGEGRSRPTAE 60
Qy 61 STGLEATFPKTTPLAQADP-AGVGTPTPTGMDCLPSCDTASAAGSSTDVDELATFPATEA 119
Db 61 STGLEATFPKTTPLAQADP-AGVGTPTPTGMDCLPSCDTASAAGSSTDVDELATFPATEA 119
Qy 120 WECELEGLLEERPALCLSPQAPFPKLGWDDDELKPKGAQIYMRFMQEHCTYDAMATSSKLV 179
Db 120 WECELEGLLEERPALCLSPQAPFPKLGWDDDELKPKGAQIYMRFMQEHCTYDAMATSSKLV 179
Qy 121 SGDEL-GLVEEKAPCPSPVLLPRLGWDDDELQKPGAVYMHFMQEHCTYDAMATSSKLV 179
Db 121 SGDEL-GLVEEKAPCPSPVLLPRLGWDDDELQKPGAVYMHFMQEHCTYDAMATSSKLV 179
Qy 180 IFDTMLEIKKAPFALVANGVRAAPLWDSKQSFVGMLTITDFFILVLRHYRSPVQIYEI 239
Db 180 IFDTMLEIKKAPFALVANGVRAAPLWDSKQSFVGMLTITDFFILVLRHYRSPVQIYEI 239
Qy 240 EHKIETWREIYLGQCFKPLVSI SPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVHLHILTH 299
Db 240 EHKIETWREIYLGQCFKPLVSI SPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVHLHILTH 299
Qy 300 KRLLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLETPALITLALDIFVDRRVSAALP 359
Db 300 KRLLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLETPALITLALDIFVDRRVSAALP 359
Qy 360 VVNECGVGLYSRFDVIHLAAQOQTYNHLDMVGEALRQRTLCLEGLVSCOPHESLGEVI 419
Db 360 VVNECGVGLYSRFDVIHLAAQOQTYNHLDMVGEALRQRTLCLEGLVSCOPHESLGEVI 419
Qy 420 DRIAREQVHRLVLDVETQHLGLGVVSLSDIILQALVLSFAGIDALGA 464
Db 420 DRIAREQVHRLVLDVETQHLGLGVVSLSDIILQALVLSFAGIDALGA 464
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RESULT 6

US-09-949-016-8261

; Sequence 8261, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

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; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8261
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-8261

Query Match      45.3%; Score 1088.5; DB 2; Length 413;
Best Local Similarity 53.9%; Pred. No. 1.5e-113;
Matches 223; Conservative 73; Mismatches 67; Indels 51; Gaps 9;

Qy 46 PPGGEGRSRPTAESTGLEATFKTTPLAQADPAGVGTPTGWDCLPSCDTASAAGSST 105
Db 41 PPDTGQ--RCPSSFQS-----PTRPPLAS-----PTHY--APSKAALAAALG- 80
Qy 106 DDVELATEFPATEAWECEGLELLEERPALCLSPQAPFPKLGWDE-LRKPGAQIYMRFMQ 164
Db 81 -----PA-EA-----GMLE-----KLEFEDEAVEDSSESGVYMRFR 110
Qy 165 EHTCYDAMATSKLVIPDTMLEIKKAPFALVANGVRAAPLWDSKQSFVGMLTITDILV 224
Db 111 SHKCYDIVPTSSKLVFDTLLQVKKAPFALVANGVRAAPLWESKQSFVGMLTITDINI 170
Qy 225 LHRYYRSPVOIYETEOHKIETWREIYLGQCFKPLVSPNDLSLFEAVYTLIKNRIHRLP 284
Db 171 LHRYYKSPMVQIYEELHETWRELYQETFKPLVNSPDSASLFDVYSLIKNKHRLP 230
Qy 285 VLDPSGNGVLHILTHKRLLKELHIFGSLPRPSFLYRTIODLGITGPRDLAVVLETA 344
Db 231 VIDPISGNALYILTHKRILKFLQFMSDMPKPAFMKQNLDELGLGTVYHIAFIHPDPTII 290
Qy 345 TALDIFDVRVSALPVNCEQGVGLYSRFDVHIAAQOTVNHLDMSVGEALRORTLCLE 404
Db 291 KALNIFERRISALPVNDESGKVDIYSKFDVINLAEKTYNNLDITVTQALQHSQYFE 350
Qy 405 GVLSQPHESLGEVIDRIAREOVHRLVLDVDETOHLLGVVSLSDILOALVLSAG 458
Db 351 GVVKCNKLEILETIVDRIVRAEVRHRLVVVNEADSVIGIISLSDILOALILTPAG 404

RESULT 7
US-08-878-989-7
; Sequence 7, Application US/08878989
; Patent No. 5885803
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl G.
; APPLICANT: Lal, Preeti
; APPLICANT: Goli, Surya K.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
; TITLE OF INVENTION: KINASES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/878,989
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0321 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 328 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PENITUT01
; CLONE: 1452972
; US-08-878-989-7

Query Match      45.0%; Score 1080.5; DB 1; Length 328;
Best Local Similarity 63.3%; Pred. No. 8.1e-113;
Matches 200; Conservative 67; Mismatches 48; Indels 1; Gaps 1;

Qy 144 KLGWDEHT-LRKPGAQIYMRFMQHEITCYDAMATSKLVIFDTMLEIKKAPFALVANGVRAA 202
Db 4 KLFEDAEVDESSESGVYMRFRSHKCYDIVPTSSKLVFDTLLQVKKAPFALVANGVRAA 63
Qy 203 PLWDSKQSFVGMLTITDILVHRYRSPVQIYEIEQHKIETWREIYLGQCFKPLVSI 262
Db 64 PLWESKQSFVGMLTITDINILHRYKSPMVQIYEELHETWRELYQETFKPLVNI 123
Qy 263 SPNDSLFEAVYTLIKNRIHRLPVLDVPSGNVHLTHKRLLKPLHIFGSLPRPSFLYRT 322
Db 124 SPDASLFDVYSLIKNKHRLPVLDIPISGNALYILTHKRILKFLQFMSDMPKPAFMKQ 183
Qy 323 IQDGLIGITGPRDLAVVLETA 458
Db 184 LDELIGITVYHIAFIHPDPTIIKALNIFVEERISALPVNDESGKVDIYSKFDVINLAE 243
Qy 383 QTYNHLDMSVGEALRORTLCLEGVLSQPHESLGEVIDRIAREOVHRLVLDVDETOHLLGV 442
Db 244 KTYNNLDITVTQALQHSQYFEGVVKCNKLEILETIVDRIVRAEVRHRLVVVNEADSVIGI 303
Qy 443 VLSLSDILOALVLSAG 458
Db 304 ISLSLSDILOALILTPAG 319

RESULT 8
US-09-272-796-7
; Sequence 7, Application US/09272796
; Patent No. 6207148
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl G.
; APPLICANT: Lal, Preeti
; APPLICANT: Goli, Surya K.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
; TITLE OF INVENTION: KINASES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive

```


;; CITY: Palo Alto
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 94304
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/272,796
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/878,989
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Billings, Lucy J J
;; REGISTRATION NUMBER: 36,749
;; REFERENCE/DOCKET NUMBER: PF-0321 US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-855-0555
;; TELEFAX: 415-845-4166
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 328 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; IMMEDIATE SOURCE:
;; LIBRARY: PENITUT01
;; CLONE: 1452972
;; US-09-272-796-7

Query Match 45.08; Score 1080.5; DB 2; Length 328;
Best Local Similarity 63.38; Pred. No. 8.1e-113;
Matches 200; Conservative 67; Mismatches 48; Indels 1; Gaps 1;

Qy 144 KLGWDD- LRKPGAQIYMRFMQHTCYDAMATSSKLVIFDTMLKIKKAFALVANGVRAA 202
Db 4 KLEPDEAVEDESGVYMRFMRSKCYDVTPTSSKLVVFDLTQVKKAFALVANGVRAA 63

Qy 203 PLWDSKKQSFVGMLTITDFILVLRHYRSPVQIYEIEQHKIETWREIYLGCCFKPLVSI 262
Db 64 PLWESKKQSFVGMLTITDFINILHRYKSPVQIYEIEEHHKIEIETWRELYLQETFKPLVNI 123

Qy 263 SPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTKRLIKLHIFGSLPRPSFLYRT 322
Db 124 SPASLFDVYSLIKNRIHRLPVLDPISGNALYILTKRLIKLHIFGSLPRPSFLYRT 183

Qy 323 IQDLGIGTFRDLAVVLETAIPILTALDIFVDRRVSALPVNVECGVGLYSRFDVHIAAQ 382
Db 184 LDELIGTYHNIAFIHPDTPILKALNIFVERRISALPVNDESKVVDIYKFDVINLAAE 243

Qy 383 QTNHLDMSVGEALRQRTCLGVLSCOPHESLGEVIDRIAREQVHRLVLDVDETOHL 442
Db 244 KTYNNLDITVQALQHRSQYFEGVQVKNCKLEILEITVIDRVRAEVHRLVVDVNEADSVGI 303

Qy 443 VLSLDILQALVLPAG 458
Db 304 ISLSLDILQALILTPAG 319

RESULT 9
US-09-359-161-6
; Sequence 6, Application US/09359161A
; Patent No. 6342656
; GENERAL INFORMATION:
; APPLICANT: Bradford, Kent J.
; APPLICANT: Dahal, Peetambar
; APPLICANT: Yang, Hong
; APPLICANT: Cooley, Michael

;; APPLICANT: Downie, Bruce
;; APPLICANT: Gee, Oliver
;; APPLICANT: The Regents of the University of California
;; TITLE OF INVENTION: Regulation of Source-Sink Relationships and Responses
;; FILE REFERENCE: 023070-095900US
;; CURRENT APPLICATION NUMBER: US/09/359,161A
;; CURRENT FILING DATE: 1999-07-21
;; NUMBER OF SEQ ID NOS: 7
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 6
;; LENGTH: 330
;; TYPE: PRT
;; ORGANISM: Rattus norvegicus
;; FEATURE:
;; OTHER INFORMATION: gamma subunit of AMP-activated protein kinase
;; OTHER INFORMATION: (AMPK-gamma)
US-09-359-161-6

Qy 140 APPKLGWDDLRKPGAQIYMRFMQHTCYDAMATSSKLVIFDTMLKIKKAFALVANGV 199
Db 9 APAPENHSQETPESNSSVYTFMKSHRCDLPTSSKLVVFDTSQVKKAFALVANGV 68

Qy 200 RAAPLWDSKKQSFVGMLTITDFILVLRHYRSPVQIYEIEQHKIETWREIYLGCCFKPL 259
Db 69 RAAPLWDSKKQSFVGMLTITDFINILHRYKSPVQIYEIEEHHKIEIETWRELYLQETFKPL 128

Qy 260 VSISPNDLSFEAVYTLIKNRIHRLPVLDPVSGNVLHILTKRLIKLHIFGSLPRPSFL 319
Db 129 VCISPNASLFDVSSLIKRIHRLPVIDPESGNTLYILTKRLIKLHIFGSLPRPSFL 188

Qy 320 YRTIQDLGIGTFRDLAVVLETAIPILTALDIFVDRRVSALPVNVECGVGLYSRFDVHIL 379
Db 189 SKSLEELQIGTYHNIAFMVTRTPVYVALGIFVQHRVSALPVNDESKVVDIYKFDVINL 248

Qy 380 AAQOTYNNHLDMSVGEALRQRTCLGVLSCOPHESLGEVIDRIAREQVHRLVLDVDETOHL 439
Db 249 AAETYNLDVSVTKALQHRSHYFEGVGLYKYLHETLEAIINRLVEAEVHRLVVDVDEHDVV 308

Qy 440 LGVVSLSLDILQALVLS 455
Db 309 KGIVSLSLDILQALVLT 324

RESULT 10
US-08-878-989-21
; Sequence 21, Application US/08878989
; Patent No. 5885803
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl G.
; APPLICANT: Lal, Preeti
; APPLICANT: Goli, Surya K.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
; TITLE OF INVENTION: KINASES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

Thu Jan 26 09:20:51 2006

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; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/878,989
; FILING DATE:
; PRIOR APPLICATION DATA:
; CLASSIFICATION: 435
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PN7450
; FILING DATE: 8 JAN 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: DC-0050
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (856) 810-1515
; TELEFAX: (856) 810-1454
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 331
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-101-146-64

; SOFTWARE: WORDPERFECT 6.0 FOR WINDOWS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/101,146
; FILING DATE: October 7, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PN7450
; FILING DATE: 8 JAN 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: DC-0050
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (856) 810-1515
; TELEFAX: (856) 810-1454
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 331
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-101-146-64

Query Match 42.3%; Score 1017; DB 2; Length 331;
Best Local Similarity 64.8%; Pred. No. 1.2e-105;
Matches 193; Conservative 53; Mismatches 52; Indels 0; Gaps 0;

Qy 158 IYMFQMOHTCYDAMATSSKLVIVDTMLEIKKAFKALVANGVRAAPLWDSKKQSFVGM 217
Db 28 VYTFMKSHRCYDLIPTSSKLVVFDTSLOVKKAFKALVANGVRAAPLWDSKKQSFVGM 87

Qy 218 ITDFILVHRYRSPVQIYEIOHKIETWREIYLOGCFKPLVSPNDLSLFEAVYTLIK 277
Db 88 ITDFINILHRYKSAVQIYELEHKIETWREVLQDSFKPLVCISPNASLFDVSSLR 147

Qy 278 NRIHRLPVLDPVSGNVLHILTHKRLKFLHIFGSLPRPSLYRTIODLGIGTFRDLAV 337
Db 148 NKIHLRPVIDESGNTLYLTHKRLKFLKLFITFPKPFMSKLSLELOLQVANIAMV 207

Qy 338 LETAPILTALDIFDVRVSALPVNVEGQVGLYSRFDVIHLAAQOTVNHLDMSVGEALR 397
Db 208 RTTTPVYVALGIFVQHRVSALPVVDEKGRVVDIYSKFDVINLAAEKTNNLDVSVTKALQ 267

Qy 398 QRTLCLEGLVSCQPHESLGEVIDRIAREQVHRLVLDVDETQHLGLGVSLDILQALVLS 455
Db 268 HRSHYFEGVLKCYLHETLEIINRLVEAEVHRLVVVDENVVKGIVSLSDILQALVLT 325

RESULT 12
US-09-272-796-21
; Sequence 21, Application US/09272796
; Patent No. 6207148
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl G.
; APPLICANT: Lal, Preeti
; APPLICANT: Goli, Surya K.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS

Query Match 42.3%; Score 1017; DB 1; Length 331;
Best Local Similarity 64.8%; Pred. No. 1.2e-105;
Matches 193; Conservative 53; Mismatches 52; Indels 0; Gaps 0;

Qy 158 IYMFQMOHTCYDAMATSSKLVIVDTMLEIKKAFKALVANGVRAAPLWDSKKQSFVGM 217
Db 28 VYTFMKSHRCYDLIPTSSKLVVFDTSLOVKKAFKALVANGVRAAPLWDSKKQSFVGM 87

Qy 218 ITDFILVHRYRSPVQIYEIOHKIETWREIYLOGCFKPLVSPNDLSLFEAVYTLIK 277
Db 88 ITDFINILHRYKSAVQIYELEHKIETWREVLQDSFKPLVCISPNASLFDVSSLR 147

Qy 278 NRIHRLPVLDPVSGNVLHILTHKRLKFLHIFGSLPRPSLYRTIODLGIGTFRDLAV 337
Db 148 NKIHLRPVIDESGNTLYLTHKRLKFLKLFITFPKPFMSKLSLELOLQVANIAMV 207

Qy 338 LETAPILTALDIFDVRVSALPVNVEGQVGLYSRFDVIHLAAQOTVNHLDMSVGEALR 397
Db 208 RTTTPVYVALGIFVQHRVSALPVVDEKGRVVDIYSKFDVINLAAEKTNNLDVSVTKALQ 267

Qy 398 QRTLCLEGLVSCQPHESLGEVIDRIAREQVHRLVLDVDETQHLGLGVSLDILQALVLS 455
Db 268 HRSHYFEGVLKCYLHETLEIINRLVEAEVHRLVVVDENVVKGIVSLSDILQALVLT 325

RESULT 11
US-09-101-146-64
; Sequence 64, Application US/09101146
; Patent No. 6124125
; GENERAL INFORMATION:
; APPLICANT: Dartmouth College, St. Vincent's Institute of
; APPLICANT: Medical Research, Kemp et al.
; TITLE OF INVENTION: No. 6124125el AMP Activated Protein Kinase
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jane Massey Licata, Esq.
; STREET: 66 E. Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PC
; OPERATING SYSTEM: WINDOWS 95
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;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Billings, Lucy J J
;; REGISTRATION NUMBER: 36,749
;; REFERENCE/DOCKET NUMBER: PF-0321 US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-855-0555
;; TELEFAX: 415-845-4166
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 21:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 331 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; IMMEDIATE SOURCE:
;; LIBRARY: GenBank
;; CLONE: 1335856
;;
US-09-272-796-21

Query Match 42.3%; Score 1017; DB 2; Length 331;
Best Local Similarity 64.8%; Pred. No. 1.2e-105;
Matches 193; Conservative 53; Mismatches 52; Indels 0; Gaps 0;

Qy 158 IYRMFQEHCTCYDAMATSSKLVIFDTMTLEIKKAFALVANGVRAAPLWDSKKQSFVGMILT 217
Db 28 VYTSFMKSHRCYDLIPTSSKLVVFDTSLOVKKAFALVTNGVRAAPLWDSKKQSFVGMILT 87
Qy 218 ITDFILVLRHYRSPVQVIEIHOHKIETWREIYLOGCFFKPLVSIISPNDSLFEAVYTLIK 277
Db 88 ITDFINILHRYKSAVQVIELEEHKIEWREYVLOQSPKPLVCISPNASLFDVAVSLIR 147
Qy 278 NRHRLPVLDPVSGNVHLTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVV 337
Db 148 NKIHLRPVIDPESGNTLYLTHKRLKFLKLFITEFPKPEFMSKLEELQIGTYANIAMV 207
Qy 338 LETAPILTALDIFVDRRVSAIPVNVCEGVVGLYSRFDVIHLAAQOQTYNHLDMVSGEALR 397
Db 208 RTTPVTVVAGIFVQHRVSALPVVDEKGRVVDIYSKFDVINLAAEKTNNLDVSVTKALQ 267
Qy 398 QRTLCLEGVLSQCPHESIGEVIDRIAREQVHRLVLDVDETQHLLGVVSLDILQALVLS 455
Db 268 HRSHYFEGVLKCYLHETLEIINRLVEAEVHRLVVVDENVVKGIVSLDILQALVLT 325

RESULT 14
US-09-949-016-10881
; Sequence 10881, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10881
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10881

Query Match 42.3%; Score 1017; DB 2; Length 336;
Best Local Similarity 64.8%; Pred. No. 1.2e-105;
Matches 193; Conservative 53; Mismatches 52; Indels 0; Gaps 0;

Qy 158 IYRMFQEHCTCYDAMATSSKLVIFDTMTLEIKKAFALVANGVRAAPLWDSKKQSFVGMILT 217
Db 33 VYTSFMKSHRCYDLIPTSSKLVVFDTSLOVKKAFALVTNGVRAAPLWDSKKQSFVGMILT 92
Qy 218 ITDFILVLRHYRSPVQVIEIHOHKIETWREIYLOGCFFKPLVSIISPNDSLFEAVYTLIK 277
Db 93 ITDFINILHRYKSAVQVIELEEHKIEWREYVLOQSPKPLVCISPNASLFDVAVSLIR 152
Qy 278 NRHRLPVLDPVSGNVHLTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVV 337
Db 153 NKIHLRPVIDPESGNTLYLTHKRLKFLKLFITEFPKPEFMSKLEELQIGTYANIAMV 212
Qy 338 LETAPILTALDIFVDRRVSAIPVNVCEGVVGLYSRFDVIHLAAQOQTYNHLDMVSGEALR 397

;;
;;
;; ORGANISM: Homo sapiens
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Db 213 RTTPVVALGIFVQHRVSALPVVDEKGRVVDIYSKFDVINLAAEKTNNLDVSVTKALQ 272
Qy 398 QRTLCLEGVLSQOPHESIGEVIDRIAREQVHRLVLDVETQHLGVSLSLQALVLS 455
Db 273 HRSHYFEGVLKCYLHETLETTINRLVEAEVHRLVVVDENDVVKGIVSLSDILQALVLT 330

RESULT 15
US-09-359-161-7
; Sequence 7, Application US/09359161A
; Patent No. 6342656
; GENERAL INFORMATION:
; APPLICANT: Bradford, Kent J.
; APPLICANT: Dahal, Peetambar
; APPLICANT: Yang, Hong
; APPLICANT: Cooley, Michael
; APPLICANT: Downie, Bruce
; APPLICANT: Gee, Oliver
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Regulation of Source-Sink Relationships and Responses
; FILE OF INVENTION: to Stress Conditions in Plants
; FILE REFERENCE: 023070-095900US
; CURRENT APPLICATION NUMBER: US/09/359,161A
; CURRENT FILING DATE: 1999-07-21
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 7
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; OTHER INFORMATION: Yeast sucrose nonfermenting protein kinase 1
; OTHER INFORMATION: kinase subunit (SNF1)
US-09-359-161-7

Query Match 19.0%; Score 457; DB 2; Length 322;
Best Local Similarity 34.2%; Pred. No. 1.9e-42;
Matches 106; Conservative 66; Mismatches 108; Indels 30; Gaps 6;
Qy 161 RFMOBHTCYDAMATSSKLVIPTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMLTITD 220
Db 24 KFLNSKTSYDVLVPSYRLVLDTSLLVKSLNVLQNSIVSAPLWDSKTSRFAGLLTTTD 83
Qy 221 FILVLRHYRSPLOIYEIOHKIETWREIYLCQCFKL-----VSIENDSLFP 269
Db 84 FINVIQYFNSP-----DKFELVDKQLDGLG-LKDIERALGVDDQLDTASIHPSRPLF 133
Qy 270 EAVYTLIKRIHRLPVLDPVSGN----VLHILTKRLKLFELHIFGSLAPRPS-FLYRTIQ 324
Db 134 EACLKMLESRGRIPLIDQDETHREIVSVLTQYRIKLFV----ALNCRETHFLKIFIG 189
Qy 325 DLIGIGTFRDLAVALLETAPILTALDIFVDRRVSAIPVNVNCEGVGLYSRFDVVIHLAAQOT 384
Db 190 DLIITQDNMKSQMTFVIDIQLTQGRVSSVPIIDENGVLINVEAYDVLGIKGGI 249
Qy 385 YNHLDMSVGEALRQRTLCLEGVLSQOPHESIGEVIDRIAREQVHRLVLDVETQHLGVS 444
Db 250 YNDLSLSVGEALMRRSDDFEGVYCTCKNDKLSTIMDNIRKARVHRFFVVDVVGRLVGVL 309
Qy 445 LSDILOALVL 454
Db 310 LSDILKYILL 319

Search completed: January 24, 2006, 22:16:25
Job time : 39.6164 secs

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OM protein - protein search, using sw model

Run on: January 24, 2006, 22:14:24 ; Search time 102.575 Seconds
(without alignments)
1890.063 Million cell updates/sec

Title: US-10-070-794A-30

Perfect score: 2403

Sequence: 1 MSFLEQENSSWPSPAVTSS.....LSDILOALVLSPPAGIDALGA 464

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:**
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:**
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:**
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:**
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	2398	99.8	489	3	US-09-826-581-6
3	2398	99.8	489	4	US-10-473-670-15
4	2398	99.8	489	4	US-10-705-137-6
5	2376	98.9	489	5	US-10-503-039-2
6	2376	98.9	489	5	US-10-503-175-6
7	2372	98.7	492	5	US-10-756-149-5028
8	2013	83.8	464	3	US-09-950-022-4
9	2013	83.8	464	6	US-11-075-134-4
10	2011	83.7	464	3	US-09-950-022-2
11	2011	83.7	464	6	US-11-075-134-2
12	2010	83.6	464	3	US-09-950-022-8
13	2010	83.6	464	6	US-11-075-134-8
14	2007	83.5	464	3	US-09-950-022-10
15	2007	83.5	464	6	US-11-075-134-10
16	2005	83.4	464	3	US-09-950-022-6
17	2005	83.4	464	6	US-11-075-134-6
18	2000	83.2	489	5	US-10-503-175-4
19	1082.5	45.0	352	5	US-10-466-162-12
20	1080.5	45.0	328	3	US-09-769-970-7
21	1080.5	45.0	328	5	US-10-466-162-14
22	1017	42.3	331	3	US-09-769-970-21
23	1017	42.3	331	5	US-10-473-127-923
24	1017	42.3	331	5	US-10-473-127-924
25	1017	42.3	331	5	US-10-473-127-927
26	1017	42.3	331	5	US-10-473-127-928
27	1017	42.3	331	5	US-10-466-162-16

28	1017	42.3	344	3	US-09-925-297-461	Sequence 461, App
29	1017	42.3	344	5	US-10-473-127-925	Sequence 925, App
30	886	36.9	488	5	US-10-450-763-50437	Sequence 50437, A
31	874.5	36.4	1207	4	US-10-108-605-71	Sequence 71, Appl
32	869.5	36.2	634	6	US-11-097-143-25527	Sequence 25527, A
33	845.5	35.2	383	5	US-10-450-763-50439	Sequence 50439, A
34	758	31.5	181	4	US-10-276-774-1611	Sequence 1611, Ap
35	494	20.6	180	4	US-10-106-698-6572	Sequence 6572, Ap
36	396	16.5	149	4	US-10-264-237-1653	Sequence 1653, Ap
37	374.5	15.6	487	5	US-10-739-930-6722	Sequence 6722, Ap
38	362	15.1	477	4	US-10-425-114-50202	Sequence 50202, A
39	357	14.9	448	4	US-10-425-115-187601	Sequence 187601, A
40	355	14.8	451	4	US-10-437-963-168583	Sequence 168583, A
41	352.5	14.7	368	4	US-10-425-114-54796	Sequence 54796, A
42	352.5	14.7	493	4	US-10-424-599-187700	Sequence 187700, A
43	352	14.6	461	4	US-10-424-599-187700	Sequence 187700, A
44	350.5	14.6	365	4	US-10-425-114-22531	Sequence 22531, A
45	347.5	14.5	497	4	US-10-425-115-274759	Sequence 274759, A

ALIGNMENTS

RESULT 1

US-10-503-175-2
; Sequence 2, Application US/10503175
; Publication No. US20050172348A1
; GENERAL INFORMATION:
; APPLICANT: Andersson, Leif
; APPLICANT: Marklund, Stefan
; TITLE OF INVENTION: Transgenic animals expressing prkg3
; FILE REFERENCE: 11145-020US1
; CURRENT APPLICATION NUMBER: US/10/503,175
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: PCT/IB03/00912
; PRIOR FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 60/353,430
; PRIOR FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-503-175-2

Query Match	100.0%	Score	2403	DB	5	Length	489
Best Local Similarity	100.0%	Pred. No.	2.6e-217				
Matches	464	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
Qy	1	MSFLEQENSSWPSPAVTSSSRIRKRAKALRWTRQKSVGEPPGQEGPRSRPTAE	60				
Db	26	MSFLEQENSSWPSPAVTSSSRIRKRAKALRWTRQKSVGEPPGQEGPRSRPTAE	85				
Qy	61	STGLEATFPKTTPLAQADPAGVCTPTGMDCLPSDCTASAGSSTDDELATFPATEAW	120				
Db	86	STGLEATFPKTTPLAQADPAGVCTPTGMDCLPSDCTASAGSSTDDELATFPATEAW	145				
Qy	121	ECELEGLLEERPALCLSPQAPFPLGWDDELKPGQAIYMRFWQHTCYDAMATSSKLVI	180				
Db	146	ECELEGLLEERPALCLSPQAPFPLGWDDELKPGQAIYMRFWQHTCYDAMATSSKLVI	205				
Qy	181	FTMLIKKAFPAFFALVANGVRAAPLWDSKKQSFVGMLTITDILVLRHYRSPVLQIYEIE	240				
Db	206	FTMLIKKAFPAFFALVANGVRAAPLWDSKKQSFVGMLTITDILVLRHYRSPVLQIYEIE	265				
Qy	241	QHKIETWREIYLGCCFKPLVSPNDLSLFEAVTYLTKNRIHRLPVLDPVSGNVLHLTHK	300				
Db	266	QHKIETWREIYLGCCFKPLVSPNDLSLFEAVTYLTKNRIHRLPVLDPVSGNVLHLTHK	325				
Qy	301	RLIKFLHIFGSLPRPSFLYRTIQDIGTFRDLAVLETAPILTALDIFVDRVSALPV	360				
Db	326	RLIKFLHIFGSLPRPSFLYRTIQDIGTFRDLAVLETAPILTALDIFVDRVSALPV	385				

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Qy 361 VNECGQVGLYSRFDVTHLAAQQTYNHLDMSVGEALRQRTLCLEGVLSQPHESLGEVID 420
Db 386 VNECGQVGLYSRFDVTHLAAQQTYNHLDMSVGEALRQRTLCLEGVLSQPHESLGEVID 445
Qy 421 RIAREQVHRLVLVDETOHLLGVVSLSDIILQALVLSPPAGIDALGA 464
Db 446 RIAREQVHRLVLVDETOHLLGVVSLSDIILQALVLSPPAGIDALGA 489

RESULT 2
US-09-826-581-6
; Sequence 6, Application US/09826581
; Patent No. US20020142310A1
; GENERAL INFORMATION:
; APPLICANT: Andersson, Lelf
; APPLICANT: Luthman, L. Holger
; APPLICANT: Marklund, Stefan
; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNIT
; FILE REFERENCE: 11145-007001
; CURRENT APPLICATION NUMBER: US/09/826,581
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 60/195,665
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-581-6

Query Match 99.8%; Score 2398; DB 3; Length 489;
Best Local Similarity 99.8%; Pred. No. 7.8e-217;
Matches 463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSFLEQENSSWSPSPAVTSSSERIRGKRRAKALRWTRQKSVVEEGPPCGGSPRSRTAE 60
Db 26 MSFLEQENSSWSPSPAVTSSSERIRGKRRAKALRWTRQKSVVEEGPPCGGSPRSRAAE 85
Qy 61 STGLEATFPKTTPLAQADPAGVGPPTGWDCLPSDCTASAAGSSTDVDELATEFPATEAW 120
Db 86 STGLEATFPKTTPLAQADPAGVGPPTGWDCLPSDCTASAAGSSTDVDELATEFPATEAW 145
Qy 121 ECEGLELEERPALCLSPQAPFPKLGWDDLRKPKCAQIYMERFMOEHTCYDAMATSSKLVI 180
Db 146 ECEGLELEERPALCLSPQAPFPKLGWDDLRKPKCAQIYMERFMOEHTCYDAMATSSKLVI 205
Qy 181 FDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMLTITDFTLVHLHYRSPVLQIYEIE 240
Db 206 FDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMLTITDFTLVHLHYRSPVLQIYEIE 265
Qy 241 QHKTETWREIYLOGCFKPLVSI SPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVHLHILTHK 300
Db 266 QHKTETWREIYLOGCFKPLVSI SPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVHLHILTHK 325
Qy 301 RLLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPV 360
Db 336 RLLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPV 385
Qy 361 VNECGQVGLYSRFDVTHLAAQQTYNHLDMSVGEALRQRTLCLEGVLSQPHESLGEVID 420
Db 386 VNECGQVGLYSRFDVTHLAAQQTYNHLDMSVGEALRQRTLCLEGVLSQPHESLGEVID 445
Qy 421 RIAREQVHRLVLVDETOHLLGVVSLSDIILQALVLSPPAGIDALGA 464
Db 446 RIAREQVHRLVLVDETOHLLGVVSLSDIILQALVLSPPAGIDALGA 489

RESULT 3
US-10-473-670-15
; Sequence 15, Application US/10473670
; Publication No. US2004010180A1
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; GENERAL INFORMATION:
; APPLICANT: RECIPON, Shirley A.; BURRILL, John D.;
; APPLICANT: MARCUS, Gregory A.; ZINGLER, Kurt A.;
; APPLICANT: TANG, Y. Tom; THORNTON, Michael;
; APPLICANT: BOROWSKY, Mark L.; BAUGHN, Mariah R.;
; APPLICANT: BURFORD, Neil; LEE, Soo Yeun;
; APPLICANT: BANDMAN, Olga; HAFALIA, April J.A.;
; APPLICANT: YAO, Monique G.; RAMKUMAR, Jayalaxmi;
; APPLICANT: CHAWLA, Narinder K.; LU, Dying Aina M.;
; APPLICANT: ARVIZU, Chandra S.; ISON, Craig H.;
; APPLICANT: DING, Li; LU, Yan;
; APPLICANT: GURURAJAN, Rajagopal; WALSH, Roderick T.;
; APPLICANT: GANDHI, Ameena R.; SWARNAKAR, Anita;
; APPLICANT: FORSTHE, Ian J.; YUE, Henry;
; APPLICANT: AU-YOUNG, Janice K.; ELLIOTT, Vicki S.;
; APPLICANT: LEE, Sally
; TITLE OF INVENTION: KINASES AND PHOSPHATASES
; FILE REFERENCE: PI-0398 USN
; CURRENT APPLICATION NUMBER: US/10/473,670
; CURRENT FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: PCT/US02/10818
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 60/282,119
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/283,588
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/283,759
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/285,589
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: US 60/287,037
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/287,036
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/288,608
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/288,712
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/289,909
; PRIOR FILING DATE: 2001-05-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PERL Program
; SEQ ID NO 15
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7474666CD1
US-10-473-670-15

Query Match 99.8%; Score 2398; DB 4; Length 489;
Best Local Similarity 99.8%; Pred. No. 7.8e-217;
Matches 463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSFLEQENSSWSPSPAVTSSSERIRGKRRAKALRWTRQKSVVEEGPPCGGSPRSRTAE 60
Db 26 MSFLEQENSSWSPSPAVTSSSERIRGKRRAKALRWTRQKSVVEEGPPCGGSPRSRAAE 85
Qy 61 STGLEATFPKTTPLAQADPAGVGPPTGWDCLPSDCTASAAGSSTDVDELATEFPATEAW 120
Db 86 STGLEATFPKTTPLAQADPAGVGPPTGWDCLPSDCTASAAGSSTDVDELATEFPATEAW 145
Qy 121 ECEGLELEERPALCLSPQAPFPKLGWDDLRKPKCAQIYMERFMOEHTCYDAMATSSKLVI 180
Db 146 ECEGLELEERPALCLSPQAPFPKLGWDDLRKPKCAQIYMERFMOEHTCYDAMATSSKLVI 205
Qy 181 FDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMLTITDFTLVHLHYRSPVLQIYEIE 240
Db 206 FDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMLTITDFTLVHLHYRSPVLQIYEIE 265
Qy 241 QHKTETWREIYLOGCFKPLVSI SPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVHLHILTHK 300
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Db 266 QHKTETWREIYLCGCPFLVSPNDLSFSAVYTLIKNRHRLPVLDPVSGNVHLHILTHK 325
Qy 301 RLLKFLHIFGSLPRPFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSAALPV 360
Db 326 RLLKFLHIFGSLPRPFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSAALPV 385
Qy 361 VNECGQVGLYSRFDVTHLAAQQTNYHLDMSVGEALRQRTLCLEGVLSQCPHESLGEVID 420
Db 386 VNECGQVGLYSRFDVTHLAAQQTNYHLDMSVGEALRQRTLCLEGVLSQCPHESLGEVID 445
Qy 421 RIAREQVHRLVLDVDETOHLLGVVSLSDILOALVLSAPGIDALGA 464
Db 446 RIAREQVHRLVLDVDETOHLLGVVSLSDILOALVLSAPGIDALGA 489

RESULT 4
US-10-705-137-6
; Sequence 6, Application US/10705137
; Publication No. US20040121385A1
; GENERAL INFORMATION:
; APPLICANT: Andersson, Leif
; APPLICANT: Luthman, L. Holger
; APPLICANT: Marklund, Stefan
; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNIT
; FILE REFERENCE: 11145-007002
; CURRENT APPLICATION NUMBER: US/10705,137
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: US 09/826,581
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 60/195,665
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-705-137-6

Query Match 99.8%; Score 2398; DB 4; Length 489;
Best Local Similarity 99.8%; Pred. No. 7.8e-217;
Matches 463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSFLEQENSSSWSPSPAVTSSSRIRGKRAKALRWTKQSVEEGPPGQEGPGRSPRTAE 60
Db 26 MSFLEQENSSSWSPSPAVTSSSRIRGKRAKALRWTKQSVEEGPPGQEGPGRSPAAE 85
Qy 61 STGLEATFPKTTPLAQADPAGVGTPTGWDCLPSDCTASAAGSTDDVELATEFPATEAW 120
Db 86 STGLEATFPKTTPLAQADPAGVGTPTGWDCLPSDCTASAAGSTDDVELATEFPATEAW 145
Qy 121 ECEGLELIERPALCLSPQAPFPKLGWDDDELKPKAQIYMRFMQEHTCYDAMATSSKLVI 180
Db 146 ECEGLELIERPALCLSPQAPFPKLGWDDDELKPKAQIYMRFMQEHTCYDAMATSSKLVI 205
Qy 181 FDTMLEIKKAPFALVANGVRAAPLWDSKQSFVGMILTITDILVHLHYRSPVQIYEIE 240
Db 206 FDTMLEIKKAPFALVANGVRAAPLWDSKQSFVGMILTITDILVHLHYRSPVQIYEIE 265
Qy 241 QHKTETWREIYLCGCPFLVSPNDLSFSAVYTLIKNRHRLPVLDPVSGNVHLHILTHK 300
Db 266 QHKTETWREIYLCGCPFLVSPNDLSFSAVYTLIKNRHRLPVLDPVSGNVHLHILTHK 325
Qy 301 RLLKFLHIFGSLPRPFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSAALPV 360
Db 326 RLLKFLHIFGSLPRPFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSAALPV 385
Qy 361 VNECGQVGLYSRFDVTHLAAQQTNYHLDMSVGEALRQRTLCLEGVLSQCPHESLGEVID 420
Db 386 VNECGQVGLYSRFDVTHLAAQQTNYHLDMSVGEALRQRTLCLEGVLSQCPHESLGEVID 445
Qy 421 RIAREQVHRLVLDVDETOHLLGVVSLSDILOALVLSAPGIDALGA 464

Db 446 RIAREQVHRLVLDVDETOHLLGVVSLSDILOALVLSAPGIDALGA 489

RESULT 5
US-10-503-039-2
; Sequence 2, Application US/10503039
; Publication No. US20050155091A1
; GENERAL INFORMATION:
; APPLICANT: Svensson, Thomas
; TITLE OF INVENTION: Prka3 gene promoter and uses thereof
; FILE REFERENCE: 11145-022US1
; CURRENT APPLICATION NUMBER: US/10/503,039
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: PCT/IB03/00762
; PRIOR FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 60/353,429
; PRIOR FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-503-039-2

Query Match 98.9%; Score 2376; DB 5; Length 489;
Best Local Similarity 98.9%; Pred. No. 9.2e-215;
Matches 459; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MSFLEQENSSSWSPSPAVTSSSRIRGKRAKALRWTKQSVEEGPPGQEGPGRSPRTAE 60
Db 26 MSFLEQENSSSWSPSPAVTSSSRIRGKRAKALRWTKQSVEEGPPGQEGPGRSPAAE 85
Qy 61 STGLEATFPKTTPLAQADPAGVGTPTGWDCLPSDCTASAAGSTDDVELATEFPATEAW 120
Db 86 STGLEATFPKTTPLAQADPAGVGTPTGWDCLPSDCTASAAGSTDDVELATEFPATEAW 145
Qy 121 ECEGLELIERPALCLSPQAPFPKLGWDDDELKPKAQIYMRFMQEHTCYDAMATSSKLVI 180
Db 146 ECEGLELIERPALCLSPQAPFPKLGWDDDELKPKAQIYMRFMQEHTCYDAMATSSKLVI 205
Qy 181 FDTMLEIKKAPFALVANGVRAAPLWDSKQSFVGMILTITDILVHLHYRSPVQIYEIE 240
Db 206 FDTMLEIKKAPFALVANGVRAAPLWDSKQSFVGMILTITDILVHLHYRSPVQIYEIE 265
Qy 241 QHKTETWREIYLCGCPFLVSPNDLSFSAVYTLIKNRHRLPVLDPVSGNVHLHILTHK 300
Db 266 QHKTETWREIYLCGCPFLVSPNDLSFSAVYTLIKNRHRLPVLDPVSGNVHLHILTHK 325
Qy 301 RLLKFLHIFGSLPRPFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSAALPV 360
Db 326 RLLKFLHIFGSLPRPFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSAALPV 385
Qy 361 VNECGQVGLYSRFDVTHLAAQQTNYHLDMSVGEALRQRTLCLEGVLSQCPHESLGEVID 420
Db 386 VNECGQVGLYSRFDVTHLAAQQTNYHLDMSVGEALRQRTLCLEGVLSQCPHESLGEVID 445
Qy 421 RIAREQVHRLVLDVDETOHLLGVVSLSDILOALVLSAPGIDALGA 464
Db 446 RIAREQVHRLVLDVDETOHLLGVVSLSDILOALVLSAPGIDALGA 489

RESULT 6
US-10-503-175-6
; Sequence 6, Application US/10503175
; Publication No. US20050172348A1
; GENERAL INFORMATION:
; APPLICANT: Andersson, Leif
; APPLICANT: Marklund, Stefan
; TITLE OF INVENTION: Transgenic animals expressing prka3
; FILE REFERENCE: 11145-020US1
; CURRENT APPLICATION NUMBER: US/10/503,175

; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: PCT/IB03/00912
; PRIOR FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 60/353,430
; PRIOR FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-503-175-6

Query Match 98.9%; Score 2376; DB 5; Length 489;
Best Local Similarity 98.9%; Pred. No. 9.2e-215;
Matches 459; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MSFLEQENSSSWPSPAVTSSSERIRGKRRAKALRWTRQKSVVEGEPGQEGPGRSPTAE 60
Db 26 MSFLEQENSSSWPSPAVTSSSERIRGKRRAKALRWTRQKSVVEGEPGQEGPGRSPTAE 85
Qy 61 STGLEATFPKTTPLAQADPAGVGTPTGWDCLPSDCTASAGSSTDDVELATEFPATEAW 120
Db 86 STGLEATFPKTTPLAQADPAGVGTPTGWDCLPSDCTASAGSSTDDVELATEFPATEAW 145
Qy 121 ECELEGLLEERPALCLSPQAPFPKLGWDDLRKFGAQIYMRFMQEHCTCYDAMATSSKLVI 180
Db 146 ECELEGLLEERPALCLSPQAPFPKLGWDDLRKFGAQIYMRFMQEHCTCYDAMATSSKLVI 205
Qy 181 FDTMLEIKKAFPAFVANGVRAAPLWDSKKQSFVGMLTITDILVLRHYRSPVQIYEIE 240
Db 206 FDTMLEIKKAFPAFVANGVRAAPLWDSKKQSFVGMLTITDILVLRHYRSPVQIYEIE 265
Qy 241 QHKIETWREIYLOGCFKPLVSI SPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHK 300
Db 266 QHKIETWREIYLOGCFKPLVSI SPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHK 325
Qy 301 RLLKFLHIFGSLPRPSFLYRTIQDLGIGTRDLAVVLETAPILTALDIFVDRRVSAALPV 360
Db 326 RLLKFLHIFGSLPRPSFLYRTIQDLGIGTRDLAVVLETAPILTALDIFVDRRVSAALPV 385
Qy 361 VNECGQVGLYSRFDVHLAAQOTYNNHLDMSVGEALRORTLCLEGVLSQPHESLGEVID 420
Db 386 VNECGQVGLYSRFDVHLAAQOTYNNHLDMSVGEALRORTLCLEGVLSQPHESLGEVID 445
Qy 421 RIAREQVHRLVLDVDETQHLGLGVVSLSDILOALVLSPAGIDALGA 464
Db 446 RIAREQVHRLVLDVDETQHLGLGVVSLSDILOALVLSPAGIDALGA 489

RESULT 7
US-10-756-149-5028
; Sequence 5028, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10756,149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5028
; LENGTH: 492
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-756-149-5028

Query Match 98.7%; Score 2372; DB 5; Length 492;
Best Local Similarity 98.7%; Pred. No. 2.2e-214;
Matches 457; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MSFLEQENSSSWPSPAVTSSSERIRGKRRAKALRWTRQKSVVEGEPGQEGPGRSPTAE 60
Db 26 MSFLEQENSSSWPSPAVTSSSERIRGKRRAKALRWTRQKSVVEGEPGQEGPGRSPTAE 85
Qy 61 STGLEATFPKTTPLAQADPAGVGTPTGWDCLPSDCTASAGSSTDDVELATEFPATEAW 120
Db 86 STGLEATFPKTTPLAQADPAGVGTPTGWDCLPSDCTASAGSSTDDVELATEFPATEAW 145
Qy 121 ECELEGLLEERPALCLSPQAPFPKLGWDDLRKFGAQIYMRFMQEHCTCYDAMATSSKLVI 180
Db 146 ECELEGLLEERPALCLSPQAPFPKLGWDDLRKFGAQIYMRFMQEHCTCYDAMATSSKLVI 205
Qy 181 FDTMLEIKKAFPAFVANGVRAAPLWDSKKQSFVGMLTITDILVLRHYRSPVQIYEIE 240
Db 206 FDTMLEIKKAFPAFVANGVRAAPLWDSKKQSFVGMLTITDILVLRHYRSPVQIYEIE 265
Qy 241 QHKIETWREIYLOGCFKPLVSI SPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHK 300
Db 266 QHKIETWREIYLOGCFKPLVSI SPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHK 325
Qy 301 RLLKFLHIFGSLPRPSFLYRTIQDLGIGTRDLAVVLETAPILTALDIFVDRRVSAALPV 360
Db 326 RLLKFLHIFGSLPRPSFLYRTIQDLGIGTRDLAVVLETAPILTALDIFVDRRVSAALPV 385
Qy 361 VNECGQVGLYSRFDVHLAAQOTYNNHLDMSVGEALRORTLCLEGVLSQPHESLGEVID 420
Db 386 VNECGQVGLYSRFDVHLAAQOTYNNHLDMSVGEALRORTLCLEGVLSQPHESLGEVID 445
Qy 421 RIAREQVHRLVLDVDETQHLGLGVVSLSDILOALVLSPAGIDALG 463
Db 446 RIAREQVHRLVLDVDETQHLGLGVVSLSDILOALVLSPAGIDPSG 488

RESULT 8
US-09-950-022-4
; Sequence 4, Application US/09950022
; Publication No. US20030017470A1
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: Novel PRKAG3 Alleles and Use fo the Same as Genetic Markers for Reproductive and Meat Quality Traits
; TITLE OF INVENTION: Reproductive and Meat Quality Traits
; FILE REFERENCE: P04668US3
; CURRENT APPLICATION NUMBER: US/09/950,022
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-950-022-4

Query Match 83.8%; Score 2013; DB 3; Length 464;
Best Local Similarity 86.0%; Pred. No. 1.5e-180;
Matches 400; Conservative 19; Mismatches 44; Indels 2; Gaps 2;

Qy 1 MSFLEQENSSSWPSPAVTSSSERIRGKRRAKALRWTRQKSVVEGEPGQEGPGRSPTAE 60
Db 1 MSFLEQENSSSWPSPAVTSSSERIRGKRRAKALRWTRQKSVVEGEPGQEGPGRSPTAE 60
Qy 61 STGLEATFPKTTPLAQADP-AGVGTPTGWDCLPSDCTASAGSSTDDVELATEFPATEA 119
Db 61 STGLEATFPKTTPLAQADP-AGVGTPTGWDCLPSDCTASAGSSTDDVELATEFPATEA 120


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Qy 300 KRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLETPILTALDIFVDRVSALP 359
Db 300 KRLKFLHIFGTLPRPSFLYRTIQDLGIGTFRDLAVVLETPILTALDIFVDRVSALP 359
Qy 360 VVNECGQVVGILYSRFDVHILAAQOQTYNHLDMNVGEALRQRTLCLEGVLSQCPHESLGEVI 419
Db 360 VVNETGVVGLYSRFDVHILAAQOQTYNHLDMNVGEALRQRTLCLEGVLSQCPHETLGEVI 419
Qy 420 DRIAREQVHRLVLVDETOHLLGVVSLSDIILQALVLSPAGIDALGA 464
Db 420 DRIAREQVHRLVLVDETOHLLGVVSLSDIILQALVLSPAGIDALGA 464

RESULT 11
US-11-075-134-2
; Sequence 2, Application US/11075134
; Publication No. US20050208551A1
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: Novel PKAG3 Alleles and Use to the Same as Genetic Markers for
; TITLE OF INVENTION: Reproductive and Meat Quality Traits
; FILE REFERENCE: P04668US3
; CURRENT APPLICATION NUMBER: US/11/075,134
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: US/09/950,022
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Sus scrofa
US-11-075-134-2

Query Match 83.7%; Score 2011; DB 6; Length 464;
Best Local Similarity 86.0%; Pred. No. 2.3e-180;
Matches 400; Conservative 19; Mismatches 44; Indels 2; Gaps 2;

Qy 1 MSFLEQENSSWSPSPAVTSSSIRIGKRAKALRWTRKSVVEEGPPGQGGPRSPRTAE 60
Db 1 MSFLEQGESRSWSPRAVTTSSRSRSHGQGNKASRWTRQEDVEEGPPGPRGQSRPVAE 60
61 STGLEATFPKTTPLAQADP-AGVCTPPTGWDCLPSCDCTASAAGSSTDVLELATEFPATEA 119
61 STGQEAATPKATPLAQAPLAEVNDPPTERDILPSCDCAASDSNTDHLGIEFSASAA 120
120 WECELEGLLEERPALCLSPQAPFPKLGWDDDELKPKGAQIYMRFMQHTCYDAMATSSKLV 179
121 SGDEL-GLVEEKPAFCPSPEVLLPRLGWDDDELQKFGAQVYMHFMQHTCYDAMATSSKLV 179
180 IFDTMLEIKKAFPAFALVANGVRAAPLWDSKKQSFVGMLTITDPIILVHRYRSPVQIYEI 239
180 IFDTMLEIKKAFPAFALVANGVRAAPLWDSKKQSFVGMLTITDPIILVHRYRSPVQIYEI 239
240 EHKIETWREIYLOGCFKPLVSI SPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVHLHILTH 299
240 EHKIETWREIYLOGCFKPLVSI SPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVHLHILTH 299
300 KRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLETPILTALDIFVDRVSALP 359
300 KRLKFLHIFGTLPRPSFLYRTIQDLGIGTFRDLAVVLETPILTALDIFVDRVSALP 359
360 VVNECGQVVGILYSRFDVHILAAQOQTYNHLDMNVGEALRQRTLCLEGVLSQCPHESLGEVI 419
360 VVNETGVVGLYSRFDVHILAAQOQTYNHLDMNVGEALRQRTLCLEGVLSQCPHETLGEVI 419
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Db 360 VVNETGVVGLYSRFDVHILAAQOQTYNHLDMNVGEALRQRTLCLEGVLSQCPHETLGEVI 419
Qy 420 DRIAREQVHRLVLVDETOHLLGVVSLSDIILQALVLSPAGIDALGA 464
Db 420 DRIAREQVHRLVLVDETOHLLGVVSLSDIILQALVLSPAGIDALGA 464

RESULT 12
US-09-950-022-8
; Sequence 8, Application US/09950022
; Publication No. US20030017470A1
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: Novel PKAG3 Alleles and Use to the Same as Genetic Markers for
; TITLE OF INVENTION: Reproductive and Meat Quality Traits
; FILE REFERENCE: P04668US3
; CURRENT APPLICATION NUMBER: US/09/950,022
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-950-022-8

Query Match 83.6%; Score 2010; DB 3; Length 464;
Best Local Similarity 85.8%; Pred. No. 2.8e-180;
Matches 399; Conservative 20; Mismatches 44; Indels 2; Gaps 2;

Qy 1 MSFLEQENSSWSPSPAVTSSSIRIGKRAKALRWTRKSVVEEGPPGQGGPRSPRTAE 60
Db 1 MSFLEQGESRSWSPRAVTTSSRSRSHGQGNKASRWTRQEDVEEGPPGPRGQSRPVAE 60
61 STGLEATFPKTTPLAQADP-AGVCTPPTGWDCLPSCDCTASAAGSSTDVLELATEFPATEA 119
61 STGQEAATPKATPLAQAPLAEVNDPPTERDILPSCDCAASDSNTDHLGIEFSASAA 120
120 WECELEGLLEERPALCLSPQAPFPKLGWDDDELKPKGAQIYMRFMQHTCYDAMATSSKLV 179
121 SGDEL-GLVEEKPAFCPSPEVLLPRLGWDDDELQKFGAQVYMHFMQHTCYDAMATSSKLV 179
180 IFDTMLEIKKAFPAFALVANGVRAAPLWDSKKQSFVGMLTITDPIILVHRYRSPVQIYEI 239
180 IFDTMLEIKKAFPAFALVANGVRAAPLWDSKKQSFVGMLTITDPIILVHRYRSPVQIYEI 239
240 EHKIETWREIYLOGCFKPLVSI SPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVHLHILTH 299
240 EHKIETWREIYLOGCFKPLVSI SPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVHLHILTH 299
300 KRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLETPILTALDIFVDRVSALP 359
300 KRLKFLHIFGTLPRPSFLYRTIQDLGIGTFRDLAVVLETPILTALDIFVDRVSALP 359
360 VVNECGQVVGILYSRFDVHILAAQOQTYNHLDMNVGEALRQRTLCLEGVLSQCPHESLGEVI 419
360 VVNETGVVGLYSRFDVHILAAQOQTYNHLDMNVGEALRQRTLCLEGVLSQCPHETLGEVI 419
420 DRIAREQVHRLVLVDETOHLLGVVSLSDIILQALVLSPAGIDALGA 464
420 DRIAREQVHRLVLVDETOHLLGVVSLSDIILQALVLSPAGIDALGA 464
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; CURRENT APPLICATION NUMBER: US/11/075,134
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: US/09/950,022
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Sus scrofa
US-11-075-134-10

Query Match	83.5%	Score 2007;	DB 6;	Length 464;
Best Local Similarity	85.8%	Pred. No. 5.4e-180;		
Matches 399;	Conservative 20;	Mismatches 44;	Indels 2;	Gaps 2;

QY	1	MSFLEQENSSWPSPAVTSSSRIRGKRRAKALRWTRKSVVEGEGPPQGEGPRSRPTAE	60
DB	1	MSFLEQGESRWPSPRAVTTSSSRSHGQGNKASRWTRQEDVEGEGPPGREGPQSRPVAE	60
QY	61	STGLEATPKTTPLAQADP-AGVGTPTGWDCLPSCDTASAGSSTDDELATEFPATEA	119
DB	61	STGQEAETPKATPLAQAAPLAEDVNPTTERDILPSCDAASASDSNTDHLGIEFSASAA	120
QY	120	WECELEGLLEERPALCLSPQAPFPKLGWDDRLKRGQAQYMRFMQHTCYDAMATSSKLV	179
DB	121	SGDEL-GLVEEKPAFCPSPEVLLPRLGWDDBLQKPGAQVYMHFMQHTCYDAMATSSKLV	179
QY	180	IFDTMLEIKKAFFALVANGVRAAPLWDSKQSFVGMLTITDFILVLRHYRSPVLQIYEI	239
DB	180	IFDTMLEIKKAFFALVANGVQAAPLWDSKQSFVGMLTITDFILVLRHYRSPVLQIYEI	239
QY	240	EQHKIETWREIYLGQCFKPLVSI SPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVHLHILTH	299
DB	240	EEHKIETWREIYLGQCFKPLVSI SPNDSLFEAVYALIKNRIHRLPVLDPVSGAVLHILTH	299
QY	300	KELLKFLHIFGSLIPRPSFLYRTIODLGIGTFRDLAVVLETAPILTALDIFVDRRVSAIP	359
DB	300	KELLKFLHIFGTLPRPSFLYRTIQDGLGTFRDLAVVLETAPILTALDIFVDRRVSAIP	359
QY	360	VVNECGQVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQRTLCLEGVLSQCPHESLGEVI	419
DB	360	VVNETGVVGLYSRFDVIHLAAQQTYNHLDNNVGEALRQRTLCLEGVLSQCPHETLGEVI	419
QY	420	DRIAREQVHRLVLDVETQHLGLGVSLSDILQALVLSPAGIDALGA	464
DB	420	DRIVEQVHRLVLDVETQHLGLGWSLSLILQALVLSPAGIDALGA	464

Search completed: January 24, 2006, 22:30:58
Job time : 103.575 secs

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OM protein - protein search, using sw model

Run on: January 24, 2006, 22:15:19 ; Search time 20.515 Seconds
(without alignments)
229.213 Million cell updates/sec

Title: US-10-070-794A-30

Perfect score: 2403

Sequence: 1 MSFLEQNSSSWSPAVTSS.....LSDIQLVLSVSPAGIDALGA 464

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 70609 seqs, 10134256 residues

Total number of hits satisfying chosen parameters: 70609

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA New:*
- 1: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep.*
 - 2: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep.*
 - 5: /cgn2_6/ptodata/1/pubppaa/US03_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep.*
 - 7: /cgn2_6/ptodata/1/pubppaa/US11_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a
* score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	111	4.6	466	7	US-11-156-084-26
2	111	4.6	466	7	US-11-156-084-33
3	111	4.6	494	7	US-11-156-084-34
4	107.5	4.5	498	6	US-10-467-657-5006
5	107.5	4.5	829	6	US-10-821-234-1179
6	102	4.2	461	7	US-11-156-084-35
7	100.5	4.2	495	7	US-11-156-084-36
8	99	4.1	330	7	US-11-156-084-230
9	92.5	3.8	529	6	US-10-632-150-44
10	92.5	3.8	529	7	US-11-073-457-44
11	92.5	3.8	529	7	US-11-073-460-44
12	92.5	3.8	554	6	US-10-467-657-8240
13	91	3.8	4374	7	US-11-128-572-2
14	90.5	3.8	909	7	US-11-076-187-4
15	90.5	3.8	1137	7	US-11-012-762-70
16	89.5	3.7	488	6	US-10-793-626-2308
17	89.5	3.7	1311	6	US-10-509-422-5
18	88.5	3.7	643	7	US-11-137-465-54
19	88	3.7	653	7	US-11-137-465-55
20	87.5	3.6	1618	6	US-10-984-645-2
21	87	3.6	619	7	US-11-052-554A-229
22	87	3.6	1251	7	US-11-043-889-22
23	86.5	3.6	506	7	US-11-055-822-946
24	86.5	3.6	867	6	US-10-467-657-2208
25	86	3.6	1225	7	US-11-053-100-50

26	85.5	3.6	158	7	US-11-055-822-948	Sequence 948, App
27	85.5	3.6	644	6	US-10-509-121-39	Sequence 39, Appl
28	85.5	3.6	7968	7	US-11-143-980-49	Sequence 49, Appl
29	85	3.5	1023	6	US-10-131-826A-200	Sequence 200, App
30	82	3.4	1005	7	US-11-080-991-90	Sequence 90, Appl
31	81.5	3.4	1841	7	US-11-057-058-63	Sequence 63, Appl
32	81	3.4	412	7	US-11-093-808-1	Sequence 1, Appl
33	81	3.4	412	7	US-11-093-808-7	Sequence 7, Appl
34	81	3.4	412	6	US-10-632-150-28	Sequence 8, Appl
35	81	3.4	621	6	US-10-632-150-28	Sequence 28, Appl
36	81	3.4	621	7	US-11-073-457-28	Sequence 28, Appl
37	81	3.4	621	7	US-11-073-460-28	Sequence 28, Appl
38	81	3.4	712	6	US-10-770-726-66	Sequence 66, Appl
39	81	3.4	761	6	US-10-453-372-126	Sequence 126, App
40	81	3.4	823	6	US-10-453-372-122	Sequence 122, App
41	81	3.4	823	6	US-10-453-372-124	Sequence 124, App
42	81	3.4	826	6	US-10-453-372-118	Sequence 118, App
43	81	3.4	826	6	US-10-453-372-156	Sequence 156, App
44	81	3.4	826	6	US-10-453-372-166	Sequence 166, App
45	81	3.4	826	6	US-10-453-372-172	Sequence 172, App

ALIGNMENTS

RESULT 1

US-11-156-084-26
; Sequence 26, Application US/11156084
; Publication No. US20060010515A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology LLC
; TITLE OF INVENTION: Controlled expression of cytokinin biosynthetic genes leads to
; FILE OF INVENTION: agronomically interesting phenotypes
; FILE REFERENCE: (38-21)
; CURRENT APPLICATION NUMBER: US/11/156,084
; CURRENT FILING DATE: 2005-06-17
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-11-156-084-26

Query Match 4.6%; Score 111; DB 7; Length 466;

Best Local Similarity 23.2%; Pred. No. 0.017;

Matches 68; Conservative 45; Mismatches 90; Indels 90; Gaps 16;

Qy	228	YYSRPLVQIYEIQKHKTWREIYLOGCFKPLVSISPNDSLFEAV-----YTLIKN	278
Db	120	YTIQAVVSKFLLDDAEDT-----ECCADVASVVDQMVVESVFGRDDLLSHGYELIKE	173
Qy	279	RIHRLPVLDPVSGNVLHILTKRLKELHFGSLPPSPFLY--RTIQDLG-IGTFR-DL	334
Db	174	-----LDPAANRHPNNHNRKINQYLSLHSGRGLPSKLYOGKTAENMGGINASRPDY	226
Qy	335	AVV-----LETAPILTALDIFVDRRVSPALPVVNECQVGVLY-----S	372
Db	227	CLICMDAETA-----VLDRYVEQRVDAMVDAGLDEVVDIYKPGADYTRGLRQSGVREFE	282
Qy	373	RFDVHILAAQOTYNHL-----DMSVGEALRQRTLCLEGLVSCOPHES-----LGEVIDRI	422
Db	283	DFLKIHL-SETCAGHLTSLNDDKVKENLRK-----ILNFPKDKLRIMLESEIDRV	334
Qy	423	-----ARQVHRLVLY-----DETQHLGLVSLSDILQALVLSPA	457
Db	335	KLNTRLLRRQRKRVSRLETVFGNTHYIDATEYILS--KSEESWNAQVVKPA	385

RESULT 2

US-11-156-084-33
; Sequence 33, Application US/11156084
; Publication No. US20060010515A1

US-10-821-234-1179

Query Match 4.5%; Score 107.5; DB 6; Length 829;
Best Local Similarity 20.5%; Pred. No. 0.084;
Matches 107; Conservative 72; Mismatches 191; Indels 151; Gaps 26;

QY 4 LEQNSSWSPATVSSSRIRGRRAKALRWTRQKSVESGEPGQEGPSPRSTAESTG 63
DB 6 LRSLSAPAWNTAAVLGL-LSSRRRGPAPACAVRSVSDGDFGY
QY 64 LEATFPKTPPAQADPAGVGPPTGWDCL---PSDCTASAAGSSTDDVELATEFPATEA 119
DB 51 -----RPLARCSPA---QTRPQWRLAINTDTWAEVARAPRHPYTKLGAREAVA 100
QY 120 WECELEGLLEBPALCLSPQAPFKLGDWDELKPGAGQIYMRFMQEHCTYDAMATSKLV 179
DB 101 ECEEEAVC---VTMCASVKY-----NIRGPA--LIPRMKTKHRY-----YIT 139
QY 180 IFDTML--EIKKAPFALVANGVRAAPLWDSKKQSFVGMLTITDILVLYHRYRSPVQIY 237
DB 140 LFSIVLLGLIATGQFWPHSIESNDWNVEKRS-----IRD-VPVVRLPADSPIPERG 192
QY 238 EIEQKIEWREIYLOGCFKPLVSPNDLSFEAVYTL-----IKNIHR----- 282
DB 193 DL-SCRMTCEDVTRCG-----FNPXNKIKVYIYALKKYVDVDFGVSNTISREYNEL 244
QY 283 -----LPVLDPVSGNVHLTHLTHKRLKFL-----HIFGSLLP 314
DB 245 LMAISDSYVTTDDINRACLFVPSIDVLNQLTRIKETAQAMAQLSRWDRTGNHLLFNMLP 304
QY 315 RPSFLYTIQDL-----GIG-----TFR---DLAVVETAPILTALDIFVDRRVGALP 359
DB 305 GGPPDYNTALDVPDRALLAGGFGFTYRQGYDVS-----PVYSPLSAEVD-----LP 354
QY 360 VVNECGGVGLYSRFDVTHLAAQOQTYNHLDMVSGEALRQRTLC---EGVLS-----COPH 412
DB 355 EKGPGQYFLLSQVGLHPYEDLEALQVKGESVILVDKTNLSEGLSVKRCRKH 414
QY 413 ELSGEVID--RIAREQVHRLVLDVETQHLGWSLSLQ 451
DB 415 ----QVFDYPOVLQEAFTCVLRGAR---LQAVLSVLQ 448

RESULT 6

US-11-156-084-35
; Sequence 35, Application US/11156084
; Publication No. US20060010515A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology LLC
; TITLE OF INVENTION: Controlled expression of cytokinin biosynthetic genes leads to
; FILE REFERENCE: (38-21)
; CURRENT APPLICATION NUMBER: US/11/156,084
; CURRENT FILING DATE: 2005-06-17
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 35
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-11-156-084-35

Query Match 4.2%; Score 102; DB 7; Length 461;
Best Local Similarity 22.4%; Pred. No. 0.11;
Matches 68; Conservative 45; Mismatches 90; Indels 100; Gaps 16;

QY 228 YRSPVQIYIEIOHKIETWREIYLOGCFKPLVSPNDLSFEAV-----YTLIKN 278
DB 105 YIYQAVVSKFLDDAAEDT-----EECCADVASVVDQDMVSVFGRDDLHSHGYELKE 158
QY 279 RIHRLPVLDPVSGNVHLTHKRLKFLHIFGSLLPSPFLYR-----TIQDL 326
DB 159 -----LDPVAANRIHPNNHKKINQYLSLHARGVLPFLSKYQKTAEVDSFFLTSRQNW 211

QY 327 G-IGTFR-DLAVV---LETAPILTALDIFVDRRVVSALPVVNECGQVGLY----- 371
DB 212 GCINASRFDYCLICMDAETA---VLDRYVEQRVDMVMDAGLLDEVYDIYKPGADYTRGL 267
QY 372 -----SRFDVHILAAQOQTYNHL-----DMSVGEALRQRTLCLEGLVSCQPHES-- 414
DB 268 RQSIGVREFEFLKIHL-SETCAGHLTSLSNDKVMKENLRK-----ILNFPKDDKLR 319
QY 415 --LGEVIDRI-----AREQVHRLV-----DETQHLGWSLSLQALVL 454
DB 320 IMLEEAIDRVKLNTRLLRQKRVSRLETVFGWNIHYIDATEYILS--KSEESWNAQVV 377
QY 455 SPA 457
DB 378 KPA 380

RESULT 7

US-11-156-084-36
; Sequence 36, Application US/11156084
; Publication No. US20060010515A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology LLC
; TITLE OF INVENTION: Controlled expression of cytokinin biosynthetic genes leads to
; FILE REFERENCE: (38-21)
; CURRENT APPLICATION NUMBER: US/11/156,084
; CURRENT FILING DATE: 2005-06-17
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 36
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-11-156-084-36

Query Match 4.2%; Score 100.5; DB 7; Length 495;
Best Local Similarity 21.8%; Pred. No. 0.17;
Matches 69; Conservative 47; Mismatches 93; Indels 107; Gaps 16;

QY 222 ILVLHRYRSPVQIYIEIOHKIETWREIYLOGCFKPLVSPNDLSFEAV----- 272
DB 113 VLVGGTHYIYQVSKFLDDAAEDT-----EECCADVASVVDQDMVSVVDQDMVSV 166
QY 273 -----YTLIKNRIHRLPVLDPVSGNVHLTHKRLKFLHIFGSLLPSPFLY-- 320
DB 167 VFGDDLHSHGYELKE-----LDPVAANRIHPNNHKKINQYLSLHARGVLPFLSKYQ 219
QY 321 RTIQDLG-IGTFR-DLAVV---LETAPILTALDIFVDRRVVSALPVVNECGQVGLY---- 371
DB 220 KTAENWGCINASRFDYCLICMDAETA---VLDRYVEQRVDMVMDAGLLDEVYDIYKPGA 275
QY 372 -----SRFDVHILAAQOQTYNHL-----DMSVGEALRQRTLCLEGLVSCQ 410
DB 276 DYTRGLRQSIGVREFEFLKIHL-SETCAGHLTSLSNDKVMKENLRK-----ILNFP 327
QY 411 PHES---LGEVIDRI-----AREQVHRLV-----DETQHLG 441
DB 328 KDKLRIMLEEAIDRVKLNTRLLRQKRVSRLETVFGWNIHYIDATEYILS 387
QY 442 VVLSLSDILQALVSPA 457
DB 388 --KSEESWNAQVVKPA 401

RESULT 8

US-11-156-084-230
; Sequence 230, Application US/11156084
; Publication No. US20060010515A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology LLC
; TITLE OF INVENTION: Controlled expression of cytokinin biosynthetic genes leads to

; TITLE OF INVENTION: agronomically interesting phenotypes

; FILE REFERENCE: (38-21)
; CURRENT APPLICATION NUMBER: US/11/156,084
; CURRENT FILING DATE: 2005-06-17
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 230
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-11-156-084-230

Query Match 4.1%; Score 99; DB 7; Length 330;

Best Local Similarity 23.9%; Pred. No. 0.13;
Matches 63; Conservative 40; Mismatches 77; Indels 84; Gaps 15;

QY 257 KPLVISPNDSLPEAV-----YTLIKRIHRLPVLDPVSGNVLHILTHKRLKFLH 307
DB 7 RSVQMLLDQMVESVFGRDDLSHGVELKE-----LDPVAARHHPNNHRKINQYLS 59
QY 308 IFGSLPRPSFLY--RTIQDILG-IGTFR-DLAVV---LETAPILTALDIFVDRRVSALPV 360
DB 60 LHASRGVLPKSLYQKTAENWGCINASRFDYCLICMDAETA---VLDRYVEQRVDAMVD 115
QY 361 VNEGQVVGLY-----SRFDVIHLAAQOITYNL-----DMSVGEA 395
DB 116 AGLLEVDVYIKPGADYTRGLRQSIGVREFEDFLKHL-SETCAGHLTSLNSNDKVMKEN 174
QY 396 LRQRTLCLEGLSCOPHES-----LGEVIDRI-----ARQVHRLVLV----- 433
DB 175 LRK-----TLNPKDDKLIMEEALDRVKLNTLRLLRRQKRVSRLEIVFGNIHYI 227
QY 434 DETQHLGLVWSLSLILQALVLSPA 457
DB 228 DATEVILS--KSESNQAQVVKPA 249

RESULT 9

US-10-632-150-44
; Sequence 44, Application US/10632150
; Publication No. US20050251871A1
; GENERAL INFORMATION:
; APPLICANT: Chiaux, D.
; APPLICANT: Pagano, M.
; APPLICANT: Latres, E.
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
; FILE REFERENCE: 5914-081
; CURRENT APPLICATION NUMBER: US/10/632,150
; CURRENT FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US/09/385,219
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-632-150-44

Query Match 3.8%; Score 92.5; DB 6; Length 529;

Best Local Similarity 18.7%; Pred. No. 1;
Matches 89; Conservative 66; Mismatches 175; Indels 145; Gaps 19;

QY 22 ERIRGKRKAKAL--RWTRQKSVEEGPPGQGEPRSRPTAESTGLEATFPKTTPLAQADP 79
DB 13 KRGARRKRGKGGREARAADGEGSGFGAEGAGARTPREAEGGSGVEEGARGIIKGD 72

QY 80 AGVGTPTPTG-----WDCLPSDCTASAAGSSTD 107
DB 73 GSVGAGKEAQGRKYKEEWRVARRREGARPRVQGGQVWAYIPGTGAAMAAAREEE 132
QY 108 VELATEFPATEWECELEGLLEERPALCLSPQAPFPKLGWDDDELKPG--AQIYMRPMQE 165
DB 133 EEAARESA-----CPAAG-----PALWRLPEVLLHMC SYLDMRALGRLAQVY-RWLWH 181
QY 166 HTCYDAMATSSKLVI FDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMLTITDFTLVL 225
DB 182 FTNCDLLRRQI-----AWASLNSGFTRLGNLMTSVPV----- 214
QY 226 HRYRSPLVQIYEIOHKIETWREIYVLOGCFKPLVSI SPNDSLFEAVYTLIKRIHRLPV 285
DB 215 -----KVSNQ-----WIVGCC-----EGI--LLKWRCSQMPW 240
QY 286 LDPVSGNVLHILTHKRLKFLHIFGSLPRPSFLYRTIQDILGIGTFRDLAV---VLETPAP 342
DB 241 MQ-LEDDALYISQANFILAYQF-----RFDGASLNROPLGVSGAGHEDVCHFLVATSH 292
QY 343 ILTALDIFVDRRVSALPVNVECGQVGLYSRFDVIHLAAQOITYNLHLDMSVGEALRQRTLC 402
DB 293 IVSAGG--DGKIG-----LGKI-----HSTFAAKYWAHQEVNCDV-----C 327
QY 403 LEGVLSQPHESLGEVIDRIAREQVHRLVLVDETQHLGLVWSLSLILQALVLSPA 457
DB 328 KGGIISPGSRDRTAKWP-LASGOLGQCLTYIQTEDQIWSVAIRPLLSFFVTGTA 381

RESULT 10

US-11-073-457-44
; Sequence 44, Application US/11073457
; Publication No. US20050260556A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIFERATIVE DISORDERS
; FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/11/073,457
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 10/042,417
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-073-457-44

Query Match 3.8%; Score 92.5; DB 7; Length 529;

Best Local Similarity 18.7%; Pred. No. 1;
Matches 89; Conservative 66; Mismatches 175; Indels 145; Gaps 19;

QY 22 ERIRGKRKAKAL--RWTRQKSVEEGPPGQGEPRSRPTAESTGLEATFPKTTPLAQADP 79
DB 13 KRGARRKRGKGGREARAADGEGSGFGAEGAGARTPREAEGGSGVEEGARGIIKGD 72
QY 80 AGVGTPTPTG-----WDCLPSDCTASAAGSSTD 107
DB 73 GSVGAGKEAQGRKYKEEWRVARRREGARPRVQGGQVWAYIPGTGAAMAAAREEE 132
QY 108 VELATEFPATEWECELEGLLEERPALCLSPQAPFPKLGWDDDELKPG--AQIYMRPMQE 165
DB 133 EEAARESA-----CPAAG-----PALWRLPEVLLHMC SYLDMRALGRLAQVY-RWLWH 181
QY 166 HTCYDAMATSSKLVI FDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMLTITDFTLVL 225
DB 182 FTNCDLLRRQI-----AWASLNSGFTRLGNLMTSVPV----- 214
QY 226 HRYRSPLVQIYEIOHKIETWREIYVLOGCFKPLVSI SPNDSLFEAVYTLIKRIHRLPV 285

Db 2842 SDALTAVSSQLEGSPMDTSSILASCTLEAEVCDTSAAGSSBPRA---GSSTPGDAPPAVA 2898
Qy 72 TPLAQADPAGVGTPTGWDCLPSPDCT--ASAGSSTDDVELATEFPATEAWECELEGLLE 129
Db 2899 EVQGRSDGSGESAQP-----PEDSSPPASSESSSTRDSAVAIS-----GADSRGILE 2945
Qy 130 ERPALCLSPQAPFPKLGWDDDELKRGQAQIYMRFMQEHCTCYDAMATSSKLVIFDTMLTIKK 189
Db 2946 E-----PLESTSEEB--DPLAGISLPEGVDFSLAALPDDIRREVQLONQOLGIRP 2993
Qy 190 AFFALVANGVRAAPLWDSKKQSFVGMLTIT----DFILVLRHYRSPVLQVIYEIEQHKIE 245
Db 2994 P-----TFTASTNSAPAVGNPGVTEVSFEFLAAL-----PRAIQEEVLAQORAE 3040
Qy 246 TWREIYQGCCKPLVSPNDLSPEAVYTLKRIHRLPVLDPVSGNVHLIFG----- 297
Db 3041 QORRELAQNA-----SSDTPMDPV-TFIQTLPSDL--RRSVLEDMEDSVLAVMPDIAAEA 3093
Qy 298 -----THKELKFLHIFG-----SLLPRPSFLYRTIQDLGI-----GTF 331
Db 3094 QALRREQARQQLMHERLFGHSSTLSALSAILRSPAFSTRLSGNRGVOYTRLAVORGTF 3153
Qy 332 R 332
Db 3154 Q 3154

RESULT 14
US-11-076-187-4
; Sequence 4, Application US/11076187
; Publication No. US20050244857A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A
; APPLICANT: Pan, James G
; APPLICANT: Gentz, Reiner L
; APPLICANT: Dixit, Vishva M
; TITLE OF INVENTION: Death Domain Containing Receptor-4
; FILE REFERENCE: PF355F3
; CURRENT APPLICATION NUMBER: US/11/076,187
; CURRENT FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: 60/035,722
; PRIOR FILING DATE: 1997-01-28
; PRIOR APPLICATION NUMBER: 60/037,829
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: 09/013,895
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 60/132,922
; PRIOR FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: 09/565,918
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/406,922
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 60/413,861
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: 10/648,786
; PRIOR FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: 60/551,768
; PRIOR FILING DATE: 2004-03-11
; PRIOR APPLICATION NUMBER: 60/608,469
; PRIOR FILING DATE: 2004-09-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 909
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-076-187-4

Query Match 3.8%; Score 90.5; DB 7; Length 909;
Best Local Similarity 20.2%; Pred. No. 3.5;
Matches 80; Conservative 47; Mismatches 114; Indels 155; Gaps 22;

Qy 34 RWTRO-----KSVEEGEPGQGEGRSPRTAESTGLEATFPKTTPLAQADPAGVGTTP 86
Db 236 RWKSKLYIVCGKSTPEK--GELEGTTTFLAPNPSFPT-PCGTTTLGFSFVPSSTFT 292
Qy 87 TGWDCILPSDCTASAAGSSTDDVELATEFPATEAWECELEGLLEERPALC---LSQAPFP 143
Db 293 SSSTYTPGDCPNFAAPRR---EVAPPYQCAD-----PILATALASDPINP 335
Qy 144 KLGWDDDELKRGQAQIYMRFMQEHCTCYDAMATSSKLVIFDTMLTIKKAPFALVANGVRAAP 203
Db 336 LQWEDSAHKPOS-----LDT--DDPATLYAVVEN---VPP 366
Qy 204 L-WDSKKQSFVGMLTITDFILVLRHYRSPVLQVIYEIEQHKIETWREIYLGQCFKPLVSI 262
Db 367 LRW-----KEFVRLGLSD-----HEIDRLQLNGR-----CLR----- 395
Qy 263 SPNDSLPEAVYTLKRIHRLPVLDPVSGNVHLIFG----- 310
Db 396 -----EAQYSLMATWRRRTPRREA---TLELL--GRVLRMDMLGLCLEDEEALCGP 442
Qy 311 -SLLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVLSALPVNCEGOVVG 369
Db 443 AALPPAPESLL-----RMGLSTVPDLLPL-----VLELLVGIYP-----SGVIG 482
Qy 370 LYSRFDVTHLAAQOQTYNHLDMVSGEALRQRTLCLEG 405
Db 483 L-----VPHL-----GDREKRDVSVCQG 500

RESULT 15
US-11-012-762-70
; Sequence 70, Application US/11012762
; Publication No. US20050244815A1
; GENERAL INFORMATION:
; APPLICANT: Georgia State University Research Foundation, Inc.
; TITLE OF INVENTION: Compositions and Methods for Viral Resistance Genes
; FILE REFERENCE: GSUL.PCT
; CURRENT APPLICATION NUMBER: US/11/012,762
; CURRENT FILING DATE: 2004-12-15
; PRIOR APPLICATION NUMBER: PCT/US03/19300
; PRIOR FILING DATE: 2003-06-19
; PRIOR APPLICATION NUMBER: US 60/390,046
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 70
; LENGTH: 1137
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-11-012-762-70

Query Match 3.8%; Score 90.5; DB 7; Length 1137;
Best Local Similarity 21.2%; Pred. No. 4.9;
Matches 77; Conservative 30; Mismatches 135; Indels 121; Gaps 16;

Qy 13 PPAVTSSEIRIG-----KRAKALRWTRQKSVERGEPPGQGEGRSPRTAESTGLE 65
Db 21 PAPERFAAVRRALGSLDNVLRKNGAGGLQRPVIRIKG-----GAHARGTALRGTD 73
Qy 66 ATFPKTTPLAQADPAGVGTPTGWDCLPSPDCTASAGSSTDDVELATEFPFA-TEAWEC-- 122
Db 74 VEL-----VIFDCLRSFGDKTCHTTEILGAIQALLESWGNP 111
Qy 123 -----ELEGLEERPA-----LCLSPQAPFPKLGWDDDELKPGQAQIYMRFMQ 164
Db 112 GPGLTFEFGPKASGILQFRLASVDQENWIDVSLVPAFDALGQLHSEVKPTPNVYSSLL 171
Qy 165 EHTCYDAMATSSKLVIFDTMLTIKKAPFALVANGVRAAPLWDSKKQSFVGMLTITDFIIV 224
Db 172 SH-COAG-----EHSACFTELKRNFNIRP-----VKLKNLILL 204
Qy 225 LHRYRSPVLQI-----YEIEQHKIETWREIYLGQCFKPLVISPNDSLFEAVYTLI 276

Db 205 VKHYRQVQTVRATLPPSYALSLITIFAW-----QCCRKDAFSLAQG---LRTVLALI 257
Qy 277 KRIH-----RLFVLDPVSGNVILHILTHKRLKFLHIFGSLIPRPSFL--YRTIQDLG 327
Db 258 QRNKHLGIFWTENYGFEDPAVGFEF-----RRQLK-----RPRPVILDPADPTWDLG 304
Qy 328 IGT 330
Db 305 NGT 307

Search completed: January 24, 2006, 22:31:44
Job time : 21.515 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 25, 2006, 20:40:11 ; Search time 713.8 Seconds

(without alignments)
4332.332 Million cell updates/sec

Title: US-10-070-794A-30

Perfect score: 2403

Sequence: 1 MSFLEGENSSWSPAVTSS.....LSDILQALVLSPIGADALGA 464

Scoring table: BLOSUM62

Xgapop 10.0	Xgapext 0.5
Ygapop 10.0	Ygapext 0.5
Fgapop 6.0	Fgapext 7.0
Delop 6.0	Delext 7.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO.spool.p/US10070794/runat_24012006_164414_8779/app.query.fasta_1.1102
-DB=N_Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-LOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10070794 @CGN 1 1 1359 @runat_24012006_164414_8779 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DEEXT=7

Database :

N_Geneseq_21:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001as:*
5: Geneseq2001bs:*
6: Geneseq2002as:*
7: Geneseq2002bs:*
8: Geneseq2003as:*
9: Geneseq2003bs:*
10: Geneseq2003cs:*
11: Geneseq2003ds:*
12: Geneseq2004as:*
13: Geneseq2004bs:*
14: Geneseq2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2403	100.0	1470	10 ADF50309	Adf50309 Human prk
2	2403	100.0	2115	4 AAD03320	Aad03320 Human AMP
3	2403	100.0	2115	12 ADP43247	Adp43247 Human AMP
4	2398	99.8	1647	5 AAH43685	Aah43685 PRKAG3 CD

5	2398	99.8	1647	12	ADP87616	Adp87616 Human NOV
6	2398	99.8	2781	8	AAD49456	Aad49456 Human kin
7	2394	99.6	2109	4	AAD03296	Aad03296 Human AMP
8	2391	99.5	2314	6	ABQ61173	Abq61173 AMP kinas
9	2372	98.7	2290	12	ADP87618	Adp87618 Human NOV
10	2372	98.7	2290	14	AEB69127	Aeb69127 Human mod
11	2013	83.8	1873	6	AAD36457	Aad36457 Pig PRKAG
12	2011	83.7	1873	4	AAD03319	Aad03319 Pig AMPK
13	2011	83.7	1873	6	AAD36456	Aad36456 Pig wild-
14	2011	83.7	2022	4	AAD03321	Aad03321 Sus scrof
15	2010	83.6	1873	6	AAD36459	Aad36459 Pig PRKAG
16	2007	83.5	1873	6	AAD36460	Aad36460 Pig PRKAG
17	2005	83.4	1873	6	AAD36458	Aad36458 Pig PRKAG
18	2002	83.3	1867	4	AAD03295	Aad03295 Pig AMPK
19	2000	83.2	1518	10	ADF50311	Adf50311 Murine pr
20	1276	53.1	9100	10	ADF50313	Adf50313 Human prk
21	1276	53.1	26000	9	AAD58250	Aad58250 Human Prk
22	1101.5	45.8	1846	14	AD280781	Ad280781 Nucleotid
23	1094	45.5	2223	4	AAH14839	Aah14839 Human CDN
24	1094	45.5	2223	6	AAH48615	Aah48615 Human ins
25	1094	45.5	2223	12	ADP87610	Adp87610 Human NOV
26	1094	45.5	2223	12	ADP87693	Adp87693 Human AMP
27	1094	45.5	2223	12	ADP87612	Adp87612 Human NOV
28	1093	45.5	2062	12	ADP43248	Adp43248 Human AMP
29	1093	45.5	2062	12	ADP21388	Adp21388 Gene PRKA
30	1093	45.5	2062	14	AEB69126	Aeb69126 Human mod
31	1089	45.3	2223	12	ADP87614	Adp87614 Human NOV
32	1088	45.3	1435	2	AAH06882	Aah06882 Disease a
33	1082.5	45.0	1157	6	AAH48614	Aah48614 Human ins
34	1059.5	44.1	2024	13	ACN42072	Acn42072 Human dia
35	1028	42.8	1328	13	ADV40979	Adv40979 Rat card1
36	1022.5	42.6	1578	6	AAH48616	Aah48616 Human ins
37	1022.5	42.6	1578	6	ABK84324	Abk84324 Human CDN
38	1022.5	42.6	1578	10	ACA56515	Aca56515 Human sig
39	1022.5	42.6	1578	10	ADK61237	Adk61237 Ovarian c
40	1022.5	42.6	1578	12	ADI56311	Adi56311 Human pol
41	1022.5	42.6	1578	12	ADP43250	Adp43250 Human AMP
42	1022.5	42.6	1578	12	ADP87691	Adp87691 Human AMP
43	1022.5	42.6	1578	12	ADP87606	Adp87606 Human NOV
44	1022.5	42.6	1578	13	ACN39423	Acn39423 Tumour-as
45	1022.5	42.6	1578	14	AEB69125	Aeb69125 Human mod

ALIGNMENTS

RESULT 1	ADP50309	ADP50309 standard; cDNA; 1470 BP.
ID	ADP50309	
AC	XX	
XX	ADP50309;	
XX		
DT	12-FEB-2004	(first entry)
XX		
DE	Human prkag3 cDNA encoding the AMPK-gamma3 subunit.	
XX		
KW	human; gene; ss; transgenic;	
KW	AMP-activated protein kinase gamma 3 subunit; Prkag3; AMPK;	
KW	energy metabolism; obesity; dyslipidaemia; insulin resistance syndrome;	
KW	type 2 diabetes; antidiabetic; anorectic; antilipaemic.	
XX		
OS	Homo sapiens.	
XX		
FX	Key	Location/Qualifiers
FT	CDS	1..1470
FT		/*tag= a
FT		/product= "AMPK-gamma 3 protein"
XX		
PN	WO2003063586-A1.	
XX		
PD	07-AUG-2003.	
XX		
PF	31-JAN-2003; 2003WO-IB000912.	
XX		

PR 01-FEB-2002; 2002US-0353430P.
 XX (AREX-) AREXIS AB.
 XX PA
 XX PI Andersson L, Marklund S;
 XX DR WPI; 2003-663404/62.
 XX DR P-PSDB; ADF50310.
 XX PT New transgenic non-human animals expressing an AMP-activated protein
 PT kinase gamma 3 subunit, useful as models for improving treatment,
 PT prevention or diagnosis of diseases related to energy metabolism, e.g.
 PT obesity or type 2 diabetes.
 XX
 XX Claim 4; SEQ ID NO 1; 46pp; English.
 XX PS
 XX CC This invention relates to novel transgenic non-human animals expressing
 CC an AMP-activated protein kinase (AMPK)-gamma 3 subunit. Specifically, it
 CC relates to the transgene pRkgs3 gene that encodes the AMPK gamma3 subunit
 CC or a variant thereof, where the nucleic acid is operably linked to a
 CC regulatory element. AMPK is involved in the regulation of energy
 CC metabolism in eukaryotic cells, and is recognised as a major regulator of
 CC lipid biosynthetic pathways due to its role in the phosphorylation and
 CC inactivation of key enzymes such as acetyl-CoA carboxylase. The present
 CC invention describes transgenic animals expressing AMPK-gamma 3 to be used
 CC as models for energy metabolism diseases and also methods for the
 CC development of drugs for the treatment or prevention of obesity,
 CC dyslipidaemia, insulin resistance syndrome or type 2 diabetes.
 CC Accordingly, the compositions of this invention have various activities
 CC including antidiabetic, anorectic and antilipemic. This polynucleotide
 CC sequence is the human pRkgs3 cDNA of the invention.
 XX
 XX SQ Sequence 1470 BP; 310 A; 444 C; 420 G; 296 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 3,89e-174 Length: 1470
 Score: 2403.00 Matches: 464
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0
 US-10-070-794A-30 (1-464) x ADF50309 (1-1470)
 QY 1 MetSerPheLeuGluGlnGluAsnSerSerSerTrpProSerProAlaValThrSerSer 20
 Db 76 ATGAGCTTCTTAGACCAAGAAACAGCAGCTCATGGCCATCACCAGCTGTGACACGAGC 135
 QY 21 SerGluArgIleArgGlyIleArgArgAlaIleValAlaLeuArgTrpThrArgGlnLysSer 40
 Db 136 TCAGAAAGAATCCGTGGGAAACCGAGGGGCCAAAGCCCTTGAGATGGACAAAGGAGGATCG 195
 QY 41 ValGluGluGlyGluProProGlyGlnGlyGlyGlyProArgSerArgProThrAlaGlu 60
 Db 196 GTGAGAGGAAGGGGAGCCACAGCTCAGGGGAGAGTCCCGGTCCAGGCCAAGCTGCTGAG 255
 QY 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla 80
 Db 256 TCCACCGGGCTGGAGGCCACATTCGCCAAGACCAACACCTTGGCTCAAGCTGATCCTGCC 315
 QY 81 GlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSerAla 100
 Db 316 GGGGTGGGCACCTCCACCAACAGGGTGGGAGCTGCCCTCCCTCTGACTGATACAGCCCTCAGCT 375
 QY 101 AlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTrp 120
 Db 376 GCAGGCTCCAGCACAGATGATGTGGAGCTGGCCACGAGTTCACGACCAAGAGCCCTGG 435
 QY 121 GluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGlnAla 140
 Db 436 GAGTGTGAGCTAGAGGCCCTGTGGAAAGAGAGGCCCTGGCCCTGTGCTGCCCGGAGGCC 495
 QY 141 ProPheProLysLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnIleTyrMet 160

Db 496 CCAATTTCCCAAGCTGGGCTGGGATGACGAACTCCGGAAACCCGGGCGCCAGATCTACATG 555
 QY 161 ArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValIle 180
 Db 556 CGCTTCATGCAGGAGCACACCTGCTACGATGCGCATGGCAACTAGCTCCAAGCTAGTATC 615
 QY 181 PheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyValArg 200
 Db 616 TTCGACACCAATGCTGGAGATCAAGAGGCTCTTTGCTCTGGTGGCAACGGTGTGG 675
 QY 201 AlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAsp 220
 Db 676 GCAGCCCTCTATGGGACCAAGACGACAGCTTTGTGGGATGCTGACCATCCTGAC 735
 QY 221 PheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGlu 240
 Db 736 TTCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 795
 QY 241 GlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeuVal 260
 Db 796 CAACATTAAGATTGAGACTGGAGGAGATCTACCTGCAAGGCTGCTTCAAGCCTCTGGTC 855
 QY 261 SerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIle 280
 Db 856 TCCATCTCTCTAATGATAGCTGTTTGAAGCTGCTTACACCTCATCAAGAACCGGATC 915
 QY 281 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 300
 Db 916 CATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 975
 QY 301 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 320
 Db 976 GGCCTGCTCAAGTTCTGACATCTTTGGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTG 1035
 QY 321 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGluThr 340
 Db 1036 CGCACTATCCAGATTGGGATCGGCACATCCGACAGCTTGGCTGTGGTCTGGAGACA 1095
 QY 341 AlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProVal 360
 Db 1096 GCACCCATCTCTGACTGCACTGCAATCTTTGTGGACCGGCTGTGCTGCACTGCTGCTG 1155
 QY 361 ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeuAla 380
 Db 1156 GTCAACGAATGTGTGAGTGTGGGCTCTATTTCCTGCTTGTGATGATTCACTGGCT 1215
 QY 381 AlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr 400
 Db 1216 GCCCAGCAAACTACACCACTGACATGATGATGGGAGAGCCCTGAGGCAGAGGACA 1275
 QY 401 LeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAsp 420
 Db 1276 CTATGCTGGAGGAGTCTCTTCTGCGAGGCCCAACGAGAGCTTTGGGGAAAGTATGATC 1335
 QY 421 ArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeu 440
 Db 1336 AGGATGTCTGGAGAGCAGGTACACAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1395
 QY 441 GlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAsp 460
 Db 1396 GGGCTGGTCTCTCTCTGACATCTTTCAGGCACCTGCTGCTGCTGCTGCTGCTGCTGCT 1455
 QY 461 AlaLeuGlyAla 464
 Db 1456 GGCCTCGGGGCC 1467
 RESULT 2
 AAD03320
 ID AAD03320 standard; cDNA; 2115 BP.
 XX AC
 XX AAD03320;
 XX

DT	13-JUN-2001	(first entry)	US-10-070-794A-30 (1-464) x AAD03320 (1-2115)
XX	Human AMPK gamma subunit muscle-specific isoform, complete PRKAG3 cDNA.		
XX	Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK;		
XX	PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;		
XX	genetic testing; carbohydrate metabolism disorder; skeletal muscle;		
XX	cystathione beta synthase; CBS; cardiant; gene therapy; ss.		
XX	Homo sapiens.		
XX	Key	Location/Qualifiers	
XX	CDS	1..1395	
XX	FT	/*tag= a	
XX	FT	/product= "Human complete Prkag3 protein"	
XX	WO200120003-A2.		
XX	22-MAR-2001.		
XX	11-SEP-2000; 2000WO-EP009896.		
XX	10-SEP-1999; 99EP-00402236.		
XX	18-MAY-2000; 2000EP-00401388.		
XX	(INRG) INRA INST NAT RECH AGRONOMIQUE.		
XX	(ANDE/) ANDERSSON L.		
XX	(LOOF/) LOOFT C.		
XX	(KALM/) KALM E.		
XX	Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;		
XX	Iannuccelli N, Gellin J, Le Roy P, Chardon P;		
XX	WPI: 2001-244810/25.		
XX	P-PSDB; AAE00223.		
XX	New variants of the gamma subunit of vertebrate adenosine monophosphate-		
XX	activated kinase for diagnosis or treatment of disorders associated with		
XX	energy metabolism such as diabetes, obesity, and myopathy.		
XX	Claim 12; Page 55-68; 71pp; English.		
XX	The present sequence is a cDNA encoding human adenosine monophosphate		
XX	(AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform,		
XX	complete PRKAG3. Mutation in prkag3 results in an altered regulation of		
XX	carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is		
XX	useful as therapeutic for treating carbohydrate metabolism disorders such		
XX	as diabetes, obesity, and disorders associated with muscle metabolism		
XX	such as myopathy and cardiovascular diseases, to modulate AMPK activity,		
XX	and for restoring a normal AMPK function. PRKAG3 sequence and its		
XX	functionally altered mutants are useful for the diagnostic evaluation,		
XX	genetic testing and prognosis of a metabolic disorder, preferably a		
XX	polymorphic marker linked to a sequence encoding PRKAG3, are useful for		
XX	detecting a dysfunction of carbohydrate metabolism resulting from the		
XX	expression of a functionally altered allele of PRKAG3. Transgenic animal		
XX	and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting		
XX	of PRKAG3 or its mutant, are useful for screening compounds able to		
XX	modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for		
XX	detecting mutations in a Prkag3 gene, or in a sequence encoding the first		
XX	cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene		
XX	therapy		
XX	Sequence 2115 BP; 460 A; 622 C; 562 G; 471 T; 0 U; 0 Other;		
SQ	Alignment Scores:		
XX	Pred. No.:	6.2e-174	Length: 2115
XX	Score:	2403.00	Matches: 464
XX	Percent Similarity:	100.00%	Conservative: 0
XX	Best Local Similarity:	100.00%	Mismatches: 0
XX	Query Match:	100.00%	Indels: 0
XX	DB:	4	Gaps: 0

QY	1	MetSerPheLeuGluGlnGluAenSerSerSerTrpProSerProAlaValThrSerSer	20
DB	1	ATGAGCTTCTTAGAGCAAGAAACAGCAGCTCATGGCCATCACCGCTGTGACCAAGCAGC	60
QY	21	SerGluArgIleArgGlyLysArgAlaLysAlaLeuArgTrpThrArgGlnLysSer	40
DB	61	TCAGAAAGAAATCCGTGGAAACCGAGGCGCAAGACCTTGAGATGACACAGGCAAGTGG	120
QY	41	ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu	60
DB	121	GTGGAGGAAGGGAGGCCACAGGTACGGGGAAAGTCCCGGTCCAGGCCAACATGCTGAG	180
QY	61	SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla	80
DB	181	TCCACCGGGCTGGAGGCCACATTCCTCCACAGACACACCTTGGCTCAAGCTGATCCTGCC	240
QY	81	GlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSerAla	100
DB	241	GGGGTGGGCACCTCCACCAACAGGGTGGGACTGGCTCCCTCTGACTGTACAGCCTCAGCT	300
QY	101	AlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTrp	120
DB	301	GCAGGGCTCCAGACAGATGATGTGGAGCTGGCCACCGAGTTCCAGCCACAGAGGCTGG	360
QY	121	GluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGlnAla	140
DB	361	GAGTGTGAGCTAGAGGCTGCTGGAAAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG	420
QY	141	ProPheProLysLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnIleTyrMet	160
DB	421	CCATTTCCCAAGCTGGGCTGGGATGACGAATCGGAAACCCCGCGGCCAGATCTACATG	480
QY	161	ArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValIle	180
DB	481	CGCTTTCATGACGAGGACACACTCTGCTAGCATGCCATGCAACTAGCTCCAAGTATGATC	540
QY	181	PheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAenGlyValArg	200
DB	541	TTCGACACCATGCTGGAGATCAAGAGGCTTCTTTGCTCTGGTGGCCAAACGGTGTGGG	600
QY	201	AlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAsp	220
DB	601	GCAGCCCTCTATGGGACACCAAGACAGAGCTTTGTGGGATGCTGACCATCACTGAC	660
QY	221	PheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGlu	240
DB	661	TTCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	720
QY	241	GlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeuVal	260
DB	721	CAACATTAAGATTGAGACCTGGAGGAGATCTACTGCAAGGCTGCTTCAAGCCTCTGGTC	780
QY	261	SerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIle	280
DB	781	TCCATCTCTCTTAATGATGACCTGTTTGAAGCTGTCTACACCTCATCAAGACCGGATC	840
QY	281	HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys	300
DB	841	CATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	900
QY	301	ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr	320
DB	901	CGCTGCTCAAGTTCCTGACATCTTTGGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTG	960
QY	321	ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGluThr	340
DB	961	CGCACTATCCAAAGATTGGGCTGCGCACATTCGAGAGCTTGGCTGTGGTGGAGACA	1020
QY	341	AlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProVal	360
DB	1021	GCACCCATCTGACTGCACTGGACATCTTTGTGGACCGGCTGTGCTGCACTGCTGCTG	1080

Qy 361 ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeuAla 380
 Db 1081 GTCAACGAATGTGTCAGGTGTCGGGCTCTATTCCCGCTTTTGATGTGATTCACCTGGCT 1140
 Qy 381 AlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr 400
 Db 1141 GCCCAGCAAACTCAACACCTGACATGATGTGGAGAAAGCCCTGAGCAGAGACA 1200
 Qy 401 LeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAsp 420
 Db 1201 CTATGTCTGGAGGAGCTCTTCTGTCAGCCACAGAGCTTTGGGGAAGTATCGAC 1260
 Qy 421 ArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeu 440
 Db 1261 AGGATTGCTCGGAGCAGGTACACAGGCTGCTGTAGTGGACGAGACCCAGCATCTCTTG 1320
 Qy 441 GlyValValSerLeuSerAspIleGlnAlaLeuValLeuSerProAlaGlyIleAsp 460
 Db 1321 GCGGTGGTCTCCCTCTCCGACATCTTCAGGCACTGGTGTCTCAGCCCTGTGGCATCGAT 1380
 Qy 461 AlaLeuGlyAla 464
 Db 1381 GCCCTCGGGGCC 1392

RESULT 3

ID ADP43247
 ADP43247 standard; DNA; 2115 BP.
 XX
 AC ADP43247;
 XX
 DT 09-SEP-2004 (first entry)
 XX
 DE Human AMP-activated protein kinase gamma subunit coding sequence.
 XX
 KW cardiovascular; neuroprotective; dermatological; cytostatic;
 KW AMPK modulator; AMPK agonist; gene therapy;
 KW adenosine monophosphate-activated protein kinase; AMPK;
 KW cardiovascular disorder; neurological disorder; metabolic disorder;
 KW dermatological disorder; neoplastic disorder; age-associated disorder;
 KW geriatric disorder; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO2004050898-A2.
 XX
 PD 17-JUN-2004.
 XX
 PF 04-DEC-2003; 2003WO-US038628.
 XX
 PR 04-DEC-2002; 2002US-0430804P.
 PR 18-JUL-2003; 2003US-0488261P.
 XX
 PA (ELIX-) ELIXIR PHARM INC.
 XX
 PI Apfeld J, O'Connor G;
 XX
 DR WPI; 2004-450740/42.
 XX
 PT Evaluating a compound, useful for treating e.g., age-related disorder,
 PT comprises contacting a polypeptide at least 85% identical to e.g., alpha
 PT adenosine monophosphate-activated protein kinase (AMPK) subunit with a
 test compound.
 XX
 PS Disclosure; SEQ ID NO 50; 160pp; English.
 XX
 CC The invention relates to a method of evaluating a compound by contacting
 CC a polypeptide comprising a sequence at least 85% identical to alpha, beta
 CC or gamma adenosine monophosphate-activated protein kinase (AMPK) subunit
 CC or a functional domain in vitro with a test compound, evaluating
 CC interaction between compound and polypeptide, contacting a cell or
 CC organism that produces the polypeptide with test compound, and evaluating
 CC a rate of aging of the cell or organism. A method comprising providing a

CC modulator of the AMPK pathway to the subject is useful for treating or
 CC preventing a disease or disorder in a subject, preferably a
 CC cardiovascular disorder, a neoplastic disorder, a metabolic disorder, a
 CC dermatological disorder, a geriatric disorder, an age-associated
 CC disorder, or a geriatric disorder. A compound that alters the expression
 CC or activity of an AMPK pathway component is useful for altering lifespan
 CC regulation in a cell or organism. This sequence represents the DNA
 CC sequence encoding one of the AMPK protein subunits.

XX SQ Sequence 2115 BP; 460 A; 622 C; 562 G; 471 T; 0 U; 0 Other;

Alignment Scores: 6.2e-174 Length: 2115
 Pred. No.: 2403.00 Matches: 464
 Score: 2403.00 Conservatives: 0
 Percent Similarity: 100.00% Mismatches: 0
 Best Local Similarity: 100.00% Indels: 0
 Query Match: 100.00% Gaps: 0
 DB: 12

US-10-070-794A-30 (1-464) x ADP43247 (1-2115)

Qy 1 MetSerPheLeuGluGlnGluAsnSerSerTyrProSerProAlaValThrSerSer 20
 Db 1 ATGAGCTTCTAGAGCAAGAAACAGCAGCTCATGGCCATCACCAGCTGTGACAGCAGC 60
 Qy 21 SerGluArgIleArgGlyLysArgAlaAlaLeuArgTyrThrArgGlnLysSer 40
 Db 61 TCAGAAAGAATCCGTGGAAACCGAGGGCCAAAGCCCTTGAGATGGACCAAGCAGAAATCG 120
 Qy 41 ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60
 Db 121 GTGAGAGAGAGGGAGGCCACACAGGTCCAGGGGAAGGTCCCGGTCCAGGCCAATGCTGAG 180
 Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla 80
 Db 181 TCCACCGGGCTGGAGGCCACATTCCTCCCAAGACCACACCTTTGGTCTCAAGCTGATCCTGCC 240
 Qy 81 GlyValGlyThrProProThrGlyTyrAspCysLeuProSerAspCysThrAlaSerAla 100
 Db 241 GGGGTGGGCATCTCCACCAACAGGGTGGAGCTGCGCTCCCTCTGACTGTACAGCTCAGCT 300
 Qy 101 AlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTrp 120
 Db 301 GCAGGCTCCAGCACAGATGATGTGAGTGGCCACGGAGTTCCAGGCCACAGAGGCGCTGG 360
 Qy 121 GluCysGluLeuGlyLeuLeuGluGluGluGluGluGluGluGluGluGluGluGlu 140
 Db 361 GAGTGTGAGCTAGAAGGCCCTGCTGGAAGAGAGGCTGCGCTGTGCTGCTGCTGCTGCTGCTG 420
 Qy 141 ProPheProLysLeuGlyTyrAspAspGluLeuArgLysProGlyAlaGlnIleTyrMet 160
 Db 421 CCATTTCCCAAGCTGGGCTGGGATGACGACTGCGATGCCATGGCACTAGCTCCCAAGCTAGTCATC 480
 Qy 161 ArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValIle 180
 Db 481 CGCTTCATGACGAGGACACCTGCTACGATGCCATGGCACTAGCTCCCAAGCTAGTCATC 540
 Qy 181 PheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyValArg 200
 Db 541 TTCGACACCATGCTGGAGATCAAGAAGGCCCTTTCTTGTCTGTGGTGGCCCAACGGTGTGGCG 600
 Qy 201 AlaAlaProLeuTyrAspSerLysGlnSerPheValGlyMetLeuThrIleThrAsp 220
 Db 601 GCAGCCCTCTATGGGACAGCAAGCAGAGCTTTTGTGGGATGCTGACCATCATCTGAC 660
 Qy 221 PheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluLeu 240
 Db 661 TTCATCTGTGTGCTGATCGCTACTACAGGTCCCGCTGGTCCAGATCTATGAGATTGAA 720
 Qy 241 GlnHisLysIleGluThrThrArgGluIleTyrLeuGlnGlyCysPheLysProLeuVal 260
 Db 721 CAACATAAGATTGAGACCTGGAGGAGATCTACCTGCAAGGCTGCTTCAAGCCTCTGGTCT 780

Qy 261 SerIleSerProAsnAppSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIle 280
 Db 781 TCCATCTCTCCTAAATGATAGCTGTTTGAAGCTGTACACCTCATCAAGACCGGATC 840
 Qy 281 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisIys 300
 Db 841 CATCGCTGCTGCTGTCTTGAACCCGGTGTGAGCAACGTAATCCACATCTCTCACACAAA 900
 Qy 301 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 320
 Db 901 CGCTGTCTCAAGTTCCTGCACATCTTGGTTCCTGTGCTGCCCGCCCTCTTCTCTTAC 960
 Qy 321 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGluThr 340
 Db 961 CGCATATCAAGATTTGGGCATCGGCACATTCGGACATTCGGCTGTGGTGTGGAGACA 1020
 Qy 341 AlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProVal 360
 Db 1021 GCACCATCTCTGACTGCACTGGACATCTTGTGGACCGCGGTGTCTGCACTGCCCTGTG 1080
 Qy 361 ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeuAla 380
 Db 1081 GTCAACGAATGTGTGCTGAGTGTGGCTCTATTCCCGCTTTGATGTGATTCACCTGGCT 1140
 Qy 381 AlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr 400
 Db 1141 GCCCAGCAAACTTCAACACCTGACATGATGATGTGGAGAACGCTTGGAGCAGAGACA 1200
 Qy 401 LeuCysLeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyValIleAsp 420
 Db 1201 CTATGTCTGGAGGAGTCTTCTTCTGTCAGCCCTTGTGGAGAGCTTGGGGAGTGTATCGAC 1260
 Qy 421 ArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeu 440
 Db 1261 AGGATTCCTGGAGAGCTGATACAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 1320
 Qy 441 GlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAsp 460
 Db 1321 GGCCTGTCTCCCTCTCCGACATCTTTCAGGCACTGTGTGTGTGTGTGTGTGTGTGTGTG 1380
 Qy 461 AlaLeuGlyAla 464
 Db 1381 GCCCTCGGGGCC 1392

AAH43685 standard; cDNA; 1647 BP.
 AAH43685;
 21-JAN-2002 (first entry)
 PRKAG3 cDNA.

Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant;
 metabolic disease; diabetes; obesity; substitution; ss.
 Homo sapiens.

Key Location/Qualifiers
 CDS 20..1489
 /tag= a.
 /product= "PRKAG3"
 variation 230
 /tag= b
 /label= C230G
 /note= "Causes P71A"
 variation 559
 /tag= c
 /label= T559C
 /note= "Silent variation"
 variation 1037
 /tag= d

FT /label= C1037T
 FT /note= "Causes R340W"

PN W0200177305-A2.

XX 18-OCT-2001.

PD 06-APR-2001; 2001WO-S0000765.

PF 07-APR-2000; 2000US-0195665P.

PR (AREX-) AREXIS AB.

XX Andersson L, Luthman H, Marklund S;

XX MPI; 2001-657170/75.

XX P-PSDB; Q0847679.

XX New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the variant.

XX Disclosure; Fig 5; 25pp; English.

XX This sequence represents the full length cDNA encoding the human AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution P71A; in exon 4 variation may be a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution R340W. There may also be nucleotide variation in intron 6. The numbering of these variations is based on the full length cDNA as given, rather than on position 1 of the open reading frame

SQ Sequence 1647 BP; 346 A; 502 C; 462 G; 337 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.09e-173 Length: 1647
 Score: 2398.00 Matches: 463
 Percent Similarity: 99.78% Conservative: 0
 Best Local Similarity: 99.78% Mismatches: 1
 Query Match: 99.79% Indels: 0
 DB: 5 Gaps: 0

US-10-070-794A-30 (1-464) x AAH43685 (1-1647)

Qy 1 MetSerPheLeuGluGlnGluAsnSerSerSerTrpProSerProAlaValThrSerSer 20

Db 95 ATGAGCTTCTTAGAGCAAGAAACAGAGCTCATGGCCATCAGCGCTGTGACGAGC 154

Qy 21 SerGluArgIleArgGlyLysArgArgAlaLysAlaLeuArgTrpThrArgGlnLysSer 40

Db 155 TCAGAAAGAAATCCGTGGAAACCGAGGGCCAAAGCCTTGAGATGGACAGCAGAGTCG 214

Qy 41 ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60

Db 215 GTGGAGGAAGGGGAGGCCACAGGTCAGGGGGAAGGTCCCGGTCCAGGCCAGCTGTGAG 274

Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla 80

Db 275 TCACCGGGCTGGAGGCCACATTCCTCCCAAGACCACACCCCTTGGCTCAAGCTGATCTGCC 334

Qy 81 GlyValGlyThrProProThrGlyTyrAspCysLeuProSerAspCysThrAlaSerAla 100

Db 335 GGGGTGGGCACTCCACCAAGAGGGTGGGACTGCTCCCTCTCTGCTGTACAGCTCAGCT 394

Qy 101 AlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTrp 120

Db 395 GCAGGCTCCAGCACAGATGATGTGGAGCTGGCCACGAGTTCCAGCACAGAGGCGCTGG 454

121 Qy GluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGlnAla 140
122 |||||
455 Db GAGTGTGAGCTAGAAAGCCCTGCTGAAGAGAGGCGCTGCCCTGTGCTGTCCCGCAGGCC 514
141 Qy ProPheProIysLeuGlyTyrAspAspGluLeuArgLysProGlyAlaGlnIleTyrMet 160
142 |||||
515 Db CCATTTCCTCCAGCTGGGCTGGGATGACGAATCGCGAACCCTGGCGCCAGATCTCATG 574
161 Qy ArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValIle 180
162 |||||
575 Db CGCTTCATGACGAGGACACCTGCTACATGATGCCATGCACTAGCTTCAAGCTAGTATC 634
181 Qy PheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyValArg 200
182 |||||
635 Db TTCGACACCATGCTGGAGATCAAGAAGGCCCTCTCTTGTCTGTGGTGGCAACGGGTGCGG 694
201 Qy AlaAlaProLeuTyrAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAsp 220
202 |||||
695 Db GCAGCCCTCTCTATGGGACAGCAAGACGAGCTTTGTGGGATGCTGACCATCACTGAC 754
221 Qy PheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGlu 240
222 |||||
755 Db TTCTATCTGTGTGCTGCTACTACAGGTCCCTCCCTGGTCCAGATCTATGAGATTGAA 814
241 Qy GlnHisLysIleGluThrTyrPheGluIleTyrLeuGlnGlyCysPheLysProLeuVal 260
242 |||||
815 Db CAACATAAGATTGAGACCTGGAGGAGATCTACCTGCAAGGCTGCTTCAAGCCCTCTGGTC 874
261 Qy SerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIle 280
262 |||||
875 Db TCCATCTCTCTAATGATGAGCTGTGTGAAGCTGTCTACACCCCTCATCAAGACCGGATC 934
281 Qy HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 300
282 |||||
935 Db CATGCCCTGCTGTCTTGACCCGGTGCAGGCAACGTACTCCACATCTCCACACAAA 994
301 Qy ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 320
302 |||||
995 Db CGCCTGCTCAAGTTCCTGCACATCTTTGGTTCCTGTGCTGCCCGGCCCTCTCTCTAC 1054
321 Qy ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGluThr 340
322 |||||
1055 Db CGCACTATCCAAAGATTTGGGCAATCGGCATCTCGAGACTTGGCTGTGGTCTGAGACA 1114
341 Qy AlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuProVal 360
342 |||||
1115 Db GCACCATCTGACTGCACTGGACATCTTTGTGGACCGCGTGTCTGCACTGCCCTGTG 1174
361 Qy ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeuAla 380
362 |||||
1175 Db GTCMAAGAAATGGTGCAGTCTGGGCGCTCTATTCCCGCTTTGATGTGATTCACCTGGCT 1234
381 Qy AlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr 400
382 |||||
1235 Db GCGCCAGCAAACTCAACACCTGACATGATGTGGGAGAAGCCCTGAGGACAGGACA 1294
401 Qy LeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAsp 420
402 |||||
1295 Db CTATGCTGGAGGAGTCTTCTCTCCAGCCGCCACGAGAGCTTGGGGAGTGTATCGAC 1354
421 Qy ArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeu 440
422 |||||
1355 Db AGGATTTGCTCGGAGCAGGTACACAGGCTGGTGTAGTGGAGCAGACCCAGCATCTCTTG 1414
441 Qy GlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAsp 460
442 |||||
1415 Db GCGGTGGTCTCCCTCTCCGACATCTTTCAGGCACCTGCTGAGCCCTGCTGGCATCGAT 1474
461 Qy AlaLeuGlyVala 464
1475 Db GCCTCTGGGGCC 1486

RESULT 5

ADP87616
ID ADP87616 standard; DNA; 1647 BP.
XX
AC ADP87616;
XX
DT 23-SEP-2004 (first entry)
XX
DE Human NOVX polypeptide encoding DNA, NOV10a.
XX
KW anorectic; antidiabetic; gene therapy; vaccine; obesity; diabetes;
KW insulin resistance; hybridization probe; chromosome mapping;
KW tissue typing; preventive medicine; pharmacogenomics; NOVX; human; gene;
KW ds.
XX
OS Homo sapiens.
XX
PN WO2004056961-A2.
XX
PD 08-JUL-2004.
XX
PF 27-OCT-2003; 2003WO-US034114.
XX
PR 25-OCT-2002; 2002US-0421239P.
PR 28-OCT-2002; 2002US-0421700P.
PR 31-OCT-2002; 2002US-0422776P.
PR 13-NOV-2002; 2002US-0426197P.
PR 20-DEC-2002; 2002US-0435498P.
PR 20-DEC-2002; 2002US-0435510P.
PR 20-DEC-2002; 2002US-0435568P.
PR 21-MAR-2003; 2003US-0456812P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Berghs C, Catterton E, Ellerman K, Ort T, Rieger D, Chaudhuri A;
XX WPI; 2004-500293/47.
XX P-PSDB; ADP87617.
XX
PT New NOVX nucleic acid molecules and polypeptides useful for preventing or
PT treating NOVX-associated disorders, e.g. diabetes, insulin resistance or
XX obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX
PS Claim 1; SEQ ID NO 73; 570pp; English.
XX
CC The invention relates to a novel isolated nucleic acid molecule
CC comprising any of the nucleotide sequences (e.g. 3634, 2127 or 2120 base
CC pairs) fully defined in the specification; or encodes any of the amino
CC acid sequences (e.g. 698, 702 or 709 amino acids) fully defined in the
CC specification. The invention further comprises: an isolated polypeptide
CC comprising any of the amino acid sequences cited above; a method for
CC identifying compounds that modulate target polypeptide activity; an
CC antibody that immunospecifically binds to the target polypeptide, where
CC the target polypeptide comprises any of the above-mentioned amino acid
CC sequences, an amino acid sequence that is at least 95% identical to the
CC above amino acid sequences, an amino acid sequence of at least one domain
CC of the above-mentioned amino acid sequences, or an amino acid sequence
CC that is at least 95% identical to the domain of the above amino acid
CC sequences; a method for identifying a potential therapeutic agent for use
CC in treatment of a pathology, where the pathology is related to aberrant
CC expression or aberrant physiological interactions of a target polypeptide
CC; and a method of screening for a modulator of activity of or of latency
CC or predisposition to a pathology associated with a target polypeptide.
CC The modulating compounds have anorectic and antidiabetic activities. The
CC nucleic acid sequences of the invention may be used in gene therapy to
CC treat disorders. The proteins of the invention are useful for identifying compounds
CC vaccine. The composition and methods are useful for identifying or treating
CC that modulate protein activity or for diagnosing, preventing or treating
CC diverse pathological conditions, such as obesity, diabetes or insulin
CC resistance. The nucleic acids are also used as hybridization probes, in
CC chromosome mapping, tissue typing, preventive medicine, and
CC pharmacogenomics. This polynucleotide sequence represents the DNA
CC encoding a NOVX polypeptide of the invention.

XX	SQ	Sequence	1647 BP; 346 A; 502 C; 462 G; 337 T; 0 U; 0 Other;
XX	Alignment Scores:		
	Pred. No.:	1.09e-173	Length: 1647
	Score:	2398.00	Matches: 463
	Percent Similarity:	99.78%	Conservative: 0
	Best Local Similarity:	99.78%	Mismatches: 1
	Query Match:	99.79%	Indels: 0
	DB:	12	Gaps: 0
XX	US-10-070-794A-30 (1-464) x ADP87616 (1-1647)		
Qy	1	MetSerPheLeuGluGlnGluAsnSerSerTrpProSerProAlaValThrSerSer	20
Db	95	ATGAGCTTCTTAGAGCAAGAAACAGCAGCTCATGGCCATCACCAGCTGTGACCGAGC	154
Qy	21	SerGluArgLeuArgGlyLysArgArgAlaLysAlaLeuArgTrpThrArgGlnLysSer	40
Db	155	TCAGAAAGAAATCCGTGGGAACGGAGGGCCAAAGCCCTTGAGATGGACAGGCGAAGTGG	214
Qy	41	ValGluGluGluGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu	60
Db	215	GTGGAGAGAGGGAGCCACAGGTCAGGGGGAAGTCCCGGTCCAGGCCAGCTGCTGAG	274
Qy	61	SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla	80
Db	275	TCCACCGGGCTGGAGGCCACATTCCTCCCAAGACCACACCCCTTGGCTCAAGCTGATCCTGCC	334
Qy	81	GlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSerAla	100
Db	335	GGGGTGGGCACTCCACCAAGAGGGTGGGACTGCCCTCCCTCTGACTGTACAGCCCTCAGCT	394
Qy	101	AlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTrp	120
Db	395	GCAGGCTCCAGCACAGATGATGTGGAGCTGGCCACGAGGATTCACGACCACAGAGGCCCTGG	454
Qy	121	GluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGlnAla	140
Db	455	GAGTGTGAGCTAGAAAGCCCTGTGGAAGAGAGGCTGCCCTGTGCTGCTCCCGCAGGCC	514
Qy	141	ProPheProLysLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnIleTyMet	160
Db	515	CCATTTCCTCCAGCTGGGCTGGGATGACGAACTGCGGAACCCCGCGCCAGATCTACATG	574
Qy	161	ArgPheMetGlnGluHisThrCysTrpAspAlaMetAlaThrSerSerLysLeuValIle	180
Db	575	CGCTTCATGACGAGGACACCTGCTACATGCCATGCCAATAGCTCCAGCTAGTATC	634
Qy	181	PheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyValArg	200
Db	635	TTGACACCATGCTGGAGATCAAGAAGCCCTTCTTCTGCTGGTGGCCACGGTGTGGG	694
Qy	201	AlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAsp	220
Db	695	GCAGCCCTCTATGGGACAGCAAGACAGAGCTTTTGTGGGATGCTGACCATCACTGAC	754
Qy	221	PheIleLeuValLeuHisArgTrpTrpArgSerProLeuValGlnIleTyGluIleGlu	240
Db	755	TTATCTCTGGTGCATCGCTACTACAGGTCCCTCTGCTGGTCCAGATCTATGAGATTGAA	814
Qy	241	GlnHisLysIleGluThrTrpArgGluIleTyLysLeuGlnGlyCysPheLysProLeuVal	260
Db	815	CAACATAAGATTGAGACCTGGAGGAGATCTACTCTGCAAGGCTGCTTCAAGCTCTGTGC	874
Qy	261	SerIleSerProAsnAspSerLeuPheGluAlaValTrpThrLeuIleLysAsnArgIle	280
Db	875	TCCATCTCTCTAATGATAGCTCTTTTGAAGCTGTCTACACCTCTCATCAAGAACCGGATC	934
Qy	281	HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys	300
Db	935	CATCGCCTGCTGTTCTTTCAGCCCGGTGTGAGGAACGTACTCCACATCTCTCACACAA	994

RESULT 6

AD49456	AD49456	standard; cDNA; 2781 BP.
XX	AD49456	
AC	AD49456	
XX	AD49456	
DT	24-MAR-2003	(first entry)
XX	Human kinase and phosphatase (KPP) -15 cDNA.	
DE	Human; kinase and phosphatase; KPP; cardiovascular; hypertension;	
XX	myocardial infarction; angina pectoris; Alzheimer's disease; epilepsy;	
KW	acquired immune deficiency syndrome; AIDS; Grave's disease; diabetes;	
KW	neurological; Parkinson's disease; cirrhosis; psoriasis; gene therapy;	
KW	hypercholesterolemia; anticonvulsant; hepatotropic; lipid myopathy;	
KW	cell proliferative disorder; cancer; cardiac; neuroprotective; enzyme;	
KW	neotrophic; ophthalmological; anorectic; cyrostatic; cataract; obesity;	
XX	gene; ss.	
OS	Homo sapiens.	
XX	Key	Location/Qualifiers
PH	CDS	21..1500
FT		/tag= a
FT		/product= "Human KPP protein"
XX	WO200283709-A2.	
PN	24-OCT-2002.	
XX	05-APR-2002; 2002WO-US010818.	
XX	06-APR-2001; 2001US-0282119P.	
PR	13-APR-2001; 2001US-0283588P.	
PR	13-APR-2001; 2001US-0283759P.	
PR	20-APR-2001; 2001US-0285589P.	
PR	27-APR-2001; 2001US-0287036P.	

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PR 27-APR-2001; 2001US-0287037P.
PR 04-MAY-2001; 2001US-0288608P.
PR 04-MAY-2001; 2001US-0288712P.
PR 09-MAY-2001; 2001US-0289909P.
PR 17-MAY-2001; 2001US-0292246P.
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Recipon SA, Burrill JD, Marcus GA, Zingler KA, Tang YT;
XX Thornton M, Borowsky ML, Baughn MR, Lee SY, Bandman O;
XX Hafalia AJA, Yao MG, Ramkumar J, Walla NK, Lu DAM, Arvizu CS;
XX Ison CH, Ding L, Lu V, Gururajan R, Walsh RT, Gandhi AR;
XX Swarnakar A, Forsythe IJ, Yue H, Au-Young JK, Elliott VS, Lee S;
XX
XX WPI; 2003-092995/08.
DR P-PSDB; RAE32034.
DR
XX New human kinases and phosphatases (KPP), useful for diagnosing, treating
XX and preventing diseases or conditions associated with the aberrant KPP
XX expression, e.g. hypertension, cancer, AIDS, diabetes, cataract,
XX psoriasis, obesity.
XX
XX Claim 5; Page 195-196; 195pp; English.
XX
XX The invention relates to human kinases and phosphatases (KPP), and their
XX corresponding nucleic acids. The polypeptides and polynucleotides of the
XX invention are useful in diagnosing, treating and preventing diseases or
XX conditions associated with the decreased expression or overexpression of
XX KPP, such as cardiovascular (e.g. hypertension, myocardial infarction,
XX angina pectoris), immune (e.g. acquired immune deficiency syndrome
XX (AIDS), Grave's disease, diabetes), neurological (e.g. Parkinson's
XX disease, Alzheimer's disease, epilepsy), disorders affecting growth and
XX development (e.g. cirrhosis, psoriasis, cataract), lipid (e.g.
XX hypercholesterolaemia, obesity, lipid myopathies), cell proliferative
XX disorders, or cancer. They are also useful in assessing the effects of
XX exogenous compounds on the expression of nucleic acid and amino acid
XX sequences of KPP. The KPP or its fragments are useful in screening
XX compounds for effectiveness as agonist or antagonist of the polypeptides,
XX or in altering the expression of the target polynucleotide and compounds
XX that specifically bind to or modulate the activity of the polypeptide.
XX The microarray is useful in monitoring and measuring protein-protein
XX interactions, drug-target interactions, and gene expression profiles. KPP
XX DNA is used in gene therapy. The present sequence is human KPP CDNA
XX
XX Sequence 2781 BP; 628 A; 795 C; 714 G; 644 T; 0 U; 0 Other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 2,13e-173 Length: 2781
XX Score: 2398.00 Matches: 463
XX Percent Similarity: 99.78% Conservative: 0
XX Best Local Similarity: 99.78% Mismatches: 1
XX Query Match: 99.79% Indels: 0
XX DB: 8 Gaps: 0
XX
XX US-10-070-794A-30 (1-464) x AAD49456 (1-2781)
XX
XX QY 1 MetSerPheLeuGluGlnGlnAlaSerSerSerSerTyrProSerProAlaValThrSerSer 20
XX
XX Db 96 ATGAGCTTCTTAGAGCAAGAAACAGCAGCTCATGGCCATCACCAGCTGTGACCAGCAGC 155
XX
XX QY 21 SerGluArgIleArgGlyLysArgAlaLysAlaLeuArgTyrThrArgGlnLysSer 40
XX
XX Db 156 TCAGAAAGAATCCGTGGGAAACCGAGGGCCAAAGCTTGTAGATGGACAAAGGCAGAGTCG 215
XX
XX QY 41 ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60
XX
XX Db 216 GTGGAGGAGAGGGAGCCACCAGGTGAGGGGAGAGTCCCGGTCCAGCCGAGCTGCTGAG 275
XX
XX QY 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla 80
XX
XX Db 276 TCCACCGGGCTGGAGCCACATTCACCAAGACACACCTTGGCTCAAGCTCATCTGCC 335
XX
XX QY 81 GlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSerAla 100

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Db 336 GGGGTGGGCACTCCACCAACAGAGGTGGACTGCCTCCCTCTGACTGTACAGCCTCAGCT 395
QY 101 AlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTyrP 120
Db 396 GCAGGCTCCAGCACAGATGATGTGGAGCTGGCCACGGAGTTCACGAGCCACAGAGGCTCG 455
QY 121 GluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysValLeuSerProGlnAla 140
Db 456 GAGTGTGAGCTAGAAGCCCTGCTGGAAAGAGAGGCTGCCCTGTGCTGCTGTCTCCCGCAGGCC 515
QY 141 ProPheProLysLeuGlyTyrAspAspGluLeuArgLysProGlyAlaGlnIleTyrMet 160
Db 516 CCATTTCCAAGCTGGGCTGGGATGACAACTCGGGAACCCCGGCGCCAGATCTCATG 575
QY 161 ArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValle 180
Db 576 CGCTTCATGAGGAGCACACTGCTAGATGCCATGGCAACTAGCTCCAAGTAGTATCATC 635
QY 181 PheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyValArg 200
Db 636 TTCGACACCATGCTGGAGATCAAGAGGCTTCTTGTCTCTGGTGGCCAAACGGTGTGGG 695
QY 201 AlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAsp 220
Db 696 GCAGCCCTCTATGGGACAGCAGACAGAGCTTTGTGGGATGCTGACCATCACTGAC 755
QY 221 PheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGlu 240
Db 756 TTCATCTGCTGCTGCATCGTACTACAGGTGCCCTCTGGTCCAGATCTATGAGATTGAA 815
QY 241 GlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeuVal 260
Db 816 CAACATAGATGTAGACTGGAGGAGATCTACTCTGCAAGGCTCTTCAAGCCCTCTGCTC 875
QY 261 SerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIle 280
Db 876 TCCATCTCTCTATGATGCTGCTTTGAAGCTGTCTACACCTCATCAAGAACCGGATC 935
QY 281 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 300
Db 936 CATCGCTGCTGCTGCTTGTACCGGTGTTCAGGCAACGTACTCCACATCTCTCACACAAA 995
QY 301 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 320
Db 996 GCGCTGCTCAAGTTCCTGACATCTTTGGTTCCCTGTGCTGCCCGGCCCTCTCTCTAC 1055
QY 321 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGluThr 340
Db 1056 CGCACTATCCAAGATTTGGGCATCGGCACATTCGAGACTTTGGTGTGCTGTGGAGACA 1115
QY 341 AlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuProVal 360
Db 1116 GCACCCATCTCTGACTGACATCTTTGTGACCGCGGTGTGTGTGCACTGCTGTG 1175
QY 361 ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeuAla 380
Db 1176 GTCAACGAATGTGGTCAGTGTGGGCTCTATTTCCTGCTTTGATGTGATTCACCTGGCT 1235
QY 381 AlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr 400
Db 1236 GCCCAGCAAACTACACCACTCGACATGATGTGGGAGAAGCCCTCAGGCAGAGGACA 1295
QY 401 LeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValleAsp 420
Db 1296 CTATGTCTGGAGGGAGTCTCTTTCTTCGCGAGCCCAACGAGAGCTTGGGGGAAGTGTAC 1355
QY 421 ArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeu 440
Db 1356 AGGATGTCTGGGAGCAGGTACACAGGCTGGTGTGTGTGGACGAGCCAGCATCTCTTG 1415
QY 441 GlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyLeAsp 460

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Db 1416 GCGTGGTCTCCCTTCGACATCTTCAGGCACTGGTGTCTCAGCCCTGCTGGCATCGAT 1475

Qy 461 AlaleuGlyAla 464
|||||

Db 1476 GCCCTCGGGGCC 1487

RESULT 7

AAD03296

ID AAD03296 standard; DNA; 2109 BP.

XX AC AAD03296;

XX DT 13-JUN-2001 (first entry)

XX DE Human AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA.

XX KW Human; gamma: subunit; adenosine monophosphate-activated kinase; AMPK;

XX KW PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;

XX KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;

XX KW cystathione beta synthase; CBS; cardiant; gene therapy; ss.

XX OS Homo sapiens.

XX FH Key

XX FT 5'UTR

XX FT 1..471

XX FT /*tag= a

XX FT CDS

XX FT 472..1389

XX FT /*tag= b

XX FT /*product= "Human Prkag3 protein"

XX FT 3'UTR

XX FT 1390..2109

XX FT /*tag= c

XX WO200120003-A2.

XX PD 22-MAR-2001.

XX PF 11-SEP-2000; 2000WO-EP009896.

XX PR 10-SEP-1999; 99EP-00402236.

XX PR 18-MAY-2000; 2000EP-00401388.

XX PA (INRG) INRA INST NAT RECH AGRONOMIQUE.

XX PA (ANDE/) ANDERSSON L.

XX PA (LOOF/) LOOFT C.

XX PA (KALM/) KALM E.

XX PI Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;

XX PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;

XX DR WPI; 2001-244810/25.

XX PS P-PSDB; AAE00221.

XX CC New variants of the gamma subunit of vertebrate adenosine monophosphate-

XX CC activated kinase for diagnosis or treatment of disorders associated with

XX CC energy metabolism such as diabetes, obesity, and myopathy.

XX CC Claim 12; Fig 2; 71pp; English.

XX CC The present sequence is a cDNA encoding human adenosine monophosphate

XX CC (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform,

XX CC PRKAG3. Mutation in Prkag3 results in an altered regulation of

XX CC carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is

XX CC useful as therapeutic for treating carbohydrate metabolism disorders such

XX CC as diabetes, obesity, and disorders associated with muscle metabolism

XX CC such as myopathy and cardiovascular diseases, to modulate AMPK activity,

XX CC and for restoring a normal AMPK function. PRKAG3 sequence and its

XX CC functionally altered mutants are useful for the diagnostic evaluation,

XX CC genetic testing and prognosis of a metabolic disorder, preferably a

XX CC carbohydrate metabolism disorder. Primers that can detect a genetic

XX CC polymorphic marker linked to a sequence encoding PRKAG3 are useful for

XX CC detecting a dysfunction of carbohydrate metabolism resulting from the

XX CC expression of a functionally altered allele of PRKAG3. Transgenic animal

XX CC and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting

CC of PRKAG3 or its mutant, are useful for screening compounds able to

CC modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for

CC detecting mutations in a Prkag3 gene, or in a sequence encoding the first

CC cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene

CC therapy

XX

SO Sequence 2109 BP; 458 A; 621 C; 560 G; 470 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	3.02e-173	Length:	2109
Score:	2394.00	Matches:	462
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	99.63%	Indels:	0
DB:	4	Gaps:	0

US-10-070-794a-30 (1-464) x AAD03296 (1-2109)

Qy 3 PheLeuGluGlnGluAenSerSerSerTTPProSerProAlaValThrSerSerSerGlu 22
|||||

Db 1 TTCTTAGCAAGAAACAGCAGCTCATGGCCATCACAGCTGTGACCCAGCTCAGAA 60
|||||

Qy 23 ArgIleArgGlyLysArgArgAlaLysAlaLeuArgTTPThrArgGlnLysSerValGlu 42
|||||

Db 61 AGAATCCGTGGAAACAGGAGGGCCAAAGCCCTTGAGATGGACAGGCAAGTCCGTGGAG 120
|||||

Qy 43 GluGlyGluProGlyGlnGlyGluGlyProArgSerArgProThrAlaGluSerThr 62
|||||

Db 121 GAAGGGAGGCCACAGCTCAGGGGAGGTCCCGGTCCAGGCCACTGCTGATGCCACC 180
|||||

Qy 63 GlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAlaGlyVal 82
|||||

Db 181 GGGCTGGAGGCCACATTTCCCAAGACCACACCCCTTGCTCAAGCTGATCTCTGCCGGGTG 240
|||||

Qy 83 GlyThrProThrGlyTTPAspCysLeuProSerSerSerCysThrAlaSerAlaAlaGly 102
|||||

Db 241 GGCACCTCCACCAACAGGGTGGGACTGCTCCCTCTGCTGTGCTGCCCGAGGCCCATTT 300
|||||

Qy 103 SerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTTPGluCys 122
|||||

Db 301 TCCAGCACAGATGATGTGGAGCTGGCCAGGAGTTCCAGCCACAGAGGCTCGGAGTGT 360
|||||

Qy 123 GluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGlnAlaProPhe 142
|||||

Db 361 GAGCTAGAAGCCCTGCTGGAAGAGAGGCGCTGCCCTGTGCTGCCCGAGGCCCATTT 420
|||||

Qy 143 ProLysLeuGlyTTPAspAspGluLeuArgLysProGlyAlaGlnIleTyrMetArgPhe 162
|||||

Db 421 CCCAAGCTGGGCTGGGATGACGAACCTGCGAAGACCCCGGCCAGATCTACATCGCTTC 480
|||||

Qy 163 MetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValIlePheAsp 182
|||||

Db 481 ATGACGAGGACACACCTGCTACGATGCCATGGCAACTAGCTCCAAAGCTAGTCACTTCGAC 540
|||||

Qy 183 ThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyValArgAlaAla 202
|||||

Db 541 ACCATGCTGGAGATCAAGAGGCTCTTTGCTGTGGTGCCCAACGGTGTGCGGCGAGCC 600
|||||

Qy 203 ProLeuTTPAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAspPheIle 222
|||||

Db 601 CCTCTATGGGACAGCAAGAGAGAGAGGCTTTTGGGGATGCTGACCATCATCTTCATC 660
|||||

Qy 223 LeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGluGlnHis 242
|||||

Db 661 CTGGTCTGCTATCGCTACTACAGGTCCCTCCCTGCTCAGATCTATGATGATGAACACAT 720
|||||

Qy 243 LysIleGluThrTTPArgGluIleTyrLeuGlnGlyCysPheLysProLeuValSerIle 262
|||||

Db 721 AAGATTGAGACCTGGAGGGAGATCTACCTGCAAGGCTGCTTCAAGCTCTGGTCTCCATC 780
|||||

Qy 263 SerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIleHisArg 282
|||||

Db 781 TCTCCTAATGATAGCCCTGTTTGAAGCTGTCTACACCCCTCATCAAGAACCGGATCCATCGC 840
|||||

QY 283 LeuProValLeuAaspProValSerGlyAsnValLeuHisIleLeuThrHisLysArgLeu 302
 DB 841 CTGCCTGTTCTTACCGGGTGTACAGCAAGTACTCCACATCTCTCCACACAAACGGCTG 900
 QY 303 LeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyrArgThr 322
 DB 901 CTCAGGTTCCTGACATCTTTGGTTCCCTGCTGCGCGCCCTCTTCTCTACCGCACT 960
 QY 323 IleGlnAaspLeuGlyIleGlyThrPheArgAaspLeuAlaValValLeuGluThrAlaPro 342
 DB 961 ATCCAGATTTGGCATCGGCACATTCGAGACTTGGCTGTGGTCTGGAGACGACACC 1020
 QY 343 IleLeuThrAlaLeuAaspIlePheValAaspArgValSerAlaLeuProValValasn 362
 DB 1021 ATCTGACTGCACTGGACATCTTTGTGACCGCGCTGTGTCTGCACCTGCCTGTGGTCAAC 1080
 QY 363 GluCysGlyGlnValValGlyLeuTyrSerArgPheAaspValIleHisLeuAlaAalaGln 382
 DB 1081 GAATGTGTGTCAGGTGTGGGGCTCTATTCCCGCTTTGATGTGATTCACCTGGCTGGCCAG 1140
 QY 383 GlnThrTyrAnHisLeuAaspMetSerValGlyGluAlaLeuArgGlnArgThrLeuCys 402
 DB 1141 CAACCTACACACCACTGGACATGATGTGTGGAGAGCCCTGAGCGACGACACTATGT 1200
 QY 403 LeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAaspArgIle 422
 DB 1201 CTGGAGGGAGTCTTCTTCCTGTCAGCCCAAGAGCTTGGGGGAAGTATCGACAGGATT 1260
 QY 423 AlaArgGluGlnValHisArgValValLeuValAaspGluThrGlnHisLeuLeuGlyVal 442
 DB 1261 GCTCGGGAGCAGGTACACAGGCTGGTGTGTGTGACAGAGACCCAGCACTCTTCTGGCGGTG 1320
 QY 443 ValSerLeuSerAaspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAaspAlaLeu 462
 DB 1321 GTCTCCCTCTCGACATCTTCAGGCACTGTGTCTCAGCCCTGTGGCATCGATCGCCCTC 1380
 QY 463 GlyAla 464
 DB 1381 GGGGCC 1386
 RESULT 8
 ID ABQ61173 standard; cDNA; 2314 BP.
 XX AC ABQ61173;
 XX DT 26-FEB-2003 (first entry)
 XX DE AMP kinase gamma 3 subunit encoding sequence.
 XX KW Neuroprotective; immunomodulator; cancer; chromosome 2; cytostatic;
 KW anti-inflammatory; gene therapy; nutritional supplement; wound; burn;
 KW ulcer; Alzheimer's disease; Huntington's disease;
 KW amyotrophic lateral sclerosis; autoimmune disorder; inflammation;
 KW vulnery; gene; ss.
 XX OS Homo sapiens.
 XX PN WO200231111-A2.
 XX PD 18-APR-2002.
 XX PF 11-OCT-2001; 2001WO-US027760.
 XX PR 12-OCT-2000; 2000US-00687527.
 XX (HYSE-) HYSEQ INC.
 XX Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao Qa, Ren F;
 XX Xue AJ, Yang Y, Wehrman T, Drmanac RT;
 XX WPI; 2002-426278/45.

DR N-PSDB; ABP43929.
 XX New polypeptides and their encoded proteins, useful as nutritional
 PT sources or supplements, or in gene therapy, particularly for treating
 PT wounds, Alzheimer's disease, amyotrophic lateral sclerosis, cancer or
 PT inflammation.
 XX Claim 1; SEQ ID # 386; 357pp + Sequence Listing; English.
 PS The invention relates to 446 newly isolated polynucleotide sequences. The
 CC activity of polynucleotides of the invention may be described as,
 CC vulnery, neuroprotective, immunomodulator, cytostatic and anti-
 CC inflammatory. Compositions comprising nucleic acids of the invention are
 CC useful for treating a mammalian subject, or as nutritional sources or
 CC supplements. These are useful in gene therapy, particularly for treating
 CC wounds, burns or ulcers, Alzheimer's disease, Huntington's disease,
 CC amyotrophic lateral sclerosis, autoimmune disorders, cancer or
 CC inflammation. The nucleic acids and polypeptides are also useful in
 CC diagnostic and research methods. The sequences given in records ABQ60788-
 CC ABQ61233 represent polynucleotides of the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 2314 BP; 513 A; 677 C; 618 G; 506 T; 0 U; 0 Other;
 SQ
 Alignment Scores: 5.76e-173 Length: 2314
 Pred. No.: 2391.00 Matches: 461
 Score: 99.78% Conservative: 2
 Percent Similarity: 99.35% Mismatches: 1
 Best Local Similarity: 99.50% Indels: 0
 Query Match: 6 Gaps: 0
 DB:
 US-10-070-794A-30 (1-464) x ABQ61173 (1-2314)
 QY 1 MetSerPheLeuGluGlnGluAasnSerSerTrrProSerProAlaValThrSerSer 20
 DB 97 ATGAGCTTCTTAGAGCAAGAAACAGCAGCTCATGGCCATCACCAGCTGTGACCAGCAGC 156
 QY 21 SerGluArgIleArgGlyLysArgArgAlaLysAlaLeuArgTrrThrArgGlnLysSer 40
 DB 157 TCAGAAAGATTCCTCGTGGAACCGGAGGCGCCAAAGCTTGAGATGGACAAAGCAGAGTCG 216
 QY 41 ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60
 DB 217 GTGGAGGAAGGGGAGCCACCAAGGTTCAGGGGAAAGGTCCCGGTCCAGGCCAGCTGCTGAG 276
 QY 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAaspProAla 80
 DB 277 TCCACCGGGCTGGAGGCCACATTCGCCAAGACCAACACCCCTTGGCTCAAGCTGATCCTGCC 336
 QY 81 GlyValGlyThrProProThrGlyTrrPaspCysLeuProSerPaspCysThrAlaSerAla 100
 DB 337 GGGGTGGGCACTCCACCAACAGGGTGGGACTGCTCCCTCTGACTGTGTACAGCTTCAGCT 396
 QY 101 AlaGlySerSerThrAaspAaspValGluLeuAlaThrGluPheProAlaThrGluAlaTrr 120
 DB 397 GCAGGCTCCAGCACAGATGATGTGGAGCTGGCCAGGAGTTCGCCAGCCACAGAGCCCTGG 456
 QY 121 GluCysGluLeuGluGlyLeuLeuGluArgProAlaLeuCysLeuSerProGlnAla 140
 DB 457 GAGTGTGAGCTAGAAAGGCTCTGGAAGAGAGGCTGCTGCTGTGCTGTGCTGCTGCTGCTG 516
 QY 141 PropheProLysLeuGlyTrrPaspAaspGluLeuArgLysProGlyAlaGlnIleTrrMet 160
 DB 517 CCATTTCCAAAGCTGGGCTGGGATGACGAACCTCGCGAAACCCCGGCGCCAGATCTACATG 576
 QY 161 ArgPheMetGlnGluHisThrCysTrrAaspAlaMetAlaThrSerSerLysLeuValIle 180
 DB 577 CGCTTTCATCGAGGAGCACACCTGCTACCATGCGCACTAGCTTCCAGCTAGCTAGCTATC 636
 QY 181 PheAaspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAasnGlyValArg 200

Db 637 TTGACACCATGCTGGAGATCAAGAGCCCTCTTTGCTCTGGTGGCCAAACGGGTGTGGG 696
 Qy 201 AlaAlaProLeuTrpAspSerLysGlnSerPheValGlyMetLeuThrIleThrAsp 220
 Db 697 GCAGCCCTCTATGGACAGCAAGAGCAGAGCTTTGTGGGGATGCTGACCATCACTGAC 756
 Qy 221 PheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGlu 240
 Db 757 TTCATCTCTGGTGGTGCATCTGCTACTACAGGTCCGCCCTGTGTCCAGATCTATGAGATTGAA 816
 Qy 241 GlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeuVal 260
 Db 817 CAACATAGATTGAGACTTGAGGGAGATCTACCTGCNAGGCTGCTTCAAGCCCTCTGGTC 876
 Qy 261 SerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIle 280
 Db 877 TCCATCTCTCTAATGATAGCTGTGTGAAGCTGTCTACACCTTCATCAAGACCGGATC 936
 Qy 281 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 300
 Db 937 CATGCCCTGCCCTGTCTTACCCGGTGTTCAGGCAACGTACTCCACATCTCTCACACAAA 996
 Qy 301 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 320
 Db 997 CGCTGCTCAAGTTCCTGACATCTTTGTGTTCCTGTGCCCCGGCCCTCTCTCTCTAC 1056
 Qy 321 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGluThr 340
 Db 1057 CGCACTATCAAGATTGGGCATCGGCACATTCGAGACATTGGCTGTGTGTGGAGACA 1116
 Qy 341 AlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProVal 360
 Db 1117 GCACCCATCTCTGACTGCATCGACATCTTTGTGACCGCGGTGTCTGCACTGCCCTGTG 1176
 Qy 361 ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeuAla 380
 Db 1177 GTCAACGAATGTGTGAGTGTGGGCTCTATTCCCGCTTTGATGTGATTCACCTGGCT 1236
 Qy 381 AlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr 400
 Db 1237 GCCCAGCAACCTACACCACTGCATCGACATGATGATGTGGAGAGCCCTGAGCAGAGACA 1296
 Qy 401 LeuCysLeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValIleAsp 420
 Db 1297 CTATGTCTGGAGGAGTCTTTCTCTGCCAGCCCAAGAGAGCTTGGGGAGTGTATCGAC 1356
 Qy 421 ArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeu 440
 Db 1357 AGGATTGCTCGGGAGCAGGTACACAGGTGTGTGTAGTGACGAGAGCCAGCATCTCTTG 1416
 Qy 441 GlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAsp 460
 Db 1417 GGCTGTGTCTCCCTCTCCGACATCTTCAGGCACTGTGTGTGTCAGCCCTGTGGCATCAT 1476
 Qy 461 AlaLeuGlyAla 464
 Db 1477 GCCCTCGGGGCC 1488

RESULT 9

ADP87618
ID ADP87618 standard; DNA; 2290 BP.

XX AC ADP87618;

XX AC ADP87618;

DT 23-SEP-2004 (first entry)

XX Human NOVX polypeptide encoding DNA, NOV10b.

XX anorectic; antidiabetic; gene therapy; vaccine; obesity; diabetes;
 KW insulin resistance; hybridization probe; chromosome mapping;
 KW tissue typing; preventive medicine; pharmacogenomics; NOVX; human; gene;
 KW ds.

XX OS Homo sapiens.

XX W02004056961-A2.

XX PN 08-JUL-2004.

XX PD 27-OCT-2003; 2003WO-US034114.

XX PF 25-OCT-2002; 2002US-0421239P.

XX PR 28-OCT-2002; 2002US-0421700P.

XX PR 31-OCT-2002; 2002US-0422776P.

XX PR 13-NOV-2002; 2002US-0426197P.

XX PR 20-DEC-2002; 2002US-0435498P.

XX PR 20-DEC-2002; 2002US-0435510P.

XX PR 21-MAR-2003; 2003US-0435568P.

XX PA (CURA-) CURAGEN CORP.

XX Berghs C, Catterton E, Ellerman K, Ort T, Rieger D, Chaudhuri A;

XX PI P-PSDB; ADP87619.

XX DR WPI: 2004-500293/47.

XX DR P-PSDB; ADP87619.

XX XX

XX PT New NOVX nucleic acid molecules and polypeptides useful for preventing or

XX PT treating NOVX-associated disorders, e.g. diabetes, insulin resistance or

XX PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

XX PS Claim 1; SEQ ID NO 75; 570pp; English.

XX CC The invention relates to a novel isolated nucleic acid molecule

XX CC comprising any of the nucleotide sequences (e.g. 3634, 2127 or 2120 base

XX CC pairs) fully defined in the specification; or encodes any of the amino

XX CC acid sequences (e.g. 698, 702 or 709 amino acids) fully defined in the

XX CC specification. The invention further comprises: an isolated polypeptide

XX CC comprising any of the amino acid sequences cited above; a method for

XX CC identifying compounds that modulate target polypeptide activity; an

XX CC antibody that immunospecifically binds to the target polypeptide; where

XX CC the target polypeptide comprises any of the above-mentioned amino acid

XX CC sequences, an amino acid sequence that is at least 95% identical to the

XX CC above amino acid sequences, an amino acid sequence of at least one domain

XX CC of the above-mentioned amino acid sequences, or an amino acid sequence

XX CC that is at least 95% identical to the domain of the above amino acid

XX CC sequences; a method for identifying a potential therapeutic agent for use

XX CC in treatment of a pathology, where the pathology is related to aberrant

XX CC expression or aberrant physiological interactions of a target polypeptide

XX CC ; and a method of screening for a modulator of activity of or of latency

XX CC or predisposition to a pathology associated with a target polypeptide.

XX CC The modulating compounds have anorectic and antidiabetic activities. The

XX CC nucleic acid sequences of the invention may be used in gene therapy to

XX CC treat disorders. The proteins of the invention may be used in creating a

XX CC vaccine. The composition and methods are useful for identifying compounds

XX CC that modulate protein activity or for diagnosing, preventing or treating

XX CC diverse pathological conditions, such as obesity, diabetes or insulin

XX CC resistance. The nucleic acids are also used as hybridization probes, in

XX CC chromosome mapping, tissue typing, preventive medicine, and

XX CC pharmacogenomics. This polynucleotide sequence represents the DNA

XX CC encoding a NOVX polypeptide of the invention.

XX SQ Sequence 2290 BP; 501 A; 674 C; 617 G; 498 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.61e-171 Length: 2290

Score: 2372.00 Matches: 457

Percent Similarity: 99.35% Conservative: 3

Best Local Similarity: 98.70% Mismatches: 3

Query Match: 98.71% Indels: 0

DB: 12 Gaps: 0

US-10-070-794A-30 (1-464) x ADP87618 (1-2290)

Qy 1 MetSerPheLeuGluGlnAenSerSerSerTrpProSerProAlaValThrSerSer 20

|||||
Db 97 ATGAGCTCTCAGAGCAGAAAAACAGCAGCTCATGGCCATCACAGCTGTGACACAGC 156
Qy 21 SerGluArgLleArgGlyLysArgAlaLysAlaLeuArgThrArgGlnLysSer 40
Db 157 TCAGAAAGATCCGTGGNAACGAGGAGGCGCAAGACCTTGAGATGGAACAAGGAGAGTCG 216
Qy 41 ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60
Db 217 GTGAGGAGGAGGAGCCACCAAGGTGAGGGGAGGTCCTCCGGTCCAGGCCAGCTGCTGAG 276
Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla 80
Db 277 TCCACCGGCTGGAGGCCACATTCCTCCAGACCAACCCCTGGCTCAAGCTGATCTCTGCC 336
Qy 81 GlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSerAla 100
Db 337 GGGGTGGGCACTCCACCAACAGGGTGGGACTGCCTCCCTCTGACTGTGTACAGCCTCAGCT 396
Qy 101 AlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTrp 120
Db 397 GCAGGCTCCAGCAGACAGATGATGTGAGCTGGCCACGGAGTTCCAGGCCACAGAGGCTGG 456
Qy 121 GluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGlnAla 140
Db 457 GAGTGTGAGCTAGAAAGGCTGCTGGNAGAGAGGCTGCCCTGTGCTGTCCCGCAGGCC 516
Qy 141 ProPheProLysLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnLileTyMet 160
Db 517 CCATTTCCAAAGCTGGGCTGGGATGACGAACCTGGCGAAACCCGGCGCCAGATCTACATG 576
Qy 161 ArgPheMetGlnGluHisThrCysTyRAspAlaMetAlaThrSerSerLysLeuValile 180
Db 577 CGCTTCATCTGAGGAGCACACCTGCTACATGCCATGCCAATAGCTTCCAAAGCTAGTCATC 636
Qy 181 PheAspThrMetLeuGluLileLysLysAlaPhePheAlaLeuValAlaAsnGlyValArg 200
Db 637 TTCGACCATGCTGGAGATCAAGNAGGCTTCTTGTCTGTGGCCACGGTGTGGGG 696
Qy 201 AlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAsp 220
Db 697 GCAGCCCTCTATGGCAGCAGCAAGAAGCAGAGCTTTGTGGGGATGCTGACCATCACTGAC 756
Qy 221 PheIleLeuValLeuHisArgTyrrTyrrArgSerProLeuValGlnLileTyrrGluIleGlu 240
Db 757 TTCACTCTGCTGCTCATCGCTACTACAGGTGCCCTCCCTGGTCCAGATCTATGAGATTGAA 816
Qy 241 GlnHisLysIleGluThrTrpArgGluIleTyrrLeuGlnGlyCysPheLysProLeuVal 260
Db 817 CAACATAAGATTGAGCTTGGAGGAGATCTACCTGCAAGGCTGCTTCAAGCCTCTGCTC 876
Qy 261 SerIleSerProAsnAspSerLeuPheGluAlaValTyrrThrLeuLileLysAsnArgIle 280
Db 877 TCCATCTCTCCCTAATGATAGCTGTTTGAAGCTGTCTACACCTCATCAAGAACCGGATC 936
Qy 281 HisArgLeuProValIleLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 300
Db 937 CATCCCTGCTGCTTCTTGGACCCGTTGTCAGGCAACGTAACCTCTTACACACAAA 996
Qy 301 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyrr 320
Db 997 CCCTGCTCAAGTTCTGTCACATCTTGGTTCCTGCTGCCCGGCCCTCTCTCTCTAC 1056
Qy 321 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGluThr 340
Db 1057 CGCACTATCCAAAGATTGGGATCGGCATCCGACATTCGAGACTTGGCTGTGTGTGGAGACA 1116
Qy 341 AlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuProVal 360
Db 1117 GCACCATCTCTGACTGCACTGACATCTTTGTGGACCGGCGGTGTGTGCTGCTGCTGTG 1176
Qy 361 ValAsnGluCysGlyGlnValValGlyLeuTyrrSerArgPheAspValIleHisLeuAla 380
|||||

1177 GTCAACGAATGTGTGTCAGGTCTGGGCTCTATTCCCGCTTTGATGTGATTCACCTGGCT 1236
Qy 381 AlaGlnGlnThrTyrrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr 400
Db 1237 GCCCAGCAAACTTACAAACCACTTGGACATGAGTGTGGAGAGCCCTTGAGGAAGAGACA 1296
Qy 401 LeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAsp 420
Db 1297 CTATGTCTGGAGGAGTCTCTTCTGCCAGCCCCACGAGAGCTTGGGGGAAGTATCGAC 1356
Qy 421 ArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeu 440
Db 1357 AGGATTGCTCGGAGCAGGTACACAGGCTGGTGTCTAGTCGACGAGACCAGCATCTCTTG 1416
Qy 441 GlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAsp 460
Db 1417 GGGTGTGTCTCCCTCTCCGACATCTTTCAGGCATGCTGTGCTCAGCCCTGCTGGCATCGAT 1476
Qy 461 AlaLeuGly 463
Db 1477 CCCTCGGG 1485
RESULT 10
AEB69127
ID AEB69127 standard; DNA; 2290 BP.
XX AC AEB69127;
XX 20-OCT-2005 (first entry)
DT Human modulator of IGFR pathway polynucleotide #4.
DE Screening; insulin growth factor receptor; IGFR; diagnosis; cancer;
KW neoplasm; cytostatic; gene; ds.
XX Homo sapiens.
OS WO2005073723-A1.
PN 11-AUG-2005.
PD 27-JAN-2005; 2005WO-US002638.
XX 28-JAN-2004; 2004US-0539837P.
PR 12-MAR-2004; 2004US-0552634P.
PR 21-JUN-2004; 2004US-0581696P.
XX (EXEL-) EXELIXIS INC.
PA (NICO/) NICOLL M.
XX Nicoll M, Friedman L, Francis-Lang H, Parks A, Shaw KJ, Zhang H;
PI Bjerke LM, Adamkewicz J, Hitz BC, Lickteig K, Jin Y;
XX WPI; 2005-582573/59.
DR P-PSDB; AEB69187.
XX Identifying a candidate insulin growth factor receptor (IGFR) pathway
PT modulating agents useful for diagnosing or treating, for e.g. cancer,
PT comprises screening for agents that modulate the activity of a modifier
PT of IGFR (MIGFR).
XX Example; SEQ ID NO 4; 334pp; English.
PS The invention relates to a method of identifying a candidate insulin
CC growth factor receptor (IGFR) pathway modulating agent comprising
CC screening for agents that modulate the activity of a modifier of IGFR
CC (MIGFR). The method comprises providing an assay system comprising an
CC MIGFR polypeptide or polynucleotide, contacting the assay system with a
CC test agent under conditions where, but for the presence of the test
CC agent, the system provides a reference activity and detecting a test
CC agent-biased activity of the assay system, where a difference between the
CC test agent-biased activity and the reference activity identifies the test
CC agent as a candidate IGFR pathway modulating agent. The invention also

CC relates to methods for modulating an IGR pathway of a cell or in a
 CC mammalian cell and a method for diagnosing a disease in a patient. The
 CC methods are useful for diagnosing or treating cancer or for identifying
 CC modulators of an IGR pathway, which may be utilized as therapeutic
 CC targets for disorders associated with defective IGR function, such as
 CC cancer. This sequence represents a human modulator of IGR pathway
 CC polynucleotide of the invention.

XX
 SQ Sequence 2290 BP; 501 A; 674 C; 617 G; 498 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1,61e-171 Length: 2290
 Score: 2372.00 Matches: 457
 Percent Similarity: 99.35% Conservations: 3
 Best Local Similarity: 98.70% Mismatches: 3
 Query Match: 98.71% Indels: 0
 DB: 14 Gaps: 0

US-10-070-794A-30 (1-464) x ABB69127 (1-2290)

Qy 1 MetSerPheLeuGluGlnGluAsnSerSerSerTrpProSerProAlaValThrSerSer 20
 Db 97 ATGAGCTCTCTAGAGCAAGAAACAGCAGCTCATGGCCATCACCAGCTGTGACCCAGCAGC 156
 Qy 21 SerGluArgIleAerGlyAerGlyAerGlyAerGlyAerGlyAerGlyAerGlyAerGly 40
 Db 157 TCAGAAAGAAATCCGTGGGAAACGGAGGCCAAAGCCTTGATGGACAAAGCAGAGTCG 216
 Qy 41 ValGluGluGlyGluProProGlyGlnGlyGlnGlyGlnGlyGlnGlyGlnGlyGlnGly 60
 Db 217 GTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 276
 Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspProAla 80
 Db 277 TCCACCGGGCTGGAGGCCACATTCACCAAGACACACACCTTGGCTCAAGCTGATCTGCC 336
 Qy 81 GlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSerAla 100
 Db 337 GGGTGGGCACTCCACCAACAGGCTGGGAGTGCCTCCCTCTGACTGTACAGCCTCAGCT 396
 Qy 101 AlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAlaTrp 120
 Db 397 GCAGGCTCCACACAGATGATGTGGCTGGCCAGGAGTTCGCCAGCCACAGAGGCTGG 456
 Qy 121 GluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGlnAla 140
 Db 457 GAGTGTGAGCTAGAGGCTCTGGAAGAGAGGCTGCCCTGTGCTGCTGCCCGCAGGCC 516
 Qy 141 ProPheProLysLeuGlyTrpAspAspGluLeuArgLysProGlyAlaGlnIleTyrMet 160
 Db 517 CCATTTCCCAAGCTGGGCTGGGATGACGAACCTGGGAAACCCGGCGGCCAGATCTACATG 576
 Qy 161 ArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValIle 180
 Db 577 CGCTTTCACGAGGAGCACCTCTGATGATGCCATGCCATGCTACCTCAAGCTAGTATC 636
 Qy 181 PheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyValArg 200
 Db 637 TTCACACCATGCTGGAGATCAAGAGGCTCTCTTGTCTGTGGTGGCAACGGTGTGGG 696
 Qy 201 AlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAsp 220
 Db 697 GCAGCCCTCTATGGGACAGCAAGACAGAGCTTTTGTGGGATGCTGACCATCAGTAC 756
 Qy 221 PheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGlu 240
 Db 757 TTCATCTCTGGTGGCATCGCTACTACAGGTCCCTCCCTGGTGGTCCAGATCTATGAGATTGA 816
 Qy 241 GlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeuVal 260
 Db 817 CAACATAGATTGAGCTGGAGGAGATCTACTCTGCAAGGCTGCTTCAAGCCTCTGGTC 876
 Qy 261 SerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIle 280

Db 877 TCCATCTCTCTATATAGCTCTTTGAAGCTGTCTACACCTCATCAAGACCGGATC 936
 Qy 281 HisArgLeuProValLeuAspProValSerGlyValAsnValLeuHisIleLeuThrHisLys 300
 Db 937 CATCGCTGCTGTCTGTGACCCGGTGTGAGCAACGTACTTCCACATCTCTCACACAAA 996
 Qy 301 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 320
 Db 997 CGCCTGCTCAAGTTCTCTGCACATCTTTGGTTTCCCTGTGCCCCGGCCCTCTCTCTAC 1056
 Qy 321 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGluThr 340
 Db 1057 CGCACTATCCAAAGATTGGGCATCGGCACATTCGAGACTTGGCTGTGGTCTGGAGACA 1116
 Qy 341 AlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProVal 360
 Db 1117 GCACCCATCTGACTGCATCGACATCTTTGTGACCGCGGTGTGTGCACTGCCTGTG 1176
 Qy 361 ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeuAla 380
 Db 1177 GTCAACGAATGTGTCAGGTCTGGGCTCTCTATTCCCGCTTTGATGTGATTCACCTGGCT 1236
 Qy 381 AlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThr 400
 Db 1237 GCCCAGCAAACTACACACCTGACATGATGATGGGAGAGCCCTGAGGAGAGGACA 1296
 Qy 401 LeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAsp 420
 Db 1297 CTATGTCTGGAGGAGTCTCTTCTGCGAGCCCGCAGAGCTTGGGGAGAGTGCATCGAC 1356
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 Db 1357 AGGATTCCTCGGAGCAGGTACACAGCTGTGTCTAGTGGAGAGACCCAGACATCTCTTG 1416
 Qy 441 GlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAsp 460
 Db 1417 GGGTGTGTCTCCCTCTCCGACATCTTTCAGGCACTGTGTCTCAGCCCTGTGTGATCGAT 1476
 Qy 461 AlaLeuGly 463
 Db 1477 CCTCGGGG 1485

RESULT 11
 AAD36457
 ID AAD36457 standard; DNA; 1873 BP.
 XX
 AC AAD36457;
 XX
 DT 09-AUG-2002 (first entry)
 XX
 DE Pig PRKAG3 polymorphic variant DNA (PRKAG3-30).
 XX
 KW AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene;
 KW screening; meat quality; single nucleotide polymorphism; SNP; pig; gene;
 KW variant; ds.
 XX
 OS Sus scrofa.
 XX
 FH Key Location/Qualifiers
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 FT /product= "Pig PRKAG3 polymorphic variant (PRKAG3-30)"
 FT replace(89, C)
 FT /*tag= b
 FT variation
 FT /standard_name= "Single nucleotide polymorphism (SNP)"
 PN WO200220850-A2.
 XX
 PD 14-MAR-2002.
 XX
 PF 10-SEP-2001; 2001WO-US028283.
 XX

Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK; PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; RN locus; chromosome 15; 88.

Sus scrofa.

Key Location/Qualifiers
CDS 1..1395
/*tag= a
/product= "Sus scrofa complete Prkag3 protein"

WO200120003-A2.

22-MAR-2001.

11-SEP-2000; 2000WO-EP009896.

10-SEP-1999; 99EP-00402236.

18-MAY-2000; 2000EP-00401388.

(INRG) INRA INST NAT RECH AGRONOMIQUE.

(ANDE/) ANDERSSON L.

(LOOF/) LOOFT C.

(KALM/) KALM E.

Anderson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;

Iannuccelli N, Gellin J, Le Roy P, Chardon P;

WPI; 2001-244810/25.

P-PSDB; AAE00222.

New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and myopathy.

Claim 12; Page 62-64; 71pp; English.

The present sequence is a cDNA encoding pig adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, complete PRKAG3. Prkag3 gene is located in the RN locus of chromosome 15. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3. Transgenic animal and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy

SQ Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4.99e-144	Length:	1873
Score:	2011.00	Matches:	400
Percent Similarity:	90.11%	Conservative:	19
Best Local Similarity:	86.02%	Mismatches:	44
Query Match:	83.69%	Indels:	2
DB:	4	Gaps:	2

US-10-070-794A-30 (1-464) x AAD03319 (1-1873)

Qy 1 MetSerPheLeuGluGlnAsnSerSerSerTrpProSerProAlaValThrSerSer 20

Db	1	ATGAGCTTCTTAGAGCAAGGAGAGAGCGCTTCATGGCCATCCCGAGCTGTAAACACCCAGC	60
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Db	61	TCAGAAAGAAGCCATGGGGACCGGGGAACAGCCCTCTAGATGGACAGCAGAGAT	120
Qy	41	ValGluGluGlyGluProProGlyGlnGlyProArgSerArgProThrAlaGlu	60
Db	121	GTAGAGGAAGGGGGCTCCGGGCCCGAGGAGGTCCCCAGTCCAGGCCAGTTGCTGAG	180
Qy	61	SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspPro---	79
Db	181	TCCACCGGCGAGGAGGCCACATTCCTCCCAAGGCCACACCTTGGCCCAAGCCGCTCCCTTG	240
Qy	80	AlaGlyValGlyThrProProThrGlyTrpAspCysLeuProSerAspCysThrAlaSer	99
Db	241	GCCGAGGTGGACAAACCCCAACAGACGGGACATCTCTCCCTCTGACTGTGGAGCCCTCA	300
Qy	100	AlaAlaGlySerSerThrAspAspValGluLeuAlaThrGluPheProAlaThrGluAla	119
Db	301	GCCTCCGACTCCAACACAGACCATCTGGATCTGGGCATAGAGTTCTCAGCCTCGCGCGC	360
Qy	120	TrpGluCysGluLeuGluGlyLeuLeuGluGluArgProAlaLeuCysLeuSerProGln	139
Db	361	TCGGGGGATGAGCTT---GGGCTGGTGAAGAGAGCCCGCTGCCCATCCCCAGAG	417
Qy	140	AlaProPheProLysLeuGlyTrpAspAspGluLeuArgLysProGlyValAlaGlnIleTr	159
Db	418	GTGCTGTATCCAGGCTGGGCTGGGATGATGAGCTGCAGAGCGGGGGCCAGGCTTAC	477
Qy	160	MetArgPheMetGlnGluHisThrCysTyAspAlaMetAlaThrSerSerLysLeuVal	179
Db	478	ATGCACCTTCATGCAGGAGCACACCTCTACGATGCCATGGCAGCCAGCTCCAAACTGTC	537
Qy	180	IlePheAspThrMetLeuGluLysLeuAlaPhePheAlaLeuValAlaAsnGlyVal	199
Db	538	ATCTTCGACACCATGCTGGAGATCAAGAGAGCCCTTCTTGGCCCTGGTGGCAACGGGCTC	597
Qy	200	ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr	219
Db	598	CGAGCGGACCTTTGTGGGACAGCAAGACAGAGCTTCGTGGGGATGTGACCATACA	657
Qy	220	AspPheIleLeuValLeuHisArgTyTrpArgSerProLeuValGlnIleTyGluIle	239
Db	658	GACTTCATCTTGGTGTGCTGACCGCTATTACAGGTCCCTCCCTGCTCCAGATCTACGAGAT	717
Qy	240	GluGlnHisLysIleGluThrTrpArgGluIleTyLeuGlnGlyCysPheLysProLeu	259
Db	718	GAAGAACATAGATTGAGACCTGGAGGGAGATCTACCTTCAAGGCTGCTTCAAGCCTCTG	777
Qy	260	ValSerIleSerProAsnAspSerLeuPheGluAlaValTyThrLeuIleLysAsnArg	279
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Qy	280	IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis	299
Db	838	ATCCACCGCTGCGGCTCTGGACCCCTGTCTCCGGGGCTGTGCTCCACATCTCCACAT	897
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Db	898	AAGCGGCTTCTCAAGTTCTTGCCACATCTTTTGGCACCTGTGCTGGCCCGCCCTCTCTC	957
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Qy	340	ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro	359
Db	1018	ACGGGGCCCATCTTGACCGGCACTGGACATCTTGTGGACCGGGCTGTGCTGCGCTGCT	1077
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Db 1078 GTGGTCAACGAACTGGACAGGTAGTGGCCCTCTACTCTCGCTTTGTGTGATCCACCTG 1137
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 Qy 440 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuValLeuSerProAlaGlyIle 459
 Db 1318 CTGGGCGTGTGCTCTCTGACATCTTCAGGCTCTGTGTCTCAGCCCTGTCTGGAATT 1377
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 AC AAD36456;
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 DT 09-AUG-2002 (first entry)
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 XX
 KW AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene;
 KW screening; meat quality; single nucleotide polymorphism; SNP; pig; gene;
 KW de.
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 OS Sus scrofa.
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 PN 14-MAR-2002.
 XX
 PF 10-SEP-2001; 2001WO-US028283.
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 PR 08-SEP-2000; 2000US-0231045P.
 PR 08-JAN-2001; 2001US-0260239P.
 PR 18-JUN-2001; 2001US-0299111P.
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 PA (IOWA) UNIV IOWA STATE RES FOUND INC.
 XX
 PI Rothschild MF, Ciobanu DC, Malek M, Piastow G;
 XX
 WI WPI; 2002-393850/42.
 DR P-PSDB; AAE22984.
 XX
 PT Screening animals to determine those likely to produce larger litters and

improved meat quality traits involves assaying for the presence of
 polymorphisms in the AMP activated protein kinase regulatory gamma
 subunit gene.
 Claim 17; Fig 1; 109pp; English.
 The invention relates to a method for screening animals to determine
 those more likely to produce large litters and improved meat quality
 traits. The method involves assaying for the presence of a genotype in
 the sample of genetic material obtained from animal. The genotype is
 characterised by polymorphism(s) in the AMP activated protein kinase
 regulatory gamma subunit (PRKAG3) gene. The method is used for screening
 animals e.g., pigs to determine those most likely to exhibit improved
 meat quality traits and to produce larger litters. The present sequence
 is pig wild-type PRKAG3 gene
 Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 4,99e-144 Length: 1873
 Score: 2011.00 Matches: 400
 Percent Similarity: 90.11% Conservatives: 19
 Best Local Similarity: 86.02% Mismatches: 44
 Query Match: 83.69% Indels: 2
 Gaps: 2
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 Db 121 GTAGAGGAGGGGGGCTCCGGGCCCGAGGGAAGTCCCGAGTCCAGGCCAGTGTCTGAG 180
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 Db 361 TCGGGGATGAGCTT---GGGCTGTGGAAGAAGCCAGCCCGCTGGCCCATCCCGAG 417
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 Qy 180 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 199
 Db 538 ATCTTCGACACCATGCTGGAGATCAAGAAGGCGCTTCTTTGGCCTGTGGTGGCCAAACGCGTC 597
 Qy 200 ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 219
 Db 598 CGAGCGGCACCTTGTGGGACAGCAAGAGCAGCTTCGTGGGATGCTGACCATCACA 657
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Db 658 GACATTCATCTTGGTGTGACCGCTATTACAGGTCCTCCCTGGTCCAGATCTACGAGATT 717
 Qy GluGlnHisLysIleGluThrTTPArgGluIleTyrLeuGlnGlyCysPheLysProLeu 259
 Db 718 GAAGACATAGATTGAGACTGGAGGAGATCTACCTTCAAGGCTGCTTCAGCCCTCTG 777
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 Qy 320 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 339
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 Qy ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuPro 359
 Db 1018 ACGGCGCCCATCTCTGACCGCACTGACATCTCTGCGACCGCGGTGTCTGCGCTGCT 1077
 Qy 360 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 379
 Db 1078 GTGTGTCAACGAACACTGGACAGTGTGTGGCTCTACTCTGCTTTGATGTATCCACTG 1137
 Qy 380 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 399
 Db 1138 GCTGCCCAACAACATACACACCTGACATGAATGTGGAGAGCCCTGAGCAGCGG 1197
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 Qy 420 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 439
 Db 1258 GACCGGATGTCCGGGAACAGGTGACCGCTGTGCTGTGATGAGACCAACACTT 1317
 Qy 440 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 459
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 Qy 460 AspAlaLeuGlyAla 464
 Db 1378 GATGCCCTCGGGGCC 1392

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AAD03321

ID AAD03321 standard; DNA; 2022 BP.

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XX AAD03321;

XX DT

XX 13-JUN-2001 (first entry)

XX DE

XX Sus scrofa PRKAG3 splice variant DNA.

XX KW

XX Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK;

XX PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;

XX genetic testing; carbohydrate metabolism disorder; skeletal muscle;

XX cystathione beta synthase; CBS; cardiac; gene therapy; ds.

XX OS

XX Sus scrofa.

XX XX

XX Location/Qualifiers

XX Key

XX 1..1545

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XX /*tag= a

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XX FT

XX FT

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XX PD

XX 22-MAR-2001.

XX XX

XX 11-SEP-2000; 2000WO-EP009896.

XX DF

XX 10-SEP-1999; 99EP-00402236.

XX PR

XX 18-MAY-2000; 2000EP-00401388.

XX XX

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XX PA

XX (ANDE/) ANDERSSON L.

XX PA

XX (LOOF/) LOOFT C.

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XX (KALM/) KALM E.

XX XX

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XX PI

XX Iannuccelli N, Gellin J, Le Roy P, Chardon P;

XX XX

XX WPI; 2001-244810/25.

XX DR

XX P-PSDB; AAE00224.

XX XX

XX Claim 12; Page 69; 71pp; English.

XX CC

XX The present sequence is pig adenosine monophosphate (AMP)-activated

XX CC

XX kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3 splice

XX CC

XX variant DNA. Prkag3 gene is located in the RN locus of chromosome 15.

XX CC

XX Mutation in Prkag3 results in an altered regulation of carbohydrate

XX CC

XX metabolism, particularly in skeletal muscle. PRKAG3 is useful as

XX CC

XX therapeutic for treating carbohydrate metabolism disorders such as

XX CC

XX diabetes, obesity, and disorders associated with muscle metabolism such

XX CC

XX as myopathy and cardiovascular diseases, to modulate AMPK activity, and

XX CC

XX for restoring a normal AMPK function. PRKAG3 sequence and its

XX CC

XX functionally altered mutants are useful for the diagnostic evaluation,

XX CC

XX genetic testing and prognosis of a metabolic disorder, preferably a

XX CC

XX carbohydrate metabolism disorder. Primers that can detect a genetic

XX CC

XX polymorphic marker linked to a sequence encoding PRKAG3, are useful for

XX CC

XX detecting a dysfunction of carbohydrate metabolism resulting from the

XX CC

XX expression of a functionally altered allele of PRKAG3. Transgenic animal

XX CC

XX and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting

XX CC

XX of PRKAG3 or its mutant, are useful for screening compounds able to

XX CC

XX modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for

XX CC

XX detecting mutations in a Prkag3 gene, or in a sequence encoding the first

XX CC

XX cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene

XX CC

XX therapy

XX XX

XX SQ

XX Sequence 2022 BP; 412 A; 623 C; 593 G; 394 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	5.5e-144	Length:	2022
Score:	2011.00	Matches:	400
Percent Similarity:	90.11%	Conservative:	19
Best Local Similarity:	86.02%	Mismatches:	44
Query Match:	83.69%	Indels:	2
DB:	4	Gaps:	2

US-10-070-794A-30 (1-464) x AAD03321 (1-2022)

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Qy 21 SerGluArgIleArgGlyLysArgArgAlaIleAlaLeuArgTrpThrArgGlnLysSer 40

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Qy 41 ValGluGluGlyGluProGlyGlnGlyGlnGlyGlnGlyGlnGlyGlnGlnGlnGln 60

Db 271 GTAGAGGAAGGGGGGCTCCGGGGCCCGAGGAGAGTCCCGAGTCCAGGCCAGGCTGCTGAG 330

Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspPro--- 79

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Db 748 CGAGCGGCACCTTTCTGGGACAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 807
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DT 09-AUG-2002 (first entry)
XX
DE Pig PRKAG3 polymorphic variant DNA (PRKAG3-199).
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KW AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene;
KW screening; meat quality; single nucleotide polymorphism; SNP; pig; gene;
KW variant; ds.
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OS Sus scrofa.
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PD 14-MAR-2002.
XX
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PR 08-SEP-2000; 2000US-0231045P.
PR 08-JAN-2001; 2001US-0260239P.
PR 18-JUN-2001; 2001US-0299111P.
XX
PA (IOWA) UNIV IOWA STATE RES FOUND INC.
XX
PI Rothschild MF, Ciobanu DC, Malek M, Plastow G;
XX
DR WPI; 2002-393850/42.
DR P-PSDB; AAE22987.
XX
PT Screening animals to determine those likely to produce larger litters and
PT improved meat quality traits involves assaying for the presence of
PT polymorphisms in the AMP activated protein kinase regulatory gamma
PT subunit gene.
XX
PS Disclosure; Page 98-100; 109pp; English.
XX
CC The invention relates to a method for screening animals to determine
CC those more likely to produce large litters and improved meat quality
CC traits. The method involves assaying for the presence of a genotype in
CC the sample of genetic material obtained from animal. The genotype is
CC characterised by polymorphism(s) in the AMP activated protein kinase
CC regulatory gamma subunit (PRKAG3) gene. The method is used for screening
CC animals e.g., pigs to determine those most likely to exhibit improved
CC meat quality traits and to produce larger litters. The present sequence
CC is pig PRKAG3 polymorphic variant DNA (PRKAG3-199)
XX
SQ Sequence 1873 BP; 383 A; 580 C; 534 G; 376 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 5,95e-144

Length: 1873

Score: 2010.00 Matches: 399

Percent Similarity: 90.11% Conservative: 20
Best Local Similarity: 85.81% Mismatches: 44
Query Match: 83.65% Indels: 2
DB: 6 Gaps: 2

US-10-070-794A-30 (1-464) x AAD36459 (1-1873)

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Qy 41 ValGluGluGlyGluProProGlyGlnGlyGluGlyProArgSerArgProThrAlaGlu 60
Db 121 GTAGAGGAAGGGGGCGCTCCGGGCGGAGGAGGTCCCCAGTCCAGGCCAGTTGCTGAG 180
Qy 61 SerThrGlyLeuGluAlaThrPheProLysThrThrProLeuAlaGlnAlaAspPro--- 79
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Db 598 CGAGCGGCACCTTTGTGGGACAGCAAGAGCAGAGCTTCGTGGGGATGCTGACCATCACA 657
Qy 220 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 239
Db 658 GACTTCATCTTGGTGTGCACCGCTATACAGGTCCCGGCTGGTCCAGATCTACGAGATT 717
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Qy 280 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 299
Db 838 ATCCACCGCTTCGCGGCTCGGACCTGTCTCCGGGGCTGTGCTCCACATCCTCACACAT 897
Qy 300 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 319
Db 898 AAGCGGCTTCTCAAGTTCTCTGCACATCTTTGGCACCTGTGCTGCGCGGCTCTCTTCTC 957
Qy 320 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGlu 339
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```
Db 958 TACGCGACCATCCAAAGATTGGGGCATCGGCACACATTCGAGACATTGGCGGTGCTGGAA 1017
Qy 340 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuPro 359
Db 1018 ACGGGCGCCATCTTGACCGGACCTGGACATCTTCGTGGACCGGCGTGTCTGCGCTGCT 1077
Qy 360 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 379
Db 1078 GTGGTCAACGAAACTGGACAGGTAGTGGGCTCTTACTCTCGCTTTGTATGTGATCCACCTG 1137
Qy 380 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 399
Db 1138 GCTGCCCCAACAAACATCAACACCTGGACATGATGTGGAGAAAGCCCTGAGGACGCGG 1197
Qy 400 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValIle 419
Db 1198 ACATGTGTCTGGAAGGCGTCTTTCTGCGCAGCCCCACGAGACCTTTGGGGGAAGTCATT 1257
Qy 420 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 439
Db 1258 GACCGGATTGTCCGGGAACAGGTGCACCGCTGTGTGCTCGTGGATGAGACCCAGCACCCT 1317
Qy 440 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 459
Db 1318 CTGGCGGTGGTGTCCCTCTCTGACATCTTTGAGGCTCTGGTGTCTCAGCCCTGCTGGAATT 1377
Qy 460 AspAlaLeuGlyAla 464
Db 1378 GATGCCCTCGGGGCC 1392
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Search completed: January 25, 2006, 22:26:39
Job time : 746.8 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 24, 2006, 21:54:27 ; Search time 83.6866 Seconds
(without alignments)
1601.338 Million cell updates/sec

Title: US-10-070-794A-4
Perfect score: 1551
Sequence: 1 MRFMQHTCYDMATSSKLV.....LSDIQLVLSPAGIDALGA 305

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1551	100.0	305	4 AAE00221	Aae00221 Human AMP
2	1551	100.0	464	4 AAE00223	Aae00223 Human AMP
3	1551	100.0	464	8 ADP43223	Adp43223 Human AMP
4	1551	100.0	489	4 AAB47679	Aab47679 PRKAG3_1
5	1551	100.0	489	6 AAE32034	Aae32034 Human kin
6	1551	100.0	489	7 ADF50310	Adf50310 Human AMP
7	1551	100.0	489	8 ADP87617	Adp87617 Human NOV
8	1550	99.9	305	4 AAE00329	Aae00329 Human Prk
9	1547	99.7	305	4 AAE00328	Aae00328 Human Prk
10	1544	99.5	489	5 AAB43929	Abp43929 AMP activ
11	1529	98.6	489	7 AAE38410	Aae38410 Human Prk
12	1529	98.6	489	7 ADF50314	Adf50314 Human AMP
13	1525	98.3	492	9 AEB69187	Adp87619 Human NOV
14	1525	98.3	492	9 AEB69187	Aeb69187 Human mod
15	1507	97.2	305	4 AAE00220	Aae00220 Pig AMPK
16	1507	97.2	464	4 AAE00222	Aae00222 Pig AMPK
17	1507	97.2	464	5 AAE22984	Aae22984 Pig wild-
18	1507	97.2	464	5 AAE22985	Aae22985 Pig PRKAG
19	1507	97.2	464	5 AAE22986	Aae22986 Pig PRKAG
20	1507	97.2	514	4 AAE00224	Aae00224 Sus scrof
21	1506	97.1	305	4 AAE00226	Aae00226 Sus scrof
22	1506	97.1	464	5 AAE22987	Aae22987 Pig PRKAG
23	1503	96.9	305	4 AAE00225	Aae00225 Sus scrof
24	1503	96.9	464	5 AAE22988	Aae22988 Pig PRKAG

25	1490	96.1	489	8 ADP87682	Adp87682 AMPK rat
26	1489	96.0	489	8 ADP43210	Adp43210 Mouse AMP
27	1479	95.4	489	7 ADF50312	Adf50312 Murine AM
28	1064	68.6	328	2 AAW8438	Aaw8438 Disease a
29	1064	68.6	328	4 AAB93432	Aab93432 Human pro
30	1064	68.6	328	5 AAO18496	Aao18496 Human ins
31	1064	68.6	328	8 ADP87611	Adp87611 Human NOV
32	1064	68.6	328	8 ADP87613	Adp87613 Human ins
33	1064	68.6	352	5 AAO18495	Aao18495 Human ins
34	1064	68.6	352	8 ADP43208	Adp43208 Human AMP
35	1064	68.6	414	9 ADZ80782	Adz80782 Amino aci
36	1064	68.6	569	8 ADP43207	Adp43207 Human AMP
37	1064	68.6	569	8 ADP43217	Adp43217 Human AMP
38	1064	68.6	569	9 AEB69186	Aeb69186 Human mod
39	1060	68.3	328	8 ADP87694	Adp87694 Human AMP
40	1059	68.3	328	8 ADP87615	Adp87615 Human NOV
41	1009	65.1	331	2 AAW29817	Aaw29817 Mammalian
42	1009	65.1	331	5 AAO18497	Aao18497 Human ins
43	1009	65.1	331	6 ABU04258	Abu04258 Human exp
44	1009	65.1	331	6 ABU04261	Abu04261 Human exp
45	1009	65.1	331	6 ABU04262	Abu04262 Human exp

ALIGNMENTS

RESULT 1
AAE00221
ID AAE00221 standard; protein; 305 AA.

XX AAE00221;

DT 13-JUN-2001 (first entry)

DE Human AMPK gamma subunit muscle-specific isoform, PRKAG3.

XX Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK;
KW PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;
KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;
KW cystathione beta synthase; CBS; cardiant; gene therapy.

OS Homo sapiens.

PN WO200120003-A2.

XX 22-MAR-2001.

PF 11-SEP-2000; 2000WO-EP009896.

XX 10-SEP-1999; 99EP-00402236.

PR 18-MAY-2000; 2000EP-00401388.

XX (INRG) INRA INST NAT RECH AGRONOMIQUE.

PA (ANDE/) ANDERSSON L.

PA (LOOF/) LOOFT C.

XX (KALM/) KALM E.

PI Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;

PI Tannuccelli N, Gallin J, Le Roy P, Chardon P;

DR WPI; 2001-244810/25.

XX N-PSDB; AAD03296.

PT New variants of the gamma subunit of vertebrate adenosine monophosphate-

PT activated kinase for diagnosis or treatment of disorders associated with
energy metabolism such as diabetes, obesity, and myopathy.
PS Claim 4; Page 55-57; 71pp; English.
XX The present sequence is human adenosine monophosphate (AMP)-activated
kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3. Mutation in
CC Prkag3 results in an altered regulation of carbohydrate metabolism,
particularly in skeletal muscle. PRKAG3 is useful as therapeutic for

CC treating carbohydrate metabolism disorders such as diabetes, obesity, and
 CC disorders associated with muscle metabolism such as myopathy and
 CC cardiovascular diseases, to modulate AMPK activity, and for restoring a
 CC normal AMPK function. PRKAG3 sequence and its functionally altered
 CC mutants are useful for the diagnostic evaluation, genetic testing and
 CC prognosis of a metabolic disorder, preferably a carbohydrate metabolism
 CC disorder. Primers that can detect a genetic polymorphic marker linked to
 CC a sequence encoding PRKAG3, are useful for detecting a dysfunction of
 CC carbohydrate metabolism resulting from the expression of a functionally
 CC altered allele of PRKAG3. Transgenic animal and host cell transformed
 CC with PRKAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant,
 CC are useful for screening compounds able to modulate AMPK activity.
 CC Nucleic acid encoding PRKAG3 is useful for detecting mutations in a
 CC Prkag3 gene, or in a sequence encoding the first cystathione beta
 CC synthase (CBS) domain of PRKAG3 and is useful in gene therapy
 XX
 SQ Sequence 305 AA;

Query Match 100.0%; Score 1551; DB 4; Length 305;
 Best Local Similarity 100.0%; Pred. No. 2.1e-165;
 Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRFQEHCTCYDAMATSSKLVIFDTMTLEIKKFAFFALVANGVRAAPLWDSKKQSFVGMLTIT 60
 DB 1 MRFQEHCTCYDAMATSSKLVIFDTMTLEIKKFAFFALVANGVRAAPLWDSKKQSFVGMLTIT 60
 QY 61 DFILVLRHYRSPVQIYEIQHKTWREIYLOQCCKPLVSIISPNDSLFEAVYTLIKNR 120
 DB 61 DFILVLRHYRSPVQIYEIQHKTWREIYLOQCCKPLVSIISPNDSLFEAVYTLIKNR 120
 QY 121 IHRPLVLDPVSGNVHLHILTHKRLKFLHIFGSLPRPSFLYRTQDLGIGTFRDLAVVLE 180
 DB 121 IHRPLVLDPVSGNVHLHILTHKRLKFLHIFGSLPRPSFLYRTQDLGIGTFRDLAVVLE 180
 QY 181 TAPILTALDIFVDRRSALPVVNECGVVGYSRFDVTHLAAQTYNHLDSVGEALRQR 240
 DB 181 TAPILTALDIFVDRRSALPVVNECGVVGYSRFDVTHLAAQTYNHLDSVGEALRQR 240
 QY 241 TLCLEGVLSQCPHESLGEVIDRIAREQVHRLVLDVDETHLHGVVSLSDILQALVLSPAGI 300
 DB 241 TLCLEGVLSQCPHESLGEVIDRIAREQVHRLVLDVDETHLHGVVSLSDILQALVLSPAGI 300
 QY 301 DALGA 305
 DB 301 DALGA 305

RESULT 2
 ID AAE00223 standard; protein; 464 AA.
 XX
 AC AAE00223;

DT 13-JUN-2001 (first entry)

XX Human AMPK gamma subunit muscle-specific isoform, complete PRKAG3.

XX Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK;
 KW PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;
 KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;
 KW cystathione beta synthase; CBS; cardiant; gene therapy.

XX Homo sapiens.

XX Key Location/Qualifiers
 PH 172..225
 FT Domain /label= CBS
 FT /note= "Cystathione beta synthase domain"
 FT Misc-difference 200
 FT /note= "RN- mutation site"
 FT Domain 253..307
 FT /label= CBS
 FT /note= "Cystathione beta synthase domain"

FT Domain 329..382
 FT /label= CBS
 FT /note= "Cystathione beta synthase domain"
 FT Domain 400..453
 FT /label= CBS
 FT /note= "Cystathione beta synthase domain"
 XX
 PN WO200120003-A2.
 XX 22-MAR-2001.
 XX 11-SEP-2000; 2000WO-EP009896.
 XX 10-SEP-1999; 99EP-00402236.
 PR 18-MAY-2000; 2000EP-00401388.
 XX (INRG) INRA INST NAT RECH AGRONOMIQUE.
 PA (ANDE/) ANDERSSON L.
 PA (LOOF/) LOOFT C.
 PA (KALM/) KALM E.
 XX
 PI Iannuccelli N, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;
 XX Iannuccelli N, Geillin J, Le Roy P, Chardon P;
 DR WPI: 2001-244810/25.
 DR N-PSDB; AAD03320.
 XX
 XX New variants of the gamma subunit of vertebrate adenosine monophosphate-
 FT activated kinase for diagnosis or treatment of disorders associated with
 FT energy metabolism such as diabetes, obesity, and myopathy.
 XX
 XX Claim 5; Fig 3; 71pp; English.

The present sequence is human adenosine monophosphate (AMP)-activated
 kinase (AMPK) gamma subunit muscle-specific isoform, complete PRKAG3.
 Mutation in prkag3 results in an altered regulation of carbohydrate
 metabolism, particularly in skeletal muscle. PRKAG3 is useful as
 CC therapeutic for treating carbohydrate metabolism disorders such as
 CC diabetes, obesity, and disorders associated with muscle metabolism such
 CC as myopathy and cardiovascular diseases, to modulate AMPK activity, and
 CC for restoring a normal AMPK function. PRKAG3 sequence and its
 CC functionally altered mutants are useful for the diagnostic evaluation,
 CC genetic testing and prognosis of a metabolic disorder, preferably a
 CC polymorphic marker linked to a sequence encoding PRKAG3 are useful for
 CC detecting a dysfunction of carbohydrate metabolism resulting from the
 CC expression of a functionally altered allele of PRKAG3. Transgenic animal
 CC and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting
 CC of PRKAG3 or its mutant, are useful for screening compounds able to
 CC modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for
 CC detecting mutations in a Prkag3 gene, or in a sequence encoding the first
 CC cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene
 CC therapy
 XX
 SQ Sequence 464 AA;

Query Match 100.0%; Score 1551; DB 4; Length 464;
 Best Local Similarity 100.0%; Pred. No. 3.8e-165;
 Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRFQEHCTCYDAMATSSKLVIFDTMTLEIKKFAFFALVANGVRAAPLWDSKKQSFVGMLTIT 60
 DB 160 MRFQEHCTCYDAMATSSKLVIFDTMTLEIKKFAFFALVANGVRAAPLWDSKKQSFVGMLTIT 219
 QY 61 DFILVLRHYRSPVQIYEIQHKTWREIYLOQCCKPLVSIISPNDSLFEAVYTLIKNR 120
 DB 220 DFILVLRHYRSPVQIYEIQHKTWREIYLOQCCKPLVSIISPNDSLFEAVYTLIKNR 279
 QY 121 IHRPLVLDPVSGNVHLHILTHKRLKFLHIFGSLPRPSFLYRTQDLGIGTFRDLAVVLE 180
 DB 280 IHRPLVLDPVSGNVHLHILTHKRLKFLHIFGSLPRPSFLYRTQDLGIGTFRDLAVVLE 339
 QY 181 TAPILTALDIFVDRRSALPVVNECGVVGYSRFDVTHLAAQTYNHLDSVGEALRQR 240

Db	340	TAPILTALDIFVDRRSALPVNCGVGLYSRFDVHLAAQOTYNHLDMSVGEALRQR	399		
Qy	241	TLCLGVLSQPHESLGEVIDRIAREQVHRLVLVDETOHLLGVVSLSDILQALVLSPAGI	300		
Db	400	TLCLGVLSQPHESLGEVIDRIAREQVHRLVLVDETOHLLGVVSLSDILQALVLSPAGI	459		
Qy	301	DALGA 305			
Db	460	DALGA 464			
RESULT 3					
ID	ADP43223	standard; protein; 464 AA.			
XX	AC	ADP43223;			
DT	09-SEP-2004	(first entry)			
XX	DE	Human AMPK gamma-3 subunit.			
XX	KW	Cardiovascular; neuroprotective; dermatological; cytostatic;			
KW	KW	AMPK modulator; AMPK agonist; gene therapy;			
KW	KW	adenosine monophosphate-activated protein kinase; AMPK;			
KW	KW	cardiovascular disorder; neurological disorder; metabolic disorder;			
KW	KW	dermatological disorder; neoplastic disorder; age-associated disorder;			
KW	KW	geriatric disorder.			
OS	XX	Homo sapiens.			
XX	PN	WO2004050898-A2.			
XX	PD	17-JUN-2004.			
XX	PF	04-DEC-2003; 2003WO-US038628.			
XX	PR	04-DEC-2002; 2002US-0430804P.			
XX	PR	18-JUL-2003; 2003US-0488261P.			
XX	PA	(ELIX-) ELIXIR PHARM INC.			
XX	PI	Apfeld J, O'Connor G;			
XX	DR	WPI; 2004-450740/42.			
XX	PT	Evaluating a compound, useful for treating e.g., age-related disorder,			
PT	PT	comprises contacting a polypeptide at least 85% identical to e.g., alpha			
PT	PT	adenosine monophosphate-activated protein kinase (AMPK) subunit with a			
XX	XX	test compound.			
PS	PS	Disclosure; SEQ ID NO 26; 160pp; English.			
XX	CC	The invention relates to a method of evaluating a compound by contacting			
CC	CC	a polypeptide comprising a sequence at least 85% identical to alpha, beta			
CC	CC	or gamma adenosine monophosphate-activated protein kinase (AMPK) subunit			
CC	CC	or a functional domain in vitro with a test compound, evaluating			
CC	CC	interaction between compound and polypeptide, contacting a cell or			
CC	CC	organism that produces the polypeptide with test compound, and evaluating			
CC	CC	a rate of aging of the cell or organism. A method comprising providing a			
CC	CC	modulator of the AMPK pathway to the subject is useful for treating or			
CC	CC	preventing a disease or disorder in a subject, preferably a			
CC	CC	cardiovascular disorder, a neurological disorder, a metabolic disorder, a			
CC	CC	dermatological disorder, a neoplastic disorder, an age-associated			
CC	CC	disorder, or a geriatric disorder. A compound that alters the expression			
CC	CC	or activity of an AMPK pathway component is useful for altering lifespan			
CC	CC	regulation in a cell or organism. This sequence represent a protein			
CC	CC	sequence of an AMPK pathway member or its homologue used in the method of			
CC	CC	the invention.			
XX	XX	Sequence 464 AA;			
SQ	XX	Query Match	100.0%;	Score 1551;	DB 8; Length 464;

Best Local Similarity 100.0%; Pred. No. 3.8e-165;					
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1	MRFMQHTCYDANATSKLVIFDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMLTIT	60		
Db	160	MRFMQHTCYDANATSKLVIFDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMLTIT	219		
Qy	61	DFILVLRHYRSPVQIYEIEQHKIETWREIYLGQCFKPLVSI SPNDSLFEAVVTLIKNR	120		
Db	220	DFILVLRHYRSPVQIYEIEQHKIETWREIYLGQCFKPLVSI SPNDSLFEAVVTLIKNR	279		
Qy	121	IHRLPVLDPVSGNVHLTHKRLKFLHIFGSLPRPSFLYRTIQDIGTFRDLAVVLE	180		
Db	280	IHRLPVLDPVSGNVHLTHKRLKFLHIFGSLPRPSFLYRTIQDIGTFRDLAVVLE	339		
Qy	181	TAPILTALDIFVDRRSALPVNCGVGLYSRFDVHLAAQOTYNHLDMSVGEALRQR	240		
Db	340	TAPILTALDIFVDRRSALPVNCGVGLYSRFDVHLAAQOTYNHLDMSVGEALRQR	399		
Qy	241	TLCLGVLSQPHESLGEVIDRIAREQVHRLVLVDETOHLLGVVSLSDILQALVLSPAGI	300		
Db	400	TLCLGVLSQPHESLGEVIDRIAREQVHRLVLVDETOHLLGVVSLSDILQALVLSPAGI	459		
Qy	301	DALGA 305			
Db	460	DALGA 464			
RESULT 4					
AAB47679	ID	AAB47679	standard; protein; 489 AA.		
XX	AC	AAB47679;			
DT	21-JAN-2002	(first entry)			
XX	DE	PRKAG3.			
XX	KW	Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant;			
KW	KW	metabolic disease; diabetes; obesity; substitution; ss.			
XX	OS	Homo sapiens.			
XX	Key	Location/Qualifiers			
FT	FT	Misc-difference 71			
FT	FT	/note= "Possible variation point P71A"			
FT	FT	Misc-difference 340			
FT	FT	/note= "Possible variation point R340W"			
XX	PN	WO200177305-A2.			
XX	PD	18-OCT-2001.			
XX	PF	06-APR-2001; 2001WO-SB000765.			
XX	PR	07-APR-2000; 2000US-0195665P.			
XX	PA	(AREX-) AREXIS AB.			
XX	XX	Andersson L, Luthman H, Marklund S;			
XX	XX	WPI; 2001-657170/75.			
XX	XX	N-PSDB; AAH43685.			
XX	XX	New variants of human AMP-activated protein kinase gamma3 subunit			
PT	PT	associated with a metabolic disease e.g. diabetes or obesity and method			
PT	PT	for determining a risk estimate of diseases in subject by detecting the			
PT	PT	variant.			
XX	PS	Disclosure; Fig 5; 25pp; English.			
XX	CC	This sequence is encoded by the full length cDNA encoding the human AMP-			
CC	CC	activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence			

CC of the PRXAG3 DNA, or a variant, is useful in determining a risk estimate
CC of a metabolic disease, such as diabetes or obesity, in a subject. The
CC variation may occur in exons 3, 4 or 10. In exon 3 variation may be a
CC substitution of a G for a C at nucleotide 320, resulting in the amino
CC acid substitution P71A; in exon 4 variation may be a substitution of a T
CC for a C at nucleotide 550; and in exon 10 variation may be a substitution
CC of a T for a C at nucleotide 1037, resulting in the amino acid
CC substitution R340W. There may also be nucleotide variation in intron 6.
CC The numbering of these variations is based on the full length cDNA,
CC rather than on position 1 of the open reading frame

XX Sequence 489 AA;

Query Match 100.0%; Score 1551; DB 4; Length 489;
Best Local Similarity 100.0%; Pred. No. 4.1e-165;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRFQEHCTCYDAMATSSKLVIFDTMLEIKKAPFAFVANGVRAAPLWDSKKQSFVGMLTIT 60
DB 185 MRFQEHCTCYDAMATSSKLVIFDTMLEIKKAPFAFVANGVRAAPLWDSKKQSFVGMLTIT 244
QY 61 DFILVLHRYRSPVQIYEIEQHKIETWREIYLQGCFFKPLVSI SPNDSLFEAVYTLIKNR 120
DB 245 DFILVLHRYRSPVQIYEIEQHKIETWREIYLQGCFFKPLVSI SPNDSLFEAVYTLIKNR 304
QY 121 IHRPLVLPDVPVSGNVHLHILTHKRLKFLHIFGSLPRPSFLYRTIQDLIGTFRDLAVLLE 180
DB 305 IHRPLVLPDVPVSGNVHLHILTHKRLKFLHIFGSLPRPSFLYRTIQDLIGTFRDLAVLLE 364
QY 181 TAPILTALDIFDVRVSLPVPVNEGQVVGYSRFDVHLAAQQTYNHLDMSVGEALRQR 240
DB 365 TAPILTALDIFDVRVSLPVPVNEGQVVGYSRFDVHLAAQQTYNHLDMSVGEALRQR 424
QY 241 TLCLEGVLSQCPHESLGEVIDRIAREQVHRLVLDVETQHLGWSLSLDILQALVLSPAGI 300
DB 425 TLCLEGVLSQCPHESLGEVIDRIAREQVHRLVLDVETQHLGWSLSLDILQALVLSPAGI 484
QY 301 DALGA 305
DB 485 DALGA 489

RESULT 5

ID AAE32034 standard; protein; 489 AA.

AC AAE32034;

DT 24-MAR-2003 (first entry)

XX Human kinase and phosphatase (KPP)-15.

XX Human; kinase and phosphatase; KPP; cardiovascular; hypertension;
KW myocardial infarction; angina pectoris; Alzheimer's disease; epilepsy;
KW acquired immune deficiency syndrome; AIDS; Grave's disease; diabetes;
KW neurological; Parkinson's disease; cirrhosis; psoriasis; gene therapy;
KW hypercholesterolaemia; anticonvulsant; hepatotropic; lipid myopathy;
KW cell proliferative disorder; cancer; cardiac; neuroprotective; enzyme;
KW nootropic; ophthalmological; anorectic; cytostatic; cataract; obesity.
OS Homo sapiens.

XX Key Location/Qualifiers
FH 197..251
FT Domain /note="CBS domain"
FT Domain 204..226
FT Domain /note="Transmembrane domain"
FT Domain 278..332
FT Domain /note="CBS domain"
FT Domain 353..406
FT Domain /note="CBS domain"
FT Domain 425..478
FT Domain /note="CBS domain"

XX WO200283709-A2.
PN 24-OCT-2002.
XX 05-APR-2002; 2002WO-US010818.
XX 06-APR-2001; 2001US-0282119P.
PR 13-APR-2001; 2001US-0283588P.
PR 13-APR-2001; 2001US-0283759P.
PR 20-APR-2001; 2001US-0285589P.
PR 27-APR-2001; 2001US-0287036P.
PR 27-APR-2001; 2001US-0287037P.
PR 04-MAY-2001; 2001US-0286080P.
PR 04-MAY-2001; 2001US-0288712P.
PR 09-MAY-2001; 2001US-0289909P.
PR 17-MAY-2001; 2001US-0292246P.
XX (INCY-) INCYTE GENOMICS INC.

XX Recipon SA, Burrill JD, Marcus GA, Zingler KA, Tang YT;
XX Thornton M, Borowsky ML, Baughn MR, Burford N, Lee SY, Bandman O;
XX Hafalia AJA, Yao MG, Rankumar J, Wallia NK, Lu DAM, Arvizu CS;
XX Ison CH, Ding L, Lu Y, Gururajan R, Walsh RT, Gandhi AR;
XX Swarnakar A, Forsythe IJ, Yue H, Au-Young JK, Elliott VS, Lee S;
XX WPI; 2003-092995/08.
DR N-PSDB; AAD49456.

XX New human kinases and phosphatases (KPP), useful for diagnosing, treating
XX and preventing diseases or conditions associated with the aberrant KPP
XX expression, e.g. hypertension, cancer, AIDS, diabetes, cataract,
XX psoriasis, obesity.

XX Claim 1; Page 176-178; 195pp; English.

XX The invention relates to human kinases and phosphatases (KPP), and their
XX corresponding nucleic acids. The polypeptides and polynucleotides of the
XX invention are useful in diagnosing, treating and preventing diseases or
XX conditions associated with the decreased expression or overexpression of
XX KPP, such as cardiovascular (e.g. hypertension, myocardial infarction,
XX angina pectoris), immune (e.g. acquired immune deficiency syndrome
XX (AIDS), Grave's disease, diabetes), neurological (e.g. Parkinson's
XX disease, Alzheimer's disease, epilepsy), disorders affecting growth and
XX development (e.g. cirrhosis, psoriasis, cataract), lipid (e.g.
XX hypercholesterolaemia, obesity, lipid myopathies), cell proliferative
XX disorders, or cancer. They are also useful in assessing the effects of
XX exogenous compounds on the expression of nucleic acid and amino acid
XX sequences of KPP. The KPP or its fragments are useful in screening
XX compounds for effectiveness as agonist or antagonist of the polypeptides,
XX or in altering the expression of the target polynucleotide and compounds
XX that specifically bind to or modulate the activity of the polypeptide.
XX The microarray is useful in monitoring or measuring protein-protein
XX interactions, drug-target interactions, and gene expression profiles. KPP
XX DNA is used in gene therapy. The present sequence is human KPP protein

XX Sequence 489 AA;

Query Match 100.0%; Score 1551; DB 6; Length 489;
Best Local Similarity 100.0%; Pred. No. 4.1e-165;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRFQEHCTCYDAMATSSKLVIFDTMLEIKKAPFAFVANGVRAAPLWDSKKQSFVGMLTIT 60
DB 185 MRFQEHCTCYDAMATSSKLVIFDTMLEIKKAPFAFVANGVRAAPLWDSKKQSFVGMLTIT 244
QY 61 DFILVLHRYRSPVQIYEIEQHKIETWREIYLQGCFFKPLVSI SPNDSLFEAVYTLIKNR 120
DB 245 DFILVLHRYRSPVQIYEIEQHKIETWREIYLQGCFFKPLVSI SPNDSLFEAVYTLIKNR 304
QY 121 IHRPLVLPDVPVSGNVHLHILTHKRLKFLHIFGSLPRPSFLYRTIQDLIGTFRDLAVLLE 180
DB 305 IHRPLVLPDVPVSGNVHLHILTHKRLKFLHIFGSLPRPSFLYRTIQDLIGTFRDLAVLLE 364

QY 181 TAPILTALDIFVDRVSALPVNCGQVGLYSRFDVHLAAQTYNHLDMVSVEALRQR 240
 DB 365 TAPILTALDIFVDRVSALPVNCGQVGLYSRFDVHLAAQTYNHLDMVSVEALRQR 424
 QY 241 TACLEGVLSQPHESLGEVIDRIAREQVHRLVLDVDETHLGLVVSLSDIQALVLSGAGI 300
 DB 425 TACLEGVLSQPHESLGEVIDRIAREQVHRLVLDVDETHLGLVVSLSDIQALVLSGAGI 484
 QY 301 DALGA 305
 DB 485 DALGA 489

RESULT 6
 ID ADF50310 standard; protein; 489 AA.
 AC ADF50310;
 XX 12-FEB-2004 (first entry)
 DT Human AMP-activated protein kinase (AMPK)-gamma 3 protein subunit.
 DE human; transgenic; AMP-activated protein kinase gamma 3 subunit; Prkg3;
 KW AMPK; energy metabolism; obesity; dyslipidaemia;
 KW insulin resistance syndrome; type 2 diabetes; antidiabetic; anorectic;
 KW antilipaeic.
 XX Homo sapiens.
 OS
 XX
 PN WO2003063586-A1.
 XX
 PD 07-AUG-2003.
 XX
 XX 31-JAN-2003; 2003WO-IB000912.
 PF
 XX
 PR 01-FEB-2002; 2002US-0353430P.
 XX
 PA (AREX-) AREXIS AB.
 XX
 XX Andersson L, Marklund S;
 XX WPI; 2003-663404/62.
 DR N-PSDB; ADF50309.
 XX
 XX New transgenic non-human animals expressing an AMP-activated protein
 PT kinase gamma 3 subunit, useful as models for improving treatment,
 PT prevention or diagnosis of diseases related to energy metabolism, e.g.
 PT obesity or type 2 diabetes.
 XX
 PS Claim 3; SEQ ID NO 2; 46pp; English.
 XX
 CC This invention relates to novel transgenic non-human animals expressing
 CC an AMP-activated protein kinase (AMPK)-gamma 3 subunit. Specifically, it
 CC relates to the transgene Prkg3 gene that encodes the AMPK gamma3 subunit
 CC or a variant thereof, where the nucleic acid is operably linked to a
 CC regulatory element. AMPK is involved in the regulation of energy
 CC metabolism in eukaryotic cells, and is recognised as a major regulator of
 CC lipid biosynthetic pathways due to its role in the phosphorylation and
 CC inactivation of key enzymes such as acetyl-CoA carboxylase. The present
 CC invention describes transgenic animals expressing AMPK-gamma 3 to be used
 CC as models for energy metabolism diseases and also methods for the
 CC development of drugs for the treatment or prevention of obesity,
 CC dyslipidaemia, insulin resistance syndrome or type 2 diabetes.
 CC Accordingly, the compositions of this invention have various activities
 CC including antidiabetic, anorectic and antilipaeic. This polypeptide
 CC sequence is the human AMPK-gamma3 protein subunit of the invention.
 XX
 SQ Sequence 489 AA;

Query Match 100.0%; Score 1551; DB 7; Length 489;
 Best Local Similarity 100.0%; Pred. No. 4.1e-165;

Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRFWQHTCYDAMATSKLVIFDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMLTIT 60
 DB 185 MRFWQHTCYDAMATSKLVIFDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMLTIT 244
 QY 61 DFILVHRYRSPVQIYEIEQHKIETWREIYLGQCFKPLVSPNDSLFEAVVTLIKNR 120
 DB 245 DFILVHRYRSPVQIYEIEQHKIETWREIYLGQCFKPLVSPNDSLFEAVVTLIKNR 304
 QY 121 IHRPLVLDPVSGNVLHILTKRLKFLHIFGSLPRPSFLYRTODIGIGTFDLAVVLE 180
 DB 305 IHRPLVLDPVSGNVLHILTKRLKFLHIFGSLPRPSFLYRTODIGIGTFDLAVVLE 364
 QY 181 TAPILTALDIFVDRVSALPVNCGQVGLYSRFDVHLAAQTYNHLDMVSVEALRQR 240
 DB 365 TAPILTALDIFVDRVSALPVNCGQVGLYSRFDVHLAAQTYNHLDMVSVEALRQR 424
 QY 241 TACLEGVLSQPHESLGEVIDRIAREQVHRLVLDVDETHLGLVVSLSDIQALVLSGAGI 300
 DB 425 TACLEGVLSQPHESLGEVIDRIAREQVHRLVLDVDETHLGLVVSLSDIQALVLSGAGI 484
 QY 301 DALGA 305
 DB 485 DALGA 489

RESULT 7
 ID ADP87617 standard; protein; 489 AA.
 AC ADP87617;
 XX 23-SEP-2004 (first entry)
 DT Human NOVX polypeptide, NOV10a.
 DE anorectic; antidiabetic; gene therapy; vaccine; obesity; diabetes;
 KW insulin resistance; hybridization probe; chromosome mapping;
 KW tissue typing; preventive medicine; pharmacogenomics; NOVX; human.
 XX Homo sapiens.
 OS
 XX WO2004056961-A2.
 PN 08-JUL-2004.
 PD
 XX 27-OCT-2003; 2003WO-US034114.
 PF
 XX 25-OCT-2002; 2002US-0421239P.
 PR 28-OCT-2002; 2002US-0421700P.
 PR 31-OCT-2002; 2002US-042276P.
 PR 13-NOV-2002; 2002US-042619P.
 PR 20-DEC-2002; 2002US-0435498P.
 PR 20-DEC-2002; 2002US-0435510P.
 PR 21-MAR-2003; 2003US-0456812P.
 XX (CURA-) CURAGEN CORP.
 PA
 XX Berghs C, Catterton E, Ellerman K, Ort T, Rieger D, Chaudhuri A;
 PI WPI; 2004-500293/47.
 XX N-PSDB; ADP87616.
 DR
 XX New NOVX nucleic acid molecules and polypeptides useful for preventing or
 PT treating NOVX-associated disorders, e.g. diabetes, insulin resistance or
 PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
 XX
 PS Claim 3; SEQ ID NO 74; 570pp; English.
 XX
 CC The invention relates to a novel isolated nucleic acid molecule
 CC comprising any of the nucleotide sequences (e.g. 3634, 2127 or 2120 base

CC pairs) fully defined in the specification; or encodes any of the amino
CC acid sequences (e.g. 698, 702 or 709 amino acids) fully defined in the
CC specification. The invention further comprises: an isolated polypeptide
CC comprising any of the amino acid sequences cited above; a method for
CC identifying compounds that modulate target polypeptide activity; an
CC antibody that immunospecifically binds to the target polypeptide, where
CC the target polypeptide comprises any of the above-mentioned amino acid
CC sequences, an amino acid sequence that is at least 95% identical to the
CC above amino acid sequences, an amino acid sequence of at least one domain
CC of the above-mentioned amino acid sequences, or an amino acid sequence
CC that is at least 95% identical to the domain of the above amino acid
CC sequences; a method for identifying a potential therapeutic agent for use
CC in treatment of a pathology, where the pathology is related to aberrant
CC expression or aberrant physiological interactions of a target polypeptide
CC; and a method of screening for a modulator of activity of or of latency
CC or predisposition to a pathology associated with a target polypeptide.
CC The modulating compounds have anorectic and antidiabetic activities. The
CC nucleic acid sequences of the invention may be used in gene therapy to
CC treat disorders. The proteins of the invention may be used in creating a
CC vaccine. The composition and methods are useful for identifying compounds
CC that modulate protein activity or for diagnosing, preventing or treating
CC diverse pathological conditions, such as obesity, diabetes or insulin
CC resistance. The nucleic acids are also used as hybridization probes, in
CC chromosome mapping, tissue typing, preventive medicine, and
CC pharmacogenomics. This sequence represents a NOVX polypeptide of the
CC invention.

XX SQ Sequence 489 AA;

Query Match 100.0%; Score 1551; DB 8; Length 489;
Best Local Similarity 100.0%; Pred. No. 4.1e-165;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRFQEHCTCYDAMATSSKLVIFDTWLEIKKFAFFALVANGVRAAPLWDSKKQSFVGMLTIT 60
DB 185 MRFQEHCTCYDAMATSSKLVIFDTWLEIKKFAFFALVANGVRAAPLWDSKKQSFVGMLTIT 244
QY 61 DFILVLHRYRSPVQVIEIQHKTWREIYLOGCFKPLVSI SPNDSLFAVYTLIKNR 120
DB 245 DFILVLHRYRSPVQVIEIQHKTWREIYLOGCFKPLVSI SPNDSLFAVYTLIKNR 304
QY 121 IHRPLVLPDPVSGNVHLTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 180
DB 305 IHRPLVLPDPVSGNVHLTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 364
QY 181 TAPILTALDIFDVRVSALPVVNECGVVGYSRFDVHLAAQQTYNHLDMSVGEALRQR 240
DB 365 TAPILTALDIFDVRVSALPVVNECGVVGYSRFDVHLAAQQTYNHLDMSVGEALRQR 424
QY 241 TLCLEGVLSQCPHESLGEVIDRIAREQVHRLVLDVDETOHLLGVVSLSDILOALVLSGPI 300
DB 425 TLCLEGVLSQCPHESLGEVIDRIAREQVHRLVLDVDETOHLLGVVSLSDILOALVLSGPI 484
QY 301 DALGA 305
DB 485 DALGA 489

RESULT 8
AAE00329
ID AAE00329 standard; protein; 305 AA.

XX AAE00329;
AC
XX
DT 13-JUN-2001 (first entry)
XX
DE Human Prkag3 V401 mutant.
XX Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK;
KW PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;
KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;
KW cystathione beta synthase; CBS; cardiac; gene therapy; mutant; mutein;
KW variant.

XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Misc-difference 40
FT FT /note= "Wild-type Val substituted with Ile"
XX
XX WO200120003-A2.
XX 22-MAR-2001.
XX 11-SEP-2000; 2000WO-EP009896.
XX 10-SEP-1999; 99EP-00402236.
XX 18-MAY-2000; 2000EP-00401388.
XX (INRG) INRA INST NAT RECH AGRONOMIQUE.
XX (ANDE/) ANDERSSON L.
XX (LOOF/) LOOFT C.
XX (KALM/) KALM E.
XX Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;
XX Iannuccelli N, Gellin J, Le Roy P, Chardon P;
XX WPI; 2001-244810/25.
XX New variants of the gamma subunit of vertebrate adenosine monophosphate-
XX activated kinase for diagnosis or treatment of disorders associated with
XX energy metabolism such as diabetes, obesity, and myopathy.
XX Disclosure; Page; 71pp; English.
XX The present sequence is a V401 mutant of human muscle-specific isoform of
XX gamma subunit of adenosine monophosphate (AMP)-activated kinase (AMPK)
XX Prkag3. This mutant sequence results in decreased glycogen content in
XX human skeletal muscle. Mutation in Prkag3 results in an altered
XX regulation of carbohydrate metabolism, particularly in skeletal muscle.
XX PRKAG3 is useful as therapeutic for treating carbohydrate metabolism
XX disorders such as diabetes, obesity, and disorders associated with muscle
XX metabolism such as myopathy and cardiovascular diseases, to modulate AMPK
XX activity, and for restoring a normal AMPK function. PRKAG3 sequence and
XX its functionally altered mutants are useful for the diagnostic
XX evaluation, genetic testing and prognosis of a metabolic disorder,
XX preferably a carbohydrate metabolism disorder. Primers that can detect a
XX genetic polymorphic marker linked to a sequence encoding PRKAG3, are
XX useful for detecting a dysfunction of carbohydrate metabolism resulting
XX from the expression of a functionally altered allele of PRKAG3.
XX Transgenic animal and host cell transformed with PRKAG3 or a
XX heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for
XX screening compounds able to modulate AMPK activity. Nucleic acid encoding
XX PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a
XX sequence encoding the first cystathione beta synthase (CBS) domain of
XX PRKAG3 and is useful in gene therapy. Note: The present sequence is not
XX shown in the specification, but is derived from the human Prkag3 sequence
XX SEQ.ID.NO.4 shown in page 57-58 of sequence listing (AAE00221)
XX
XX Sequence 305 AA;

Query Match 99.9%; Score 1550; DB 4; Length 305;
Best Local Similarity 99.7%; Pred. No. 2.7e-165;
Matches 304; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRFQEHCTCYDAMATSSKLVIFDTWLEIKKFAFFALVANGVRAAPLWDSKKQSFVGMLTIT 60
DB 1 MRFQEHCTCYDAMATSSKLVIFDTWLEIKKFAFFALVANGVRAAPLWDSKKQSFVGMLTIT 60
QY 61 DFILVLHRYRSPVQVIEIQHKTWREIYLOGCFKPLVSI SPNDSLFAVYTLIKNR 120
DB 61 DFILVLHRYRSPVQVIEIQHKTWREIYLOGCFKPLVSI SPNDSLFAVYTLIKNR 120
QY 121 IHRPLVLPDPVSGNVHLTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 180
DB 121 IHRPLVLPDPVSGNVHLTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 180

QY 181 TAPILTALDIFVDRVSALPVNNECGVGVGLYSRFDVHLAAQTYNHLDMVSGEALRQR 240
 DB 181 TAPILTALDIFVDRVSALPVNNECGVGVGLYSRFDVHLAAQTYNHLDMVSGEALRQR 240
 QY 241 TLCLEGVLSQCPHESLGEVIDRIAREQVHRLVLDVDETOHLLGVVSLSDILQALVLSPAGI 300
 DB 241 TLCLEGVLSQCPHESLGEVIDRIAREQVHRLVLDVDETOHLLGVVSLSDILQALVLSPAGI 300
 QY 301 DALGA 305
 DB 301 DALGA 305

RESULT 9
 ID AAE00328
 XX AAE00328 standard; protein; 305 AA.

AC AAE00328;

DT 13-JUN-2001 (first entry)

XX Human Prkag3 R41Q mutant.

XX Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK;
 KW Prkag3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;
 KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;
 KW cystathione beta synthase; CBS; cardiant; gene therapy; mutant; mutein;
 KW variant.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT Misc-difference 41 /note= "Wild-type Arg substituted with Gln"

XX WO200120003-A2.

XX 22-MAR-2001.

XX 11-SEP-2000; 2000WO-EP009896.

XX 10-SEP-1999; 99EP-00402236.

XX 18-MAY-2000; 2000EP-00401388.

XX (INRG) INRA INST NAT RECH AGRONOMIQUE.
 PA (ANDE/) ANDERSSON L.
 PA (LOOF/) LOOFT C.
 PA (KALM/) KALM E.

XX Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;
 PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;

XX WPI; 2001-244810/25.

XX New variants of the gamma subunit of vertebrate adenosine monophosphate-
 FT activated kinase for diagnosis or treatment of disorders associated with
 FT energy metabolism such as diabetes, obesity, and myopathy.

XX Disclosure; Page: 71pp; English.

XX The present sequence is a R41Q mutant of human muscle-specific isoform of
 CC gamma subunit of adenosine monophosphate (AMP)-activated kinase (AMPK)
 CC Prkag3. This mutant sequence results in increased glycogen content in
 CC human skeletal muscle. Mutation in Prkag3 results in an altered
 CC regulation of carbohydrate metabolism, particularly in skeletal muscle.
 CC Prkag3 is useful as therapeutic for treating carbohydrate metabolism
 CC disorders such as diabetes, obesity, and disorders associated with muscle
 CC metabolism such as myopathy and cardiovascular diseases, to modulate AMPK
 CC activity, and for restoring a normal AMPK function. Prkag3 sequence and
 CC its functionally altered mutants are useful for the diagnostic
 CC evaluation, genetic testing and prognosis of a metabolic disorder,
 CC preferably a carbohydrate metabolism disorder. Primers that can detect a

CC genetic polymorphic marker linked to a sequence encoding PRKAG3, are
 CC useful for detecting a dysfunction of carbohydrate metabolism resulting
 CC from the expression of a functionally altered allele of PRKAG3.
 CC Transgenic animal and host cell transformed with PRKAG3 or a
 CC heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for
 CC screening compounds able to modulate AMPK activity. Nucleic acid encoding
 CC PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a
 CC sequence encoding the first cystathione beta synthase (CBS) domain of
 CC PRKAG3 and is useful in gene therapy. Note: The present sequence is not
 CC shown in the specification, but is derived from the human Prkag3 sequence
 CC SEQ.ID.NO.4 shown in page 57-58 of sequence listing (AAE00221)

XX SQ Sequence 305 AA;

Query Match 99.7%; Score 1547; DB 4; Length 305;
 Best Local Similarity 99.7%; Pred. No. 5.9e-165;
 Matches 304; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRFMQEHTCYDAMATSSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMILTIT 60
 DB 1 MRFMQEHTCYDAMATSSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMILTIT 60
 QY 61 DFILVLRHYRSPVLQIYEIEQHKIETWREIYLOGCFKPLVSLSPNDSLFEAVVTLIKNR 120
 DB 61 DFILVLRHYRSPVLQIYEIEQHKIETWREIYLOGCFKPLVSLSPNDSLFEAVVTLIKNR 120
 QY 121 IHRPLVLDPVSGNVHLHTKRLKFLHIFGSLLPSPFLYRTIQDLGIGTFRDLAVVLE 180
 DB 121 IHRPLVLDPVSGNVHLHTKRLKFLHIFGSLLPSPFLYRTIQDLGIGTFRDLAVVLE 180
 QY 181 TAPILTALDIFVDRVSALPVNNECGVGVGLYSRFDVHLAAQTYNHLDMVSGEALRQR 240
 DB 181 TAPILTALDIFVDRVSALPVNNECGVGVGLYSRFDVHLAAQTYNHLDMVSGEALRQR 240
 QY 241 TLCLEGVLSQCPHESLGEVIDRIAREQVHRLVLDVDETOHLLGVVSLSDILQALVLSPAGI 300
 DB 241 TLCLEGVLSQCPHESLGEVIDRIAREQVHRLVLDVDETOHLLGVVSLSDILQALVLSPAGI 300
 QY 301 DALGA 305
 DB 301 DALGA 305

RESULT 10

ABP43929
 ID ABP43929 standard; protein; 489 AA.

XX AC ABP43929;

XX 26-FEB-2003 (first entry)

XX AMP activated protein kinase gamma 3 subunit.

XX Neuroprotective; immunomodulator; cancer; chromosome 2; cytostatic;
 KW anti-inflammatory; gene therapy; nutritional supplement; wound; burn;
 KW ulcer; Alzheimer's disease; Huntington's disease;
 KW amyotrophic lateral sclerosis; autoimmune disorder; inflammation;
 KW vulnery.

XX Homo sapiens.

XX WO200231111-A2.

XX 18-APR-2002.

XX 11-OCT-2001; 2001WO-US027760.

XX 12-OCT-2000; 2000US-00687527.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
 PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;

XX	DR	WPI; 2002-426278/45.
XX	DR	N-PSDB; ABQ61173.
XX	XX	
PT	XX	New polypeptides and their encoded proteins, useful as nutritional
PT	XX	sources or supplements, or in gene therapy, particularly for treating
PT	XX	wounds, Alzheimer's disease, amyotrophic lateral sclerosis, cancer or
PT	XX	inflammation.
XX	XX	
PS	XX	Claim 20; SEQ ID # 832; 357pp + Sequence Listing; English.
XX	XX	
CC	XX	The invention relates to 446 newly isolated polynucleotide sequences. The
CC	XX	activity of polynucleotides of the invention may be described as,
CC	XX	vulnerable, neuroprotective, immunomodulator, cytostatic and anti-
CC	XX	inflammatory. Compositions comprising nucleic acids of the invention are
CC	XX	useful for treating a mammalian subject, or as nutritional sources or
CC	XX	supplements. These are useful in gene therapy, particularly for treating
CC	XX	wounds, burns or ulcers, Alzheimer's disease, Huntington's disease,
CC	XX	amyotrophic lateral sclerosis, autoimmune disorders, cancer or
CC	XX	inflammation. The nucleic acids and polypeptides are also useful in
CC	XX	diagnostic and research methods. The sequences given in records ABP43544-
CC	XX	ABP43989 represent polypeptides encoded by polynucleotides of the
CC	XX	invention. NOTE: The sequence data for this patent did not form part of
CC	XX	the printed specification, but was obtained in electronic format directly
CC	XX	from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX	XX	
SQ	XX	Sequence 489 AA;
Query Match 99.5%; Score 1544; DB 5; Length 489;		
Best Local Similarity 99.3%; Pred. No. 2.5e-164; Indels 0; Gaps 0;		
Matches 303; Conservative 2; Mismatches 0;		
Qy	1	MRFQEHCTCYDAMATSSKLVIFDTMLTKKFAFFALVANGVRAAPLWDSKKQSFVGMLTIT 60
Db	185	NRFFIEHTCYDAMATSSKLVIFDTMLTKKFAFFALVANGVRAAPLWDSKKQSFVGMLTIT 244
Qy	61	DFILVLRHYRSPLVQIYEIEQHKIETWREIYLOGCFKPLVSI SPNDSLFEAVVTLIKNR 120
Db	245	DFILVLRHYRSPLVQIYEIEQHKIETWREIYLOGCFKPLVSI SPNDSLFEAVVTLIKNR 304
Qy	121	IHRPLVDPVSGNVHLHTHKKLLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 180
Db	305	IHRPLVDPVSGNVHLHTHKKLLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 364
Qy	181	TAPILTALDIFVDRVSALPVVNECGQVVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQR 240
Db	365	TAPILTALDIFVDRVSALPVVNECGQVVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQR 424
Qy	241	TLCLEGVLSQPHESLGEVIDRIAREQVHRLVLDVDETOHLLGVVSLSDIQLVLSPAGI 300
Db	425	TLCLEGVLSQPHESLGEVIDRIAREQVHRLVLDVDETOHLLGVVSLSDIQLVLSPAGI 484
Qy	301	DALGA 305
Db	485	DALGA 489
RESULT 11		
AAE38410		
ID	AAE38410	standard; protein; 489 AA.
XX	AC	AAE38410;
XX	AC	
XX	XX	20-NOV-2003 (first entry)
DT	DT	
XX	XX	Human Prkag3 protein.
DE	XX	
XX	XX	Human; Prkag3; transcription; therapy; prevention; energy metabolism;
KW	KW	obesity; dyslipidaemia; insulin resistance syndrome; type II diabetes;
KW	KW	anorectic; antilipaemic; antidiabetic.
XX	XX	
OS	XX	Homo sapiens.
XX	XX	
PN	XX	WO2003064465-A2.
XX	XX	
PD	XX	07-AUG-2003.
XX	XX	
PF	XX	31-JAN-2003; 2003WO-IB000762.
XX	XX	
PR	XX	01-FEB-2002; 2002US-0353429P.
XX	XX	
PA	XX	(AREX-) AREXIS AB.
XX	XX	
PI	XX	Svensson T;
XX	XX	
DR	XX	WPI; 2003-636796/60.
DR	XX	N-PSDB; AAD58250.
XX	XX	
PT	XX	Novel isolated nucleic acid encoding human Prkag3 promoter capable of
PT	XX	directing transcription of a heterologous coding sequence, useful for
PT	XX	screening compounds which modulate human Prkag3 promoter activity.
PT	XX	screening compounds which modulate human Prkag3 promoter activity.
XX	XX	
PS	XX	Disclosure; Page 52-53; 53pp; English.
XX	XX	
CC	XX	The present invention relates to novel human Prkag3 promoter capable of
CC	XX	directing transcription of a heterologous coding sequence, useful for
CC	XX	screening compounds which modulate human Prkag3 promoter activity. The
CC	XX	invention is useful for treating or preventing diseases related to energy
CC	XX	metabolism e.g. obesity, dyslipidaemia, insulin resistance syndrome or
CC	XX	type II diabetes. The present sequence is human Prkag3 protein
XX	XX	
SQ	XX	Sequence 489 AA;
Query Match 98.6%; Score 1529; DB 7; Length 489;		
Best Local Similarity 98.7%; Pred. No. 1.2e-162; Indels 0; Gaps 0;		
Matches 301; Conservative 1; Mismatches 3;		
Qy	1	MRFQEHCTCYDAMATSSKLVIFDTMLTKKFAFFALVANGVRAAPLWDSKKQSFVGMLTIT 60
Db	185	MRFQEHCTCYDAMATSSKLVIFDTMLTKKFAFFALVANGVRAAPLWDSKKQSFVGMLTIT 244
Qy	61	DFILVLRHYRSPLVQIYEIEQHKIETWREIYLOGCFKPLVSI SPNDSLFEAVVTLIKNR 120
Db	245	DFILVLRHYRSPLVQIYEIEQHKIETWREIYLOGCFKPLVSI SPNDSLFEAVVTLIKNR 304
Qy	121	IHRPLVDPVSGNVHLHTHKKLLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 180
Db	305	IHRPLVDPVSGNVHLHTHKKLLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 364
Qy	181	TAPILTALDIFVDRVSALPVVNECGQVVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQR 240
Db	365	TAPILTALDIFVDRVSALPVVNECGQVVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQR 424
Qy	241	TLCLEGVLSQPHESLGEVIDRIAREQVHRLVLDVDETOHLLGVVSLSDIQLVLSPAGI 300
Db	425	TLCLEGVLSQPHESLGEVIDRIAREQVHRLVLDVDETOHLLGVVSLSDIQLVLSPAGI 484
Qy	301	DALGA 305
Db	485	DALGA 489
RESULT 12		
ADF50314		
ID	ADF50314	standard; protein; 489 AA.
XX	AC	ADF50314;
XX	AC	
XX	XX	12-FEB-2004 (first entry)
DT	DT	
XX	XX	Human AMPK-gamma 3 protein subunit (SeqID 6).
DE	XX	
XX	XX	human; transgenic; AMP-activated protein kinase gamma 3 subunit; Prkag3;
KW	KW	AMPK; energy metabolism; obesity; dyslipidaemia;
KW	KW	insulin resistance syndrome; type 2 diabetes; antidiabetic; anorectic;
XX	XX	
OS	XX	antilipaemic.

XX OS Homo sapiens.
 XX PN WO2003063586-A1.
 XX AC ADP87619;
 XX PD 07-AUG-2003.
 XX DT 31-JAN-2003; 2003WO-IB000912.
 XX DE 01-FEB-2002; 2002US-0353430P.
 XX KW (AREX-) AREXIS AB.
 XX KW Anderson L, Marklund S;
 XX OS WPI; 2003-663404/62.
 XX PN N-PSDB; ADF50313.
 XX PD New transgenic non-human animals expressing an AMP-activated protein
 PT kinase gamma 3 subunit, useful as models for improving treatment,
 PT prevention or diagnosis of diseases related to energy metabolism, e.g.
 PT obesity or type 2 diabetes.
 XX PS Example 1; SEQ ID NO 6; 46pp; English.
 XX CC This invention relates to novel transgenic non-human animals expressing
 CC an AMP-activated protein kinase (AMPK)-gamma 3 subunit. Specifically, it
 CC relates to the transgene Prkg3 gene that encodes the AMPK gamma3 subunit
 CC or a variant thereof, where the nucleic acid is operably linked to a
 CC regulatory element. AMPK is involved in the regulation of energy
 CC metabolism in eukaryotic cells, and is recognised as a major regulator of
 CC lipid biosynthetic pathways due to its role in the phosphorylation and
 CC inactivation of key enzymes such as acetyl-CoA carboxylase. The present
 CC invention describes transgenic animals expressing AMPK-gamma 3 to be used
 CC as models for energy metabolism diseases and also methods for the
 CC development of drugs for the treatment or prevention of obesity,
 CC dyslipidemia, insulin resistance syndrome or type 2 diabetes.
 CC According to the compositions of this invention have various activities
 CC including antidiabetic, anorectic and antilipemic. This polypeptide
 CC sequence is the human AMPK-gamma3 protein subunit of the invention.
 XX SQ Sequence 489 AA;
 Query Match 98.6%; Score 1529; DB 7; Length 489;
 Best Local Similarity 98.7%; Pred. No. 1.2e-162;
 Matches 301; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MRFMQHTCYDAMATSSKLVIFDTMLIKKAPFALVANGVRAAPLWDSKQSFVGMLTIT 60
 DB 185 MRFMQHTCYDAMATSSKLVIFDTMLIKKAPFALVANGVRAAPLWDSKQSFVGMLTIT 244
 QY 61 DFILVHLRYRSPVLQVIEIQHKEIETWREIYLGCCFKPLVSPNDLSPEAVVTLIKNR 120
 DB 245 DFILVHLRYRSPVLQVIEIQHKEIETWREIYLGCCFKPLVSPNDLSPEAVVTLIKNR 304
 QY 121 IHRPLVLDPVSGNVHLTHLTKRLKLFHIFGSLLPSPFLYRTQDLIGTFRDLAVVLE 180
 DB 305 IHRPLVLDPVSGNVHLTHLTKRLKLFHIFGSLLPSPFLYRTQDLIGTFRDLAVVLE 364
 QY 181 TAPILTALDIFDVRVSALPVNCEGVGLYSRFDVIHLAAQOTYHLDMSVGEALRQR 240
 DB 365 TAPILTALDIFDVRVSALPVNCEGVGLYSRFDVIHLAAQOTYHLDMSVGEALRQR 424
 QY 241 TLCLEGLVSCQPESLGEVIDRIAREQVHRLVLDVDETOHLLGVVSLDIIQALVLSPAGI 300
 DB 425 TLCLEGLVSCQPESLGEVIDRIAREQVHRLVLDVDETOHLLGVVSLDIIQALVLSPAGI 484
 QY 301 DALGA 305
 DB 485 DALGA 489

ADP87619
 ID ADP87619 standard; protein; 492 AA.
 XX AC ADP87619;
 XX DT 23-SEP-2004 (first entry)
 XX DE Human NOVX polypeptide, NOV10b.
 XX KW anorectic; antidiabetic; gene therapy; vaccine; obesity; diabetes;
 KW insulin resistance; hybridization probe; chromosome mapping;
 KW tissue typing; preventive medicine; pharmacogenomics; NOVX; human.
 XX OS Homo sapiens.
 XX PN WO2004056961-A2.
 XX PD 08-JUL-2004.
 XX DT 27-OCT-2003; 2003WO-US034114.
 XX DE 25-OCT-2002; 2002US-0421239P.
 XX PR 28-OCT-2002; 2002US-0421700P.
 XX PR 31-OCT-2002; 2002US-0422776P.
 XX PR 13-NOV-2002; 2002US-0426197P.
 XX PR 20-DEC-2002; 2002US-0435498P.
 XX PR 20-DEC-2002; 2002US-0435510P.
 XX PR 20-DEC-2002; 2002US-0435568P.
 XX PR 21-MAR-2003; 2003US-0456812P.
 XX PA (CURA-) CURAGEN CORP.
 XX BG Berghs C, Catterton E, Ellerman K, Ort T, Rieger D, Chaudhuri A;
 XX WPI; 2004-500293/47.
 XX N-PSDB; ADP87618.
 XX New NOVX nucleic acid molecules and polypeptides useful for preventing or
 PT treating NOVX-associated disorders, e.g. diabetes, insulin resistance or
 PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
 XX Claim 3; SEQ ID NO 76; 570pp; English.
 The invention relates to a novel isolated nucleic acid molecule
 comprising any of the nucleotide sequences (e.g. 3634, 2127 or 2120 base
 pairs) fully defined in the specification; or encodes any of the amino
 acid sequences (e.g. 698, 702 or 709 amino acids) fully defined in the
 specification. The invention further comprises: an isolated polypeptide
 comprising any of the amino acid sequences cited above; a method for
 identifying compounds that modulate target polypeptide activity; an
 antibody that immunospecifically binds to the target polypeptide; where
 the target polypeptide comprises any of the above-mentioned amino acid
 sequences, an amino acid sequence that is at least 95% identical to the
 above amino acid sequences, an amino acid sequence of at least one domain
 of the above-mentioned amino acid sequences, or an amino acid sequence
 that is at least 95% identical to the domain of the above amino acid
 sequences; a method for identifying a potential therapeutic agent for use
 in treatment of a pathology, where the pathology is related to aberrant
 expression or aberrant physiological interactions of a target polypeptide
 ; and a method of screening for a modulator of activity of or of latency
 or predisposition to a pathology associated with a target polypeptide.
 The modulating compounds have anorectic and antidiabetic activities. The
 nucleic acid sequences of the invention may be used in gene therapy to
 treat disorders. The proteins of the invention may be used in creating a
 vaccine. The composition and methods are useful for identifying compounds
 that modulate protein activity or for diagnosing, preventing or treating
 diverse pathological conditions, such as obesity, diabetes or insulin
 resistance. The nucleic acids are also used as hybridization probes, in
 chromosome mapping, tissue typing, preventive medicine, and
 pharmacogenomics. This sequence represents a NOVX polypeptide of the
 invention.

Sequence 492 AA;
 XX SQ

CC	screening for agents that modulate the activity of a modifier of IGFR (MIGFR). The method comprises providing an assay system comprising an MIGFR polypeptide or polynucleotide, contacting the assay system with a test agent under conditions where, but for the presence of the test agent, the system provides a reference activity and detecting a test agent-biased activity of the assay system, where a difference between the test agent-biased activity and the reference activity identifies the test agent as a candidate IGFR pathway modulating agent. The invention also relates to methods for modulating an IGFR pathway of a cell or in a mammalian cell and a method for diagnosing a disease in a patient. The methods are useful for diagnosing or treating cancer or for identifying modulators of an IGFR pathway, which may be utilized as therapeutic targets for disorders associated with defective IGFR function, such as cancer. This sequence represents a human modulator of IGFR pathway polypeptide of the invention.
XX	Sequence 492 AA;
SQ	Query Match 98.3%; Score 1525; DB 9; Length 492; Best Local Similarity 98.4%; Pred. No. 3.5e-162; Matches 299; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy	1 MRPMQEHCTCYDAMATSSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGM
Db	185 MRPIEHTCYDAMATSSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGM
Qy	61 DFILVLRHYRSPVLQIYEIEQHKIETWREIYLQGCPLVSI SPNDLSLFEAVYTLIKNR
Db	245 DFILVLRHYRSPVLQIYEIEQHKIETWREIYLQGCPLVSI SPNDLSLFEAVYTLIKNR
Qy	121 IHRLPVLDPVSGNVHLTHKRLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLAVVLE
Db	305 IHRLPVLDPVSGNVHLTHKRLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLAVVLE
Qy	181 TAPILTALDIFVDRRVSALPVNCGQVGLYSRFDVIHLAAQOTYNHLDMSVGEALRQR
Db	365 TAPILTALDIFVDRRVSALPVNCGQVGLYSRFDVIHLAAQOTYNHLDMSVGEALRQR
Qy	241 TLCLEGLVSCOPHESLGEVIDRIAREQVHRLVLDVDETHLLGVVLSLSDILQALVLS
Db	425 TLCLEGLVSCOPHESLGEVIDRIAREQVHRLVLDVDETHLLGVVLSLSDILQALVLS
Qy	301 DALG 304
Db	485 DPSG 488
RESULT 15	
AAE00220	standard; protein; 305 AA.
XX	AAE00220;
XX	13-JUN-2001 (first entry)
DE	Pig AMPK gamma subunit muscle-specific isoform, PRKAG3.
XX	Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK; PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; RN locus; chromosome 15.
OS	Sus scrofa.
XX	Key
XX	Domain
FT	13..66
FT	/label= CBS
FT	/note= "Cystathione beta synthase domain"
FT	94..148
FT	/label= CBS
FT	/note= "Cystathione beta synthase domain"
FT	170..223

FT /label= CBS
FT /note= "Cystathione beta synthase domain"
FT 241..294
FT /label= CBS
FT /note= "Cystathione beta synthase domain"
XX
XX WO200120003-A2.
XX
XX 22-MAR-2001.
XX
XX 11-SEP-2000; 2000WO-EP009896.
XX
XX 10-SEP-1999; 99EP-00402236.
XX 18-MAY-2000; 2000EP-00401388.
XX
XX (INRG) INRA INST NAT RECH AGRONOMIQUE.
XX (ANDE/) ANDERSSON L.
XX (LOOF/) LOOFT C.
XX (KALM/) KALM E.
XX
XX Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;
XX Iannuccelli N, Gellin J, Le Roy P, Chardon P;
XX
XX WPI: 2001-244810/25.
XX N-PSDB; AAD03295.
XX

New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and myopathy.

Claim 4; Fig 2; 71pp; English.

The present amino acid sequence is pig adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3. Prkag3 gene is located in the RN locus of chromosome 15. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3. Transgenic animal and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy

Sequence 305 AA;

Query Match 97.2%; Score 1507; DB 4; Length 305;
Best Local Similarity 97.0%; Pred. No. 1.9e-160;
Matches 296; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 1 MRFQHECTYDAMATSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMLTIT 60
DB 1 MRFQHECTYDAMATSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMLTIT 60
QY 61 DFILVLRHYRSPVQIYEIEHQHETWRIYIYQGCPLVSI SPNDSLFEAVYTLIKNR 120
DB 61 DFILVLRHYRSPVQIYEIEHQHETWRIYIYQGCPLVSI SPNDSLFEAVYTLIKNR 120
QY 121 IHRPLVLPDPSGVNLHILTHKRLKFLHIFGSLLPSPFLYRTIQDLCIGTFRDLAVLE 180
DB 121 IHRPLVLPDPSGAVLHILTHKRLKFLHIFGTLPPSPFLYRTIQDLCIGTFRDLAVLE 180
QY 181 TAPILTALDIFVDRRVSALPVNVECGVGLYSRFDVIHLAAOQTYNHLDMNSVGEALRQR 240

Db 181 TAPILTALDIFVDRRVSALPVNVECGVGLYSRFDVIHLAAOQTYNHLDMNSVGEALRQR 240
QY 241 TLCLEGVLSQPHESLGEVIDRIAREQVHRLVLDVDETHLLGVVSLSDIILQALVLSPAGI 300
Db 241 TLCLEGVLSQPHETLGEVIDRIVREQVHRLVLDVDETHLLGVVSLSDIILQALVLSPAGI 300
QY 301 DALGA 305
Db 301 DALGA 305

Search completed: January 24, 2006, 22:08:48
Job time : 84.6866 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 24, 2006, 22:02:17 ; Search time 19.4343 Seconds
(without alignments)
1510.014 Million cell updates/sec

Title: US-10-070-794A-4
Perfect score: 1551
Sequence: 1 MRFQHEHTCYDAMATSSKLV.....LSLDLQALVLSPAGIDALGA 305

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1007	64.9	330	2 T10759	AMP-activated prot
2	485	31.3	478	2 T25899	hypothetical prote
3	457	29.5	322	1 RGBYC3	regulatory protein
4	372.5	24.0	274	2 S67444	probable 5'-AMP-ac
5	243.5	15.7	391	2 B86222	hypothetical prote
6	217	14.0	443	2 T25854	Pv42 protein - kid
7	214	13.8	379	2 T10971	hypothetical prote
8	207.5	13.4	460	2 T24248	hypothetical prote
9	189.5	12.2	352	2 F86287	hypothetical prote
10	188.5	12.2	629	2 T18227	hypothetical prote
11	188	12.1	424	2 T46197	hypothetical prote
12	176	11.3	399	2 D96832	hypothetical prote
13	163	10.5	447	2 B96720	hypothetical prote
14	161.5	10.4	392	2 G75056	dehydrogenase PAB0
15	155.5	10.0	392	2 D71175	hypothetical prote
16	148.5	9.6	250	2 C90449	conserved hypotet
17	148	9.5	92	2 T50087	probable 5'-AMP-ac
18	147.5	9.5	280	1 H64452	conserved hypotet
19	146	9.4	313	1 H69030	conserved hypotet
20	141.5	9.1	157	1 F69185	yhcv homolog MTH64
21	140	9.0	527	2 S46088	hypothetical prote
22	139	9.0	152	2 AF2282	hypothetical prote
23	139	9.0	300	1 S08244	conserved hypotet
24	138.5	8.9	421	2 C64475	hypothetical prote
25	138	8.9	485	1 JC4998	IMP dehydrogenase
26	137	8.8	284	1 H69355	conserved hypotet
27	136.5	8.8	527	2 S64060	probable membrane
28	134	8.6	1286	2 A12195	two-component hybr
29	130.5	8.4	792	2 A84308	chloride channel [

30 129.5 8.3 1344 2 AD2103 two-component hybr
31 126.5 8.2 168 1 A64478 hypothetical prote
32 126 8.1 486 1 E71456 IMP dehydrogenase
33 125.5 8.1 157 2 AF3344 IMP dehydrogenase
34 123.5 8.0 287 2 F72780 IMP dehydrogenase
35 122 7.9 282 2 C75148 hypothetical prote
36 120.5 7.8 223 2 T36952 conserved hypotet
37 120.5 7.8 278 2 A72781 probable acetoin u
38 120.5 7.8 284 1 H69232 M1225-related pro
39 119 7.7 122 2 B69119 yhcV homolog MTH18
40 119 7.7 485 2 E75015 IMP dehydrogenase
41 116.5 7.5 382 2 AD2762 conserved hypotet
42 116.5 7.5 382 2 C97543 hypothetical prote
43 115.5 7.4 285 1 C71188 conserved hypotet
44 115 7.4 482 2 C72264 IMP dehydrogenase
45 114.5 7.4 215 2 H72290 conserved hypotet

ALIGNMENTS

RESULT 1

T10759
AMP-activated protein kinase (EC 2.7.1.1.) gamma chain - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T10759
R/Woods, A.; Cheung P, C.F.; Smith, F.C.; Davison, M.D.; Scott, J.; Berl, R.K.; Carling, J. Biol. Chem. 271, 10282-10290, 1996
A/Title: Characterization of AMP-activated protein kinase beta and gamma subunits: Assem
A/Reference number: 206738; MUID:96215327; PMID:8626596
A/Accession: T10759
A/Status: translated from GS/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-330 <WOO>
A/Cross-references: UNIPROT:P80385; UNIPARC:UPI00001250B4; EMBL:X95578; NID:g1185270; PI
A/Experimental source: strain wislar
C/Complex: heterotrimer; alpha, beta and gamma chains
C/Function:
A/Description: is responsible for the regulation of fatty acid synthesis by phosphorylat
C/Superfamily: CAT3 protein
C/Keywords: fatty acid biosynthesis; phosphotransferase

Query Match 64.9%; Score 1007; DB 2; Length 330;
Best Local Similarity 65.3%; Pred. No. 8.6e-79;
Matches 192; Conservative 52; Mismatches 50; Indels 0; Gaps 0;
QY 3 FMOEHTCYDAMATSSKLVIPDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMLTITDF 62
DB 31 FMKSHRCYDLIPTSSKLVVFDTSQVKKAFALVTNGVRAAPLWDSKKQSFVGMLTITDF 90
QY 63 ILVLRHYRSPVQIYEIEQHKIETWREIYLOQCFPLVSI SPNDSLFEAVYTLIKNRIH 122
DB 91 INILHRYKSAVQIYELEHKIETWREVLQSFPLVCISPNASLFDVSSLIKNKIH 150
QY 123 RLPVLPVSGNVLIHLTHRLKLLKFLHIFGSLRPSPFLYRTIQDLGIGTFDRDLAVILETA 182
DB 151 RLPVIDPESGNTLYLTHRKILKFLKLFITEFPKPEFMSKSLBELQIGTVANIAMVRTTT 210
QY 183 PILTALDIFVDRVSLPVPVNECGVQVGLYSRFDVTHLAAQQTYNHLDMSVGEALRORTL 242
DB 211 PVVVALGIFVQHRVSAIPVVDKRGVVVDIYSKEDVINLAAEKTNNLDVSVTKALQHRSH-270
QY 243 CLEGVSLQCPHESGLGVDRVAREQVHRLVVDQTHLLQGVSLSDTLQALVLVS 296
DB 271 YFEGVLKCYLHETLEAIINRLVEAEVHRLVVVDHVDVKGIVSLSDILQALVLT 324

RESULT 2

T25899
hypothetical protein T20F7.6 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

Db 18 FISRSTSYDLVTSFRIIVFDVTLVFKTSLSLLTLNNIVSAPLWDSSEANKFAGLLTWADF 77
 Qy 63 ILVLHRYRSPV--QIYEIEQHKTETWRIYQ-GCFKP-LVSI SPNDSLFVAVYTLIK 118
 Db 78 VNIKYQSSPEAEADIKFELLGUREVERKIGALPETIYVHPHMSLMDACLAMSK 137
 Qy 119 NRHLRPLVDPVSGN-----VLHILTHKRLKFLHIFGSLLPSPFLYRT-IDOLGIGTF 172
 Db 138 SRARIEPLID-VDETGETSEMIVSVLTQYRILKET-----SNCKETAMLRVPLNQMTIGTW 192
 Qy 173 RDLAVLETPALITLALDI FVDRRVSALPVNVEGQVVLGYSRDFVHLAAQOQYNNHLDMS 232
 Db 193 SNLATASMETKVDVVKMLAEKNISAVPIVNSEGTLLNVYESVDVHMLIQDGDYNSLDLS 252
 Qy 233 VGEALRQRTLCLEGLVSCQ 251
 Db 253 VGEALLKRPANFDGVHTCR 271
 RESULT 5
 B66222
 hypothetical protein [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C:Accession: B66222
 R:Theologian, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 ansen, N.P.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: B66222
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-391 <STO>
 A:Cross-references: UNIPROT:O04028; UNIPARC:UPI00000AB393; GB:AE005172; NID:g2342682; P
 C:Genetics:
 A:Map position: 1
 Query Match 15.7%; Score 243.5; DB 2; Length 391;
 Best Local Similarity 29.5%; Pred. No. 3.6e-13;
 Matches 79; Conservative 53; Mismatches 89; Indels 47; Gaps 12;
 Qy 39 GVRAAPLWDSKQSFVGMFLITPILVLRHY--YRSPVQIYIEQHKTETWRE--IYLQ 94
 Db 121 GIPLAPLWDFGKQFVGVLPGLDFILRLGTHGSLNTE-ESELTHTIAAWKEGKAHIS 179
 Qy 95 GCF-----KPLVSI SPNDSLFVAVYTLIKRIHRLPVL-----DPVSGNVHLHILTHK 141
 Db 180 RQYDGGSRPRLPVQGVYDNLKVALKILQNKVAAPVIYSSLDQGSYPOLLHLASLS 239
 Qy 142 RLK-----FLHIFGSLLPSPFLYRTIDOLGIGTF-----RDLAVLETPALITA 187
 Db 240 GILKICRYFRHSSSL-----PILQPICSIPIGTWVPRIGSSSKPLATLRPHASLGSA 295
 Qy 188 LDIFVDRRVSALPVNVEGQVVLGYSRDFVHLAAQOQYNN--HL-DMSVGEALR--QRTL 242
 Db 296 LALLVQAEVSIPIVDNDLSLDIYSRSDITALAKAKYAIHLDDMTVHQALQLQGDAS 355
 Qy 243 CLEGLVLS-----CQPHESLGEVIDRIA 264
 Db 356 PPGIFNGQRCHMCLRSDSLKVYMERLA 383
 RESULT 6
 T25854
 hypothetical protein T01B6.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
 C:Accession: T25854
 R:Johnson, D.
 submitted to the EMBL Data Library, August 1996
 A:Description: The sequence of C. elegans cosmid T01B6.
 A:Reference number: Z20100
 A:Accession: T25854
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-443 <JOH>
 A:Cross-references: UNIPARC:UPI000017B39; EMBL:U67950; PIDN:AAB07568.1; GSPDB:GN00028;
 A:Experimental source: strain Bristol N2; clone T01B6
 C:Genetics:
 A:Gene: CESP:T01B6.3
 A:Map position: X
 A:Introns: 5/3; 45/2; 72/1; 105/3; 153/3; 179/2; 200/3; 225/3; 255/3; 349/3; 397/2
 Query Match 14.0%; Score 217; DB 2; Length 443;
 Best Local Similarity 26.2%; Pred. No. 8e-11;
 Matches 83; Conservative 59; Mismatches 117; Indels 58; Gaps 12;
 Qy 3 FMOEHTCYDAMATSSKLVIPFDITMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMFLT---- 58
 Db 81 FMSIITCYDLPQPHSSLVVFDGKTCKVAAVHALSQHGHIAAVVNTDTKYQAEVFNMGHC 140
 Qy 59 ITDFILVL--HRYRSPVQIYIEQHKTETWRIYQ-GCFKP-LVSI SPNDSLFVAVYTL 116
 Db 141 LTAILLVAGNRVASKTL-----VEFLKEIGSGN-----LICGVQNSVWEAANII 187
 Qy 117 IKNRHRLPVLDP--PVSGNVHLHILTHKRLK-----FLHIFGSLLPSPFL 160
 Db 188 SHNKISFVPFDITIPKGPGLYFLTPRMILQETVLKLSDFGDAILLHV-----R 237
 Qy 161 YRTIQLDGTGTFD--LAVLETPALITLALDI FVDRRVSALPVNVEGQVVLGYSRDFVI 218
 Db 238 QATLDQKKGITWMDVILKIGLNTT-IEEAIKMSERKMTPIPVNDFPKQIVNMLARKDII 296
 Qy 219 -HLAAQOQYNNHLDMSVGEALRQRTLCLEGLVLS-----CQPHESLGEVIDRIA QVHRLVL 273
 Db 297 LEIMSHQGNFHDH-----LKEPVKILQSLRSLVYGRSSYTFETVAKMTSDKSLPI 351
 Qy 274 VDETQHLLGVVSLSDIL 290
 Db 352 IDEGKEILAVVSCDIL 368
 RESULT 7
 T10971
 Pv42 protein - kidney bean
 C:Species: Phaseolus vulgaris (kidney bean)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
 C:Accession: T10971
 R:Abbe, H.
 submitted to the EMBL Data Library, November 1995
 A:Reference number: Z17236
 A:Accession: T10971
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-379 <ABE>
 A:Cross-references: UNIPROT:Q41108; UNIPARC:UPI00000ACD11; EMBL:U40713; NID:g1113940; P
 Query Match 13.8%; Score 214; DB 2; Length 379;
 Best Local Similarity 23.5%; Pred. No. 1.2e-10;
 Matches 85; Conservative 73; Mismatches 122; Indels 82; Gaps 17;
 Qy 4 MOEHTCYDAMATSSKLVIPFDITMLEIKKAPFALVANGVRAAPL-----W-----DS 48
 Db 17 LKEKKVKDMMVGKRLVEVPYTTASLAQIMNTLVANKIVAVPVAAAPQGMVAGGSMVES 76
 Qy 49 KQQS-----FVGMFLITDFILVL-----HRYRSPVQIYIEQHKTETWRIY----LQ 95
 Db 77 DKQTGAVRKHYIGMVTMLDILAHAGDHLSCGDNITQ--DLDRMSDSVSSIGHSEFEG 134

Qy 96 CFKPLVSI SPNDLSFEAVYTLIKNRIHRLVLPVDSG---NV-----LHLTH 140
Db 135 L--SLWTLNPTNMLDCMEVFSKG-VHRAMV--PVDGLEENVASGVELTESASSYQMLTQ 189
Qy 141 KRLIKFLHIFGSLPRPSFLYRTIQLGIGTFRDLAUVLETAPIITLALDIFVDRRYSALP 200
Db 190 MDMLKFLHGGAEI--HSILSRVQDLGADTVQIYAIT-DRTKLVHAIKCLKKAMLNAPV 246
Qy 201 W-----NECGQVGLYSRFDV--IHLLAAQOTYNHLD-MSVGEALRQRTL 242
Db 247 IVRATGVGDHKKQLNGRCRKLIGTSATDLRCHISLSKSWLGISALAFTEVRSSPL 306
Qy 243 CLEG-----VLSCQPHESLGEVIDRIAREQVHRLVLDVDETHLLGVVSLSDILQ 291
Db 307 YSESDMQNRGSSRRELTVCAESPLSEVIEKAVTSHVRVWVVDQEGLLGVVSLTDVIR 366
Qy 292 AL 293
Db 367 VI 368

RESULT 8
T24248
hypothetical protein R53.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T24248
R:Wilkinson, J.
submitted to the EMBL Data Library, October 1995
A:Reference number: Z19863
A:Accession: T24248
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-460 <WIL>
A:Cross-references: UNIPROT:Q22022; UNIPARC:UPI0000082652; EMBL:Z66515; PIDN:CAA91351.1;
A:Experimental source: clone R53
C:Genetics:
A:Gene: CESP:R53.7
A:Map position: 2
A:Introns: 30/1; 133/1; 407/3

Query Match 13.4%; Score 207.5; DB 2; Length 460;
Best Local Similarity 23.3%; Pred. No. 5.5e-10;
Matches 73; Conservative 68; Mismatches 127; Indels 45; Gaps 11;
Qy 2 RFMQBHTCYDAMATSSKLVIFDTMLEIKKAFALVANGVRAAPLWDSKKQSFV--GMLTI 59
Db 141 QYMSVVVDVLECPNNSKVIIDASTPTTRAFIRMDHNITTLIVDTSDBRHKVKNILTL 200
Qy 60 TDFILVLRHYRSPLVQIYEIOHKIETWREIYLQGCFKPLVSI SPNDLSLFEAVYTLKN 119
Db 201 TDCLNAIRN--ETPPADQGVLRASDI-----LSG--NQLVSVSISSKILDLCBELHQN 249
Qy 120 RIHRLVLPVDSGNNVHLHILTKRLKFLHIFGSLPRPSFLYRTIQLGIGTFRDLAUVL 179
Db 250 RLHRVVVLDDAK-EVNNIISVRRVIAIHKQNRSLHFAQWLKSLGMSAIGTWENVAVIS 308
Qy 180 ETAPILTALDIFVDRRVSALPVNCGQVGLYSRFDVHLLAAQOTYNHLL-----DMS 232
Db 309 QNETVIRAWEDMIGFHYALPVDSKQNVIGVITKIDICKALPR---NFIEPKRWLQETK 365
Qy 233 VGEALRQRTLCLGVLSCQPHESLGEVIDRIAREQVHRLVLDVDETHLLGVV 284
Db 366 VSDILH---ICKSQIL-ISSADSVQVLDTL-----LAGDTQSFAFHNGKAIGVI 412
Qy 285 SLSDILQALVLSP 297
Db 413 SLTDFLSHLRSP 425

RESULT 9
F86287

hypothetical protein F91L27 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: F86287
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: F86287
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-352 <STO>
A:Cross-references: UNIPROT:Q9XI37; UNIPARC:UPI000004825C; GB:AE005172; NID:G5103830; PFI
C:Genetics:
A:Map position: 1

Query Match 12.2%; Score 189.5; DB 2; Length 352;
Best Local Similarity 23.2%; Pred. No. 1.4e-08;
Matches 81; Conservative 59; Mismatches 128; Indels 81; Gaps 13;
Qy 8 TCYDAMATSSKLVIFDTMLEIKKAFALVANGVRAAPL-----W-----DSKKQS 52
Db 17 TANDLTVRNRRLVEVPYVATLTSAMNTLVNISALPVAAAPPGHGIGAGGSMINESDKQT 76
Qy 53 -----FVGMLTITDFIL-----VLHRYRSPVQIYEIOHKIE---TWREIYLQGC 96
Db 77 GVVRKYIGILTMLDLIAHIAGEDSNLSLDLRKMSQVSSIIGHCLEGLSLW----- 128
Qy 97 FKPLVSI SPNDLSFEAVYTLIKNRIH--LPVLDPVSGN-----VLHILTHK 141
Db 129 -----TLNPTVSLCEMEVFSKG-IHRLVPESSISNNTIAGVELIESASAYKMLTQM 182
Qy 142 RLLKFL--HIFGSLPRPSFLYRTIQLGIGTFRDLAUVLETAPIITLALDIFVDRRYSAL 199
Db 183 DLLRFLKXHHFDDL---KTVLSRSISDLG-AVNDVSVYAITERTTVSNAINVMKGALLNAV 238
Qy 200 PVVN-----ECGQVGLYSRFDVHLLAAQOTYNHLDMSVGEALRQRTLCL 244
Db 239 PIVHAPDIAQEDHQLVNGRHKRVIGTFSATDLKGCRLELOTLWLPITALEFTKTSKE 298
Qy 245 EGVLSQCPHESLGEVIDRIAREQVHRLVLDVDETHLLGVVSLSDILQAL 293
Db 299 REVVSCGVSTMEAEIEKVTVRGVHRVWVMDQOGLLGQVSLTDIIRSL 347

RESULT 10
T18227
hypothetical protein - yeast (Candida albicans)
C:Species: Candida albicans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18227
R:Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, November 1998
A:Reference number: Z18831
A:Accession: T18227
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-629 <BAR>
A:Cross-references: UNIPROT:Q94035; UNIPARC:UPI0000069ECC; EMBL:AL033501; NID:e1341022;
C:Genetics:
A:Note: Ca41C10.01c

Query Match 12.2%; Score 188.5; DB 2; Length 629;
Best Local Similarity 24.3%; Pred. No. 3.5e-08;
Matches 76; Conservative 60; Mismatches 136; Indels 41; Gaps 11;

Qy	13	MATSSKLVIPDTWLEIKKAFVALVANGVRAAPLWDSKK--QSFVGLMTI-----TDFIL	64
Db	149	LTESNKLISHTSHSVQSAFETLLKYNLTSPVSVISKSDPHDLTNCLTFDYSDLNTVLLL	208
Qy	65	VLHRYRSPJ-----VOIYBIOH-----KIETWREIYLGQCFK-----PLVSVIS	104
Db	209	IMNKINYSELNVDGIDPNISPOEHRHEFTQTISKAKRGEVPVEFTIKLHPKNPTIKFN	368
Qy	105	PNDLSFEAVYVTLKRIHRLPVLDPVSGNVLHILTHKRLKFLHIFOSLLPRPSP-LYRT	163
Db	269	ETDTLFSVMETI-GNGVHRIAITNEEGNKITGILSQRRLLIKYMWENARREPSLDFYLTST	327
Qy	164	IQDLGIGTFRDLAVLETAPILTALDI FVDRRVSAALPVNCEGQVGLYERFDVIHLAAQ	223
Db	328	LQDLKLGSSNPI -TYIEDQMLEALHKMFNERVSSLAVIDRSRTLIGNISVIDVKNVTS	386
Qy	224	QTYNHLDMSV---GEALRQRTLCEG-----VLSCQPHESLGEVIDRIAREQVHRLVLV	274
Db	387	KNSHLLFKSVLNFISVNLQKGI -EEGQDQFPI FHVNNQTSIGRVIAKL VATOSHRLWIV	445
Qy	275	DETQHLLGVVSVLS 287	
Db	446	DSSROASSMSAS 458	

RESULT 11

T46197
T46197
Hypothetical protein T8P19.40 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: T46197
R:Choiene, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; Sarrailhe, B.; Drouot, J.-L.; Gouy, M.
Submitted to the Protein Sequence Database, December 1999
A:Reference number: Z23008
A:Accession: T46197
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-424 <CHO>
A:Cross-references: UNIPROT:Q9S7W6; UNIPARC:UIP00000AB74R; EMBL:AL133315
A:Experimental source: cultivar Columbia; BAC clone T8P19
C:Genetics:
A:Map position: 3
A:Introns: 69/1; 126/3; 178/3; 270/3; 325/2
A>Note: T8P19.40

[illegible]

RESULT 12

hypothetical protein F18B13.17 [imported] - Arabidopsis thaliana
C Species: Arabidopsis thaliana (mouse-ear cress)
C Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C Accession: D96832
R Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White
anin, N.F.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.
Chen, C.W.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin
C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A Reference number: A86141; MUID:21016719; PMID:11130712
A Accession: D96832
A Status: preliminary
A Molecule type: DNA
A Residues: 1-399 <STO>
A Cross-references: UNIPROT:Q9SSD0; UNIPARC:UPI000009F89F; GB:AE005173; NID
C Genetics:
A Gene: F18B13.17
A Map position: 1

Query Match	11.3%	Score 176;	DB 2;	Length 399;
Best Local Similarity	25.2%;	Pred. No. 2.3e-07;		
Matches	90;	Conservative 58;	Mismatches 109;	Indels 100; Gaps 19;
QY	8	TCYDAMATSKLVIFDTMLEIKAFALVANGVRAAPL-----W-----	46	
DB	65	TLGDALNTM-----TILGIKP-----VANRVRAVPAKPGQWLGAAGSMIVELDKQS	112	
QY	47	DSKKQSFVGMLTITDFIL-----VLHRYVRSPLVQIYEIEQHKIETWREIYLGCFF	97	
DB	113	GSARKQYIGWVTMLDVVAHAGDDGSEGLDKQWAAPVSSIIHCPEGLSLW-----	163	
QY	98	KPLVSTSPNDLSFEAVYTLIKRIHRLPVLDPVSGNVLHILTKRLKLFHIGSL--LP	155	
DB	164	----SLNPNTSIMDCMELMSKG-IHR--VLVPLDSNTENI--TGPELVESASAVMLSQMD	215	
QY	156	RPSFLYRTTQDL-GI--GTFRDLAVVLETAPLIT-----ALDIFVDRVRSALPVVNEC	205	
DB	216	LISFFPDQSSQLHGILSHVTYTLDSAIHTNLTVAATSOARVKDAIQCMSIAMLNAVPIFEAS	275	
QY	206	GO-----VUGLYSRFDV--IHLAAQTYNHLDMSVGSAIRQ--RTLCEG--	246	
DB	276	GGEGDHKQLVDGKNRRVVGTFSSADLKGCHLALRSW--LPINALRFEVEKIPRTILFTAA	333	
QY	247	-----VLSCQPHESLGEVIDRIAREQVHRLVLVDTEQHLGLGVVSLSDILOALVLIS	296	
DB	334	TSTPGRELVTCHVTSTLAQVIMHVTTKRVHRRVWVVDONGLOGLVSLTDII--AVVRS	389	

RESULT 13

Record: 13
Accession: B96720
Hypothesized protein T17F3.17 [imported] - Arabidopsis thaliana
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C.Accession: B96720
C.R: Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, P.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A.Reference number: A86141; PMID:21016719; PMID:11130712

RESULT 2

US-10-473-670-15
 ; Sequence 15, Application US/10473670
 ; Publication No. US20040110180A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RECIPON, Shirley A.; BURRILL, John D.;
 ; APPLICANT: MARCUS, Gregory A.; ZINGLER, Kurt A.;
 ; APPLICANT: TANG, Y. Tom; THORNTON, Michael;
 ; APPLICANT: BOROWSKY, Mark L.; BAUGHN, Mariah R.;
 ; APPLICANT: BURFORD, Neil; LEE, Soo Yeun;
 ; APPLICANT: BANDMAN, Olga; HAFALIA, April J.A.;
 ; APPLICANT: YAO, Monique G.; RAMKUMAR, Jayalaxmi;
 ; APPLICANT: CHAWLA, Narinder K.; LU, Dyrung Aina M.;
 ; APPLICANT: ARVIZU, Chandra S.; ISON, Craig H.;
 ; APPLICANT: DING, Li; LU, Yan;
 ; APPLICANT: GURURAJAN, Rajagopal; WALSH, Roderick T.;
 ; APPLICANT: GANDHI, Ameer R.; SWARNAKAR, Anita;
 ; APPLICANT: FORSYTHE, Ian J.; YUE, Henry;
 ; APPLICANT: AU-YOUNG, Janice K.; ELLIOTT, Vicki S.;
 ; APPLICANT: LEE, Sally
 ; TITLE OF INVENTION: KINASES AND PHOSPHATASES
 ; FILE REFERENCE: PI-0398 USN
 ; CURRENT APPLICATION NUMBER: US/10/473,670
 ; CURRENT FILING DATE: 2003-10-01
 ; PRIOR APPLICATION NUMBER: PCT/US02/10818
 ; PRIOR FILING DATE: 2002-04-05
 ; PRIOR APPLICATION NUMBER: US 60/282,119
 ; PRIOR FILING DATE: 2001-04-06
 ; PRIOR APPLICATION NUMBER: US 60/283,588
 ; PRIOR FILING DATE: 2001-04-13
 ; PRIOR APPLICATION NUMBER: US 60/283,759
 ; PRIOR FILING DATE: 2001-04-13
 ; PRIOR APPLICATION NUMBER: US 60/285,589
 ; PRIOR FILING DATE: 2001-04-20
 ; PRIOR APPLICATION NUMBER: US 60/287,037
 ; PRIOR FILING DATE: 2001-04-27
 ; PRIOR APPLICATION NUMBER: US 60/287,036
 ; PRIOR FILING DATE: 2001-04-27
 ; PRIOR APPLICATION NUMBER: US 60/288,608
 ; PRIOR FILING DATE: 2001-05-04
 ; PRIOR APPLICATION NUMBER: US 60/288,712
 ; PRIOR FILING DATE: 2001-05-04
 ; PRIOR APPLICATION NUMBER: US 60/289,909
 ; PRIOR FILING DATE: 2001-05-09
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 15
 ; LENGTH: 489
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No: 7474666CD1
 US-10-473-670-15

Query Match 100.0%; Score 1551; DB 4; Length 489;
 Best Local Similarity 100.0%; Pred. No. 3,4e-148;
 Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRFMQHTCYDAMATSSKLVIPTDMLTKKFAFFALVANGVRAAPLWDSKKQSFVGMLTIT 60
 Db 185 MRFMQHTCYDAMATSSKLVIPTDMLTKKFAFFALVANGVRAAPLWDSKKQSFVGMLTIT 244
 Qy 61 DFILVLRYSPLVQIYEIOHKIETWREIYLQGCFFPLVSPNDSLFPAVYTLIKNR 120
 Db 245 DFILVLRYSPLVQIYEIOHKIETWREIYLQGCFFPLVSPNDSLFPAVYTLIKNR 304
 Qy 121 IHRLPVLPVSGNVHLTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 180
 Db 305 IHRLPVLPVSGNVHLTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 364

Qy 181 TAPILTALDIFVDRRVVSALPVVNECGQVGLYSRFDVHLAAQQTYNHLDMSVGEALRQR 240
 Db 365 TAPILTALDIFVDRRVVSALPVVNECGQVGLYSRFDVHLAAQQTYNHLDMSVGEALRQR 424
 Qy 241 TLCLEGVLSQPHESLGEVIDRIAREQVHRVLVDETHQLLGVVSLSDIILQALVLSPAGI 300
 Db 425 TLCLEGVLSQPHESLGEVIDRIAREQVHRVLVDETHQLLGVVSLSDIILQALVLSPAGI 484
 Qy 301 DALGA 305
 Db 485 DALGA 489

RESULT 3

US-10-705-137-6
 ; Sequence 6, Application US/10705137
 ; Publication No. US20040121385A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Andersson, Leif
 ; APPLICANT: Luthman, L. Holger
 ; APPLICANT: Marklund, Stefan
 ; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNIT
 ; FILE REFERENCE: 11145-007002
 ; CURRENT APPLICATION NUMBER: US/10/705,137
 ; CURRENT FILING DATE: 2003-11-10
 ; PRIOR APPLICATION NUMBER: US 09/826,581
 ; PRIOR FILING DATE: 2001-04-05
 ; PRIOR APPLICATION NUMBER: US 60/195,665
 ; PRIOR FILING DATE: 2000-04-07
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 6
 ; LENGTH: 489
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-705-137-6

Query Match 100.0%; Score 1551; DB 4; Length 489;
 Best Local Similarity 100.0%; Pred. No. 3,4e-148;
 Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRFMQHTCYDAMATSSKLVIPTDMLTKKFAFFALVANGVRAAPLWDSKKQSFVGMLTIT 60
 Db 185 MRFMQHTCYDAMATSSKLVIPTDMLTKKFAFFALVANGVRAAPLWDSKKQSFVGMLTIT 244
 Qy 61 DFILVLRYSPLVQIYEIOHKIETWREIYLQGCFFPLVSPNDSLFPAVYTLIKNR 120
 Db 245 DFILVLRYSPLVQIYEIOHKIETWREIYLQGCFFPLVSPNDSLFPAVYTLIKNR 304
 Qy 121 IHRLPVLPVSGNVHLTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 180
 Db 305 IHRLPVLPVSGNVHLTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 364
 Qy 181 TAPILTALDIFVDRRVVSALPVVNECGQVGLYSRFDVHLAAQQTYNHLDMSVGEALRQR 240
 Db 365 TAPILTALDIFVDRRVVSALPVVNECGQVGLYSRFDVHLAAQQTYNHLDMSVGEALRQR 424
 Qy 241 TLCLEGVLSQPHESLGEVIDRIAREQVHRVLVDETHQLLGVVSLSDIILQALVLSPAGI 300
 Db 425 TLCLEGVLSQPHESLGEVIDRIAREQVHRVLVDETHQLLGVVSLSDIILQALVLSPAGI 484
 Qy 301 DALGA 305
 Db 485 DALGA 489

RESULT 4

US-10-503-175-2
 ; Sequence 2, Application US/10503175
 ; Publication No. US20050172348A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Andersson, Leif
 ; APPLICANT: Marklund, Stefan

```

; TITLE OF INVENTION: Transgenic animals expressing prkag3
; FILE REFERENCE: 11145-020US1
; CURRENT APPLICATION NUMBER: US/10/503,175
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: PCT/IB03/00912
; PRIOR FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 60/353,430
; PRIOR FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-503-175-2

Query Match      100.0%; Score 1551; DB 5; Length 489;
Best Local Similarity 100.0%; Pred. No. 3.4e-148;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRPMQHTCYDAMATSSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMILTIT 60
Db 185 MRPMQHTCYDAMATSSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMILTIT 244

Qy 61 DFILVLHRYRSPVQIYIEIOHKIETWREIYLOQCFKPLVSI SPNDSLFEAVYTLIKNR 120
Db 245 DFILVLHRYRSPVQIYIEIOHKIETWREIYLOQCFKPLVSI SPNDSLFEAVYTLIKNR 304

Qy 121 IHRPLVLPDPSGNVLHILTHKLLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 180
Db 305 IHRPLVLPDPSGNVLHILTHKLLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 364

Qy 181 TAPILTALDIFVDRRVSALPVVNECGQVGLYSRFDVIHLAAQQTNYNHLDM SVGEALRQR 240
Db 365 TAPILTALDIFVDRRVSALPVVNECGQVGLYSRFDVIHLAAQQTNYNHLDM SVGEALRQR 424

Qy 241 TLCLEGLVSCQPHEISGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDILOALVLS PAGI 300
Db 425 TLCLEGLVSCQPHEISGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDILOALVLS PAGI 484

Qy 301 DALGA 305
Db 485 DALGA 489

RESULT 5
US-10-503-039-2
; Sequence 2, Application US/10503039
; Publication No. US20050155091A1
; GENERAL INFORMATION:
; APPLICANT: Svensson, Thomas
; TITLE OF INVENTION: prkag3 gene promoter and uses thereof
; FILE REFERENCE: 11145-022US1
; CURRENT APPLICATION NUMBER: US/10/503,039
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: PCT/IB03/00762
; PRIOR FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 60/353,429
; PRIOR FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-503-039-2

Query Match      98.6%; Score 1529; DB 5; Length 489;
Best Local Similarity 98.7%; Pred. No. 5.7e-146;
Matches 301; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MRPMQHTCYDAMATSSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMILTIT 60
Db 185 MRPMQHTCYDAMATSSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMILTIT 244

Qy 61 DFILVLHRYRSPVQIYIEIOHKIETWREIYLOQCFKPLVSI SPNDSLFEAVYTLIKNR 120
Db 245 DFILVLHRYRSPVQIYIEIOHKIETWREIYLOQCFKPLVSI SPNDSLFEAVYTLIKNR 304

Qy 121 IHRPLVLPDPSGNVLHILTHKLLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 180
Db 305 IHRPLVLPDPSGNVLHILTHKLLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 364

Qy 181 TAPILTALDIFVDRRVSALPVVNECGQVGLYSRFDVIHLAAQQTNYNHLDM SVGEALRQR 240
Db 365 TAPILTALDIFVDRRVSALPVVNECGQVGLYSRFDVIHLAAQQTNYNHLDM SVGEALRQR 424

Qy 241 TLCLEGLVSCQPHEISGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDILOALVLS PAGI 300
Db 425 TLCLEGLVSCQPHEISGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDILOALVLS PAGI 484

Qy 301 DALGA 305
Db 485 DALGA 489

RESULT 6
US-10-503-175-6
; Sequence 6, Application US/10503175
; Publication No. US20050172348A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Leif
; APPLICANT: Marklund, Stefan
; TITLE OF INVENTION: Transgenic animals expressing prkag3
; FILE REFERENCE: 11145-020US1
; CURRENT APPLICATION NUMBER: US/10/503,175
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: PCT/IB03/00912
; PRIOR FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 60/353,430
; PRIOR FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-503-175-6

Query Match      98.6%; Score 1529; DB 5; Length 489;
Best Local Similarity 98.7%; Pred. No. 5.7e-146;
Matches 301; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MRPMQHTCYDAMATSSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMILTIT 60
Db 185 MRPMQHTCYDAMATSSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMILTIT 244

Qy 61 DFILVLHRYRSPVQIYIEIOHKIETWREIYLOQCFKPLVSI SPNDSLFEAVYTLIKNR 120
Db 245 DFILVLHRYRSPVQIYIEIOHKIETWREIYLOQCFKPLVSI SPNDSLFEAVYTLIKNR 304

Qy 121 IHRPLVLPDPSGNVLHILTHKLLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 180
Db 305 IHRPLVLPDPSGNVLHILTHKLLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 364

Qy 181 TAPILTALDIFVDRRVSALPVVNECGQVGLYSRFDVIHLAAQQTNYNHLDM SVGEALRQR 240
Db 365 TAPILTALDIFVDRRVSALPVVNECGQVGLYSRFDVIHLAAQQTNYNHLDM SVGEALRQR 424

Qy 241 TLCLEGLVSCQPHEISGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDILOALVLS PAGI 300
Db 425 TLCLEGLVSCQPHEISGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDILOALVLS PAGI 484

Qy 301 DALGA 305
Db 485 DALGA 489

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RESULT 7
US-10-756-149-5028
; Sequence 5028, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10756,149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5028
; LENGTH: 492
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-756-149-5028

Query Match      98.3%; Score 1525; DB 5; Length 492;
Best Local Similarity 98.4%; Pred. No. 1.5e-145;
Matches 299; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      1 MRFQEHCTCYDAMATSSKLVIFDTMLEIKKAFPAFFALVANGVRAAPLWDSKKQSFVGMLTIT 60
Db      185 MRFIEHCTCYDAMATSSKLVIFDTMLEIKKAFPAFFALVANGVRAAPLWDSKKQSFVGMLTIT 244

Qy      61 DFILVHLHRYRSPVQIYEIEQHKTWREIYLOGCPKPLVSI SPNDSLFEAVVTLIKNR 120
Db      245 DFILVHLHRYRSPVQIYEIEQHKTWREIYLOGCPKPLVSI SPNDSLFEAVVTLIKNR 304

Qy      121 IHRLPVLDPVSGNVHLTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 180
Db      305 IHRLPVLDPVSGNVHLTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 364

Qy      181 TAPILTALDIFVDRRVSALPVVNECGVVGLYSRFDVHILAAQOTYNNHLDMSVGEALRQR 240
Db      365 TAPILTALDIFVDRRVSALPVVNECGVVGLYSRFDVHILAAQOTYNNHLDMSVGEALRKR 424

Qy      241 TLCLEGVLSQCPHESLGEVIDRIAREQVHRLVLDVDETOHLLGVVSLSDILOALVLSPAGI 300
Db      425 TLCLEGVLSQCPHESLGEVIDRIAREQVHRLVLDVDETOHLLGVVSLSDILOALVLSPAGI 484

Qy      301 DALG 304
Db      485 DSPG 488

RESULT 8
US-09-950-022-2
; Sequence 2, Application US/09950022
; Publication No. US20030017470A1
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: Novel PRKAG3 Alleles and Use fo the Same as Genetic Markers for
; TITLE OF INVENTION: Reproductive and Meat Quality Traits
; FILE REFERENCE: P04668US3
; CURRENT APPLICATION NUMBER: US/09/950,022
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0

Qy      1 MRFQEHCTCYDAMATSSKLVIFDTMLEIKKAFPAFFALVANGVRAAPLWDSKKQSFVGMLTIT 60
Db      160 MRFQEHCTCYDAMATSSKLVIFDTMLEIKKAFPAFFALVANGVRAAPLWDSKKQSFVGMLTIT 219

Qy      61 DFILVHLHRYRSPVQIYEIEQHKTWREIYLOGCPKPLVSI SPNDSLFEAVVTLIKNR 120
Db      161 DFILVHLHRYRSPVQIYEIEQHKTWREIYLOGCPKPLVSI SPNDSLFEAVVTLIKNR 120
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; SEQ ID NO 2
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-950-022-2

Query Match      97.2%; Score 1507; DB 3; Length 464;
Best Local Similarity 97.0%; Pred. No. 9e-144;
Matches 296; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy      1 MRFQEHCTCYDAMATSSKLVIFDTMLEIKKAFPAFFALVANGVRAAPLWDSKKQSFVGMLTIT 60
Db      160 MRFQEHCTCYDAMATSSKLVIFDTMLEIKKAFPAFFALVANGVRAAPLWDSKKQSFVGMLTIT 219

Qy      61 DFILVHLHRYRSPVQIYEIEQHKTWREIYLOGCPKPLVSI SPNDSLFEAVVTLIKNR 120
Db      220 DFILVHLHRYRSPVQIYEIEQHKTWREIYLOGCPKPLVSI SPNDSLFEAVVTLIKNR 279

Qy      121 IHRLPVLDPVSGNVHLTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 180
Db      280 IHRLPVLDPVSGNVHLTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 339

Qy      181 TAPILTALDIFVDRRVSALPVVNECGVVGLYSRFDVHILAAQOTYNNHLDMSVGEALRQR 240
Db      340 TAPILTALDIFVDRRVSALPVVNECGVVGLYSRFDVHILAAQOTYNNHLDMSVGEALRQR 399

Qy      241 TLCLEGVLSQCPHESLGEVIDRIAREQVHRLVLDVDETOHLLGVVSLSDILOALVLSPAGI 300
Db      400 TLCLEGVLSQCPHESLGEVIDRIAREQVHRLVLDVDETOHLLGVVSLSDILOALVLSPAGI 459

Qy      301 DALGA 305
Db      460 DALGA 464

RESULT 9
US-09-950-022-4
; Sequence 4, Application US/09950022
; Publication No. US20030017470A1
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: Novel PRKAG3 Alleles and Use fo the Same as Genetic Markers for
; TITLE OF INVENTION: Reproductive and Meat Quality Traits
; FILE REFERENCE: P04668US3
; CURRENT APPLICATION NUMBER: US/09/950,022
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-950-022-4

Query Match      97.2%; Score 1507; DB 3; Length 464;
Best Local Similarity 97.0%; Pred. No. 9e-144;
Matches 296; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy      1 MRFQEHCTCYDAMATSSKLVIFDTMLEIKKAFPAFFALVANGVRAAPLWDSKKQSFVGMLTIT 60
Db      160 MRFQEHCTCYDAMATSSKLVIFDTMLEIKKAFPAFFALVANGVRAAPLWDSKKQSFVGMLTIT 219

Qy      61 DFILVHLHRYRSPVQIYEIEQHKTWREIYLOGCPKPLVSI SPNDSLFEAVVTLIKNR 120
Db      161 DFILVHLHRYRSPVQIYEIEQHKTWREIYLOGCPKPLVSI SPNDSLFEAVVTLIKNR 120
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Db 220 DFILVLRHRYRSPVQIYIEIEEHKIEIETWREIYLGCCFKPLVSPNDLSLFEAVYALIKNR 279
Qy 121 IHRPLVLDPVSGNVHLHILTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 180
Db 280 IHRPLVLDPVSGAVLHILTHKRLKFLHIFGTLPRPSFLYRTIQDLGIGTFRDLAVVLE 339
Qy 181 TAPILTALDIFVDRRVSALPVNCGVGLYSRFDVHLAAQOTYVHLDMSVGEALRQR 240
Db 340 TAPILTALDIFVDRRVSALPVNCGVGLYSRFDVHLAAQOTYVHLDMSVGEALRQR 399
Qy 241 TLCLEGLVSCQPHEISLEGEVIDRIAREQVHRLVLVDETOHLLGVVSLSDIILQALVLSGAGI 300
Db 400 TLCLEGLVSCQPHEISLEGEVIDRIAREQVHRLVLVDETOHLLGVVSLSDIILQALVLSGAGI 459
Qy 301 DALGA 305
Db 460 DALGA 464

RESULT 10
US-09-950-022-6
; Sequence 6, Application US/09950022
; Publication No. US20030017470A1
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: Novel PRKAG3 Alleles and Use for the Same as Genetic Markers for
; FILE REFERENCE: P04668US3
; CURRENT APPLICATION NUMBER: US/09/950,022
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-950-022-6

Query Match 97.2%; Score 1507; DB 3; Length 464;
Best Local Similarity 97.0%; Pred. No. 9e-144;
Matches 296; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMLTIT 60
Db 160 MRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMLTIT 219
Qy 61 DFILVLRHRYRSPVQIYIEIEEHKIEIETWREIYLGCCFKPLVSPNDLSLFEAVYALIKNR 120
Db 220 DFILVLRHRYRSPVQIYIEIEEHKIEIETWREIYLGCCFKPLVSPNDLSLFEAVYALIKNR 279
Qy 121 IHRPLVLDPVSGNVHLHILTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 180
Db 280 IHRPLVLDPVSGAVLHILTHKRLKFLHIFGTLPRPSFLYRTIQDLGIGTFRDLAVVLE 339
Qy 181 TAPILTALDIFVDRRVSALPVNCGVGLYSRFDVHLAAQOTYVHLDMSVGEALRQR 240
Db 340 TAPILTALDIFVDRRVSALPVNCGVGLYSRFDVHLAAQOTYVHLDMSVGEALRQR 399
Qy 241 TLCLEGLVSCQPHEISLEGEVIDRIAREQVHRLVLVDETOHLLGVVSLSDIILQALVLSGAGI 300
Db 400 TLCLEGLVSCQPHEISLEGEVIDRIAREQVHRLVLVDETOHLLGVVSLSDIILQALVLSGAGI 459
Qy 301 DALGA 305
Db 460 DALGA 464

RESULT 12
US-11-075-134-4
; Sequence 4, Application US/11075134
; Publication No. US20050208551A1
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: Novel PRKAG3 Alleles and Use for the Same as Genetic Markers for
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Db 220 DFILVLRHRYRSPVQIYIEIEEHKIEIETWREIYLGCCFKPLVSPNDLSLFEAVYALIKNR 279
Qy 121 IHRPLVLDPVSGNVHLHILTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 180
Db 280 IHRPLVLDPVSGAVLHILTHKRLKFLHIFGTLPRPSFLYRTIQDLGIGTFRDLAVVLE 339
Qy 181 TAPILTALDIFVDRRVSALPVNCGVGLYSRFDVHLAAQOTYVHLDMSVGEALRQR 240
Db 340 TAPILTALDIFVDRRVSALPVNCGVGLYSRFDVHLAAQOTYVHLDMSVGEALRQR 399
Qy 241 TLCLEGLVSCQPHEISLEGEVIDRIAREQVHRLVLVDETOHLLGVVSLSDIILQALVLSGAGI 300
Db 400 TLCLEGLVSCQPHEISLEGEVIDRIAREQVHRLVLVDETOHLLGVVSLSDIILQALVLSGAGI 459
Qy 301 DALGA 305
Db 460 DALGA 464

RESULT 10
US-09-950-022-6
; Sequence 6, Application US/09950022
; Publication No. US20030017470A1
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: Novel PRKAG3 Alleles and Use for the Same as Genetic Markers for
; FILE REFERENCE: P04668US3
; CURRENT APPLICATION NUMBER: US/09/950,022
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-950-022-6

Query Match 97.2%; Score 1507; DB 3; Length 464;
Best Local Similarity 97.0%; Pred. No. 9e-144;
Matches 296; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMLTIT 60
Db 160 MRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMLTIT 219
Qy 61 DFILVLRHRYRSPVQIYIEIEEHKIEIETWREIYLGCCFKPLVSPNDLSLFEAVYALIKNR 120
Db 220 DFILVLRHRYRSPVQIYIEIEEHKIEIETWREIYLGCCFKPLVSPNDLSLFEAVYALIKNR 279
Qy 121 IHRPLVLDPVSGNVHLHILTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 180
Db 280 IHRPLVLDPVSGAVLHILTHKRLKFLHIFGTLPRPSFLYRTIQDLGIGTFRDLAVVLE 339
Qy 181 TAPILTALDIFVDRRVSALPVNCGVGLYSRFDVHLAAQOTYVHLDMSVGEALRQR 240
Db 340 TAPILTALDIFVDRRVSALPVNCGVGLYSRFDVHLAAQOTYVHLDMSVGEALRQR 399
Qy 241 TLCLEGLVSCQPHEISLEGEVIDRIAREQVHRLVLVDETOHLLGVVSLSDIILQALVLSGAGI 300
Db 400 TLCLEGLVSCQPHEISLEGEVIDRIAREQVHRLVLVDETOHLLGVVSLSDIILQALVLSGAGI 459
Qy 301 DALGA 305
Db 460 DALGA 464

RESULT 12
US-11-075-134-4
; Sequence 4, Application US/11075134
; Publication No. US20050208551A1
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: Novel PRKAG3 Alleles and Use for the Same as Genetic Markers for
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Db 220 DFILVLRHRYRSPVQIYIEIEEHKIEIETWREIYLGCCFKPLVSPNDLSLFEAVYALIKNR 279
Qy 121 IHRPLVLDPVSGNVHLHILTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 180
Db 280 IHRPLVLDPVSGAVLHILTHKRLKFLHIFGTLPRPSFLYRTIQDLGIGTFRDLAVVLE 339
Qy 181 TAPILTALDIFVDRRVSALPVNCGVGLYSRFDVHLAAQOTYVHLDMSVGEALRQR 240
Db 340 TAPILTALDIFVDRRVSALPVNCGVGLYSRFDVHLAAQOTYVHLDMSVGEALRQR 399
Qy 241 TLCLEGLVSCQPHEISLEGEVIDRIAREQVHRLVLVDETOHLLGVVSLSDIILQALVLSGAGI 300
Db 400 TLCLEGLVSCQPHEISLEGEVIDRIAREQVHRLVLVDETOHLLGVVSLSDIILQALVLSGAGI 459
Qy 301 DALGA 305
Db 460 DALGA 464

RESULT 11
US-11-075-134-2
; Sequence 2, Application US/11075134
; Publication No. US20050208551A1
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: Novel PRKAG3 Alleles and Use for the Same as Genetic Markers for
; FILE REFERENCE: P04668US3
; CURRENT APPLICATION NUMBER: US/11/075,134
; PRIOR FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: US/09/950,022
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Sus scrofa
US-11-075-134-2

Query Match 97.2%; Score 1507; DB 6; Length 464;
Best Local Similarity 97.0%; Pred. No. 9e-144;
Matches 296; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMLTIT 60
Db 160 MRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMLTIT 219
Qy 61 DFILVLRHRYRSPVQIYIEIEEHKIEIETWREIYLGCCFKPLVSPNDLSLFEAVYALIKNR 120
Db 220 DFILVLRHRYRSPVQIYIEIEEHKIEIETWREIYLGCCFKPLVSPNDLSLFEAVYALIKNR 279
Qy 121 IHRPLVLDPVSGNVHLHILTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 180
Db 280 IHRPLVLDPVSGAVLHILTHKRLKFLHIFGTLPRPSFLYRTIQDLGIGTFRDLAVVLE 339
Qy 181 TAPILTALDIFVDRRVSALPVNCGVGLYSRFDVHLAAQOTYVHLDMSVGEALRQR 240
Db 340 TAPILTALDIFVDRRVSALPVNCGVGLYSRFDVHLAAQOTYVHLDMSVGEALRQR 399
Qy 241 TLCLEGLVSCQPHEISLEGEVIDRIAREQVHRLVLVDETOHLLGVVSLSDIILQALVLSGAGI 300
Db 400 TLCLEGLVSCQPHEISLEGEVIDRIAREQVHRLVLVDETOHLLGVVSLSDIILQALVLSGAGI 459
Qy 301 DALGA 305
Db 460 DALGA 464

RESULT 12
US-11-075-134-4
; Sequence 4, Application US/11075134
; Publication No. US20050208551A1
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: Novel PRKAG3 Alleles and Use for the Same as Genetic Markers for
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; TITLE OF INVENTION: Reproductive					
; FILE REFERENCE: and Meat Quality Traits					
; FILE REFERENCE: P04668US3					
; CURRENT APPLICATION NUMBER: US/11/075,134					
; CURRENT FILING DATE: 2005-03-08					
; PRIOR APPLICATION NUMBER: US/09/950,022					
; PRIOR FILING DATE: 2001-09-10					
; PRIOR APPLICATION NUMBER: 60/231045					
; PRIOR FILING DATE: 2000-09-08					
; PRIOR APPLICATION NUMBER: 60/260,239					
; PRIOR FILING DATE: 2001-01-08					
; PRIOR APPLICATION NUMBER: 60/299,111					
; PRIOR FILING DATE: 2001-06-18					
; NUMBER OF SEQ ID NOS: 21					
; SOFTWARE: PatentIn version 3.1					
; SEQ ID NO 4					
; LENGTH: 464					
; TYPE: PRT					
; ORGANISM: Sus scrofa					
US-11-075-134-4					
Query Match 97.2%; Score 1507; DB 6; Length 464;					
Best Local Similarity 97.0%; Pred.No.9e-144;					
Matches 296; Conservative 4; Mismatches 5; Indels 0; Gaps 0;					
Qy	1	MRFMQEHTCYDAMATSSKLVI	FDTMLEIKKAPFALVANGVRAA	PWDSSKKQSFGVGLTIT	60
Dd	160	MHFMQEHTCYDAMATSSKLVI	FDTMLEIKKAPFALVANGVRAA	PWDSSKKQSFGVGLTIT	219
Qy	61	DFILVLHRYRSPLVQIYEIEQH	KIETWREIYLGCGFKPLVSIS	PNDSLFEAVTYLIKNR	120
Dd	220	DFILVLHRYRSPLVQIYEIEEH	KIETWREIYLGCGFKPLVSIS	PNDSLFEAVTYLIKNR	279
Qy	121	IHLRPVLDPSGVNVLTHLTKRL	LKFHIHGSLLPRPSFLYRTIQD	LGIOTFRDLAVVLE	180
Dd	280	IHLRPVLDPSGAVNLTHLTKRL	LKFHIHGSLLPRPSFLYRTIQD	LGIOTFRDLAVVLE	339
Qy	181	TAPILTALDIFVDRRVSALPVN	ECSGQVGVIYSRFDVHIAAQYT	NHLDMSVGEALRQR	240
Dd	340	TAPILTALDIFVDREVSAIPVN	ETGQVGVIYSRFDVHIAAQYT	NHLDMSVGEALRQR	399
Qy	241	TLCEGLVSCQPHESLGEVIDRI	AREQVHRVLVDETOHLLGVVSL	SDDILOALVLSAGI	300
Dd	400	TLCEGLVSCQPHELTGEVIDRI	VREQVHRVLVDETOHLLGVVSL	SDDILOALVLSAGI	459
Qy	301	DALCA 305			
Dd	460	DALCA 464			
RESULT 13					
US-11-075-134-6					
; Sequence 6, Application US/11075134					
; Publication No. US20050208551A1					
; GENERAL INFORMATION:					
; APPLICANT: Rothschild, Max					
; APPLICANT: Ciobanu, Dan					
; APPLICANT: Malek, Massoud					
; APPLICANT: Plastow, Graham					
; TITLE OF INVENTION: Novel PKAK3 Alleles and Use fo the Same as Genetic Markers for					
; TITLE OF INVENTION: Reproductive					
; TITLE OF INVENTION: and Meat Quality Traits					
; FILE REFERENCE: P04668US3					
; CURRENT APPLICATION NUMBER: US/11/075,134					
; CURRENT FILING DATE: 2005-03-08					
; PRIOR APPLICATION NUMBER: US/09/950,022					
; PRIOR FILING DATE: 2001-09-10					
; PRIOR APPLICATION NUMBER: 60/231045					
; PRIOR FILING DATE: 2000-09-08					
; PRIOR APPLICATION NUMBER: 60/260,239					
; PRIOR FILING DATE: 2001-01-08					
; PRIOR APPLICATION NUMBER: 60/299,111					
; PRIOR FILING DATE: 2001-06-18					

Qy	61	DFILVLRHYRSPVLQVIYEIIOHKIETWREIYLOGCFKPLVSISPNDSLFEAVYTILKNR	120
Dd	220	DFILVLRHYRSPVLQVIYEIBEHKIETWREIYLOGCFKPLVSISPNDSLFEAVYALIKNR	279
Qy	121	IHRLPVLDPPVSGNVLIHLTHKRLLKFPHIFGSLLPRPSFLXYRTIQDLGITGFDRDLAVLIE	180
Dd	280	IHRLPVLDPPVSGAVLIHLTHKRLLKFPHIFGTLLPRPSFLXYRTIQDLGITGFDRDLAVLIE	339
Qy	181	TAPILTALDIPVDRRVSALPVMNEGGQVGLYSRFDVTIHLAAQTYNHLDMSVSGBALRQR	240
Dd	340	TAPTILTALDIPVDRRVSALPVMNETGVGVLSYRFDTIHLAAQTYNHLDMNMVGEALRQR	399
Qy	241	TLCLEGLVSCOPHESLSGVIDIRAREQVHRVLVLVDETQHLLCGVWSLSITLQALVLSPAGI	300
Dd	400	TLCLEGLVSCOPHETLGEVIDIRVREQVHRVLVLVDETQHLLCGVWSLSDTLQALVLSPAGI	459
Qy	301	DALGA 305 	
Dd	460	DALGA 464 	

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US-11-075-134-8
; Sequence 8, Application US/11075134
; Publication No. US20050208551A1
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: Novel PFKF3 Alleles and Use for the Same as Genetic Markers for
; TITLE OF INVENTION: Reproductive
; TITLE OF INVENTION: and Meat Quality Traits
; FILE OF INVENTION: P04668US3
; CURRENT APPLICATION NUMBER: US/11/075,134
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: US/09/950,022
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Sus scrofa
US-11-075-134-8

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Best Local Similarity	96.7%;	Pred. No. 1.1e-143;		
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QY	1	MRFQEHCTCDAMATSSKLIVDFMTLSEIKKAPFALVANGVRAAAPLWDSKKQSFVGMLTIT	60	
DB	160	MHFQEHCTCDAMATSSKLIVDFMTLSEIKKAPFALVANGVRAAAPLWDSKKQSFVGMLTIT	219	
QY	61	DFILVLHRYRSPLVQVYEIEQHKIETWREIYLOGCFKPLVSIISPNDSLFEAVYTLIKNR	120	
DB	220	DFILVLHRYRSPLVQVYEIESEHKIETWREIYLOGCFKPLVSIISPNDSLFEAVYALIKNR	279	
QY	121	IHRLLPVLDPVSGNVLHLTHLKRLLKFLHI FGSLLPRPSFLYRTIQDLGIGFRDLAVVLE	180	
DB	280	IHRLLPVLDPVSGAVLHLTHLKRLLKFLHI FGTLPLPRPSFLYRTIQDLGIGFRDLAVVLE	339	
QY	181	TAPILTALDITFVDRRSALPVNCEGGVGLYSRFDVHILAAQOTYNHLDMSVGEALRQR	240	
DB	340	TAPILTALDITFVDRRSALPVNCEGGVGLYSRFDVHILAAQOTYNHLDNMVGEALRQR	399	
QY	241	TLCLEGVLSQCPHESLGEVDRITAREQVHRLVLDVETQHLLGVVLSLSDILQALVLSPAGI	300	

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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 24, 2006, 22:02:17 ; Search time 29.5657 Seconds
(without alignments)
1510.014 Million cell updates/sec

Title: US-10-070-794A-30
Perfect score: 2403
Sequence: 1 MSFLEQNSSWSPAVTSS.....LSDILOALVLSPPAGIDALGA 464

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1028	42.8	330	2 T10759	AMP-activated prot
2	488	20.3	478	2 T25899	hypothetical prote
3	457	19.0	322	1 RBYC3	regulatory protein
4	375.5	15.6	274	2 S67444	probable 5'-AMP-ac
5	243.5	10.1	331	2 B86222	hypothetical prote
6	222	9.2	443	2 T25854	hypothetical prote
7	215.5	9.0	460	2 T24248	Pv42 protein - kid
8	214	8.9	379	2 T10371	hypothetical prote
9	198	8.2	424	2 T46197	hypothetical prote
10	197	8.2	629	2 T18227	hypothetical prote
11	189.5	7.9	352	2 F86287	hypothetical prote
12	179	7.4	399	2 D96832	hypothetical prote
13	163	6.8	447	2 B96720	hypothetical prote
14	163	6.8	527	2 S46088	hypothetical prote
15	161.5	6.7	392	2 G75056	dehydrogenase PAB0
16	155.5	6.5	322	2 D71175	hypothetical prote
17	149	6.2	280	1 H64452	conserved hypotet
18	148.5	6.2	250	2 C90449	conserved hypotet
19	148	6.2	92	2 T50087	probable 5'-AMP-ac
20	146	6.1	313	1 E69030	conserved hypotet
21	141.5	5.9	157	1 F69185	yhcV homolog MTH64
22	139	5.8	152	2 AF2282	hypothetical prote
23	139	5.8	300	1 S08244	conserved hypotet
24	138.5	5.8	421	2 C64475	hypothetical prote
25	138	5.7	485	1 JC4998	IMP dehydrogenase
26	137	5.7	284	1 H69355	conserved hypotet
27	136.5	5.7	527	2 S64060	probable membrane
28	134	5.6	1286	2 A12195	two-component hybr
29	130.5	5.4	792	2 A84308	chloride channel [

30	129.5	5.4	1344	2 AD2103	two-component hybr
31	126.5	5.3	168	1 A64478	hypothetical prote
32	126	5.2	486	1 E71456	IMP dehydrogenase
33	125.5	5.2	157	2 AF3344	IMP dehydrogenase
34	123.5	5.1	287	2 F72780	hypothetical prote
35	122	5.1	282	2 C75148	hypothetical prote
36	120.5	5.0	223	2 T36952	conserved hypotet
37	120.5	5.0	278	2 A72781	probable acetoin u
38	120.5	5.0	284	1 H69232	Yjv25-related pro
39	119	5.0	122	2 B69119	yhcV homolog MTH18
40	119	5.0	485	2 E75015	IMP dehydrogenase
41	116.5	4.8	382	2 AD2762	conserved hypotet
42	116.5	4.8	382	2 C97543	hypothetical prote
43	115.5	4.8	285	1 C71188	conserved hypotet
44	115.5	4.8	895	2 T03446	probable transcript
45	115	4.8	482	2 C72264	IMP dehydrogenase

ALIGNMENTS

RESULT 1

T10759
AMP-activated protein kinase (EC 2.7.1.1-) gamma chain - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T10759
R;Woods, A.; Cheung P, C.F.; Smith, F.C.; Davison, M.D.; Scott, J.; Beri, R.K.; Carling, J. Biol. Chem. 271, 10282-10290, 1996
A;Title: Characterization of AMP-activated protein kinase beta and gamma subunits: Assem
A;Reference number: 206738; MUID:96215327; PMID:8626596
A;Accession: T10759
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-330 <HOO>
A;Cross-references: UNIPROT:P80385; UNIPARC:UPI00001250B4; EMBL:X95578; NID:g1185270; PI
A;Experimental source: strain Wistar
C;Complex: heterotrimer; alpha, beta and gamma chains
C;Function:
A;Description: is responsible for the regulation of fatty acid synthesis by phosphorylat
C;Superfamily: CAT3 protein
C;Keywords: fatty acid biosynthesis; phosphotransferase

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Best Local Similarity 62.3%; Pred.No.1.4e-73;
Matches 197; Conservative 56; Mismatches 63; Indels 0; Gaps 0;

QY	140	APPKLGWDELKPGCAQIYMRFMQEHCTCYDAMATSSKLVIFDTMLEIKKAPFALVANGV	199
DB	9	APAPENEHSQETPSNSSVYTTFMKSHRCVLDIPTSSKLVVFDTSLOVKKAFALVTNGV	68
QY	200	RAAPLWDSKKQSPVGMLTITDFILVLRHYRSPLVQIYEIEQHKIETWREIYLQGCFKPL	259
DB	69	RAAPLWDSKKQSPVGMLTITDFINILHRYKSAVQIYELEEHKIETWREIVYLDQSFPL	128
QY	260	VSISPNDLSFEAVYTLIKRIHRLPVLDPVSGNVLHILTKRLKLFHIFGLSPFSFL	319
DB	129	VCISPNASLFDVSSLI RNKHILPVIDPSGNLTLYLTHKRLKLFKLFITFPKPEFM	188
QY	320	YRTIQDLGTGTRDLAVLLETAPILTALDIFVDRRSALPVPVNECGVGLYRFRDVIHL	379
DB	189	SKSLEELQIGTGVANIAMVRITTPVYVALGIFVQHRVSALPVPVDEKGRVVDIYSKFDVINL	248
QY	380	AAQOTVNHLDMSVGEALRORTLCLEGLVSCQPHESIGEVIDRIARQVHRLVLVDEQHL	439
DB	249	AAEKTNNLDVSVTKALQHRSHYFEGVLKCYLHLEALINRLVAEVHRLVVDHVV	308
QY	440	LGWVSLSDILQALVLS	455
DB	309	KGIVSLSDILQALVLT	324

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[illegible]

C:Genetics:
A;Note: Ca41C0.01c

Query Match 8.2%; Score 197; DB 2; Length 629;
Best Local Similarity 22.4%; Pred. No. 1.6e-07;
Matches 106, Conservative 79; Mismatches 197; Indels 92; Gaps 20;

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Db :
4 PPQPROMPKSPRLSTSTSGPSAPVNLGSPRPSPOLQHQPSSASTSST-----TST 56
Qy 98 ASAGSTDDVEATEEPATEAW-----ECEGLELLEERPALCLSPQAPFFKLGM--- 147
Db :
57 ATTGGGIS-----ATAPGSTOYHLHHHPSRKTSIVELLSPPLPTDNDPIHQLSLRH 111
Qy 148 -----DDELAKPGAQIYMRFQEHTC-----YDMATSKGLVIFDTMLSIKKA 190
Db :
112 ASTSSNKSSQSOTAPGSTA---ITNHAFSLVDNSEIPLTETESKNLISHSHSVQA 167
Qy 191 FFALVANGVRAAPLWSKK--QSFVGMLTI-----TDFILVLHYRRSP-----VQ 235
Db :
168 FETLLKNTLTSVPVISKSDPHDLTNCLTPDYSDLANTYLLIMKINYSSELNVDDIGDPN 227
Qy 236 IYIEIQH-----KIETWEIYLQCFK-----PLVSISPNDLSFEAVYTILKRIRH 282
Db :
228 ISPPERHEFVTQTISKARCEEVPEVFIIKHPKNPFKEFNETDTLFSVMETL-GNGVHR 286
Qy 283 LPVLDPVSGNVLHILTHKRLKFLHFISGLLPRSP-LYRTIODLGIGTFRDLAHVLETA 341
Db :
287 IATNEBGNKITGLSORRLIKTWENARRFPSSLDFLTSTLOQLKGSNPI-TTYEDQ 345
Qy 342 PIITALDIFVDRRVSAIPVNNEGQGVGLYSREFDVIHLAAQQTYNHLMSV----GEALR 397
Db :
346 MLTEALKHMENERVSSLAVIDRSKTLIGNISIVDVKNVTSSKNSHLLFKSVLNFIYNLS 405
Qy 398 QRTLCLEG-----VLSQCPHSEIGEVIDRTAREQVHRLVLVDETOHLLGVVSL 446
Db :
406 QKGI-BEGODQPFIFHNNQTSLSGRVIAKLVAQSHRLWIVDSSROASSMSSAS 458

RESULT 11
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C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: F86287
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Pedersen, N.A.; Kaul, S.; White, O.; Alonso,
Chen, N.F.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
Nature 408, 816-820, 2000
A:A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: AB6141; MUID:21016719; PMID:11130712
A:Accession: F86287
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-352 <STO>
A:Cross-references: UNIPROT:Q9X137; UNIPARC:UIP000004825C; GB:AB005172; NID:g5103830; PT
C:Genetics:
A:Map position: 1

Query Match 7.9%; Score 189.5; DB 2; Length 352;
Best Local Similarity 23.2%; Pred. No. 2.8e-07;
Matches 81, Conservative 59; Mismatches 128; Indels 81; Gaps 13;

Qy 167 TCYDAMATSKSLVIPDTMLSIKKAFFALVANGVRAAPL-----W-----DSKQOS 211
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17 TAKDLTVRNRLRVPEVPTYATLSHAMNTLVANSIALPVAAPPGHWITGAGGSMTMESDKQT 76

C:Genetics:
A;Note: Ca41C0.01c

Query Match 8.2%; Score 197; DB 2; Length 629;
Best Local Similarity 22.4%; Pred. No. 1.6e-07;
Matches 106, Conservative 79; Mismatches 197; Indels 92; Gaps 20;

Qy 46 PPOGEGPRG-RPTAESTGLEAT-----PPK-TTPLAQADPAGVGPPTPGWDCLPSCDT 97
Db :
4 PPQPROMPKSPRLSTSTSGPSAPVNLGSGRPSPPOLQHQPSSASTSST-----TST 56
Qy 98 ASAGSTDDVEATEEPATEAW-----ECELEGLEERPALCLSPQAFFKLGM--- 147
Db :
57 ATTGGGIS-----ATAPGSTOYHLHHHPSRKTSIVELLSPPLPTDNDPIHQLSLRH 111
Qy 148 -----DDELAKPGAQIYMRFQEHTC-----YDMATSKGLVIFDTMLSIKKA 190
Db :
112 ASTSSNKSSQSOTAPGSTA----ITNHAFSLVDNSEIPLTETESKNLISHSHSVQSA 167
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Db :
168 FETLLKNTLTSVPVISKSDPHDLTNCLTPDYSDLNLYLLIMKINYSSELNVDDIGDPN 227
Qy 236 IYIEIQH-----KIETWEIYLQCCK-----PLVSISPNDLSFEAVYTILKRIRH 282
Db :
228 ISQPERHEFVTQTISKARCEEVPEVFIIKHPKNPFKEFNEDTLFSVMETL-GNGVHR 286
Qy 283 LPVLDPVSGNVLHILTHKRLKFLHFISGLLPRSP-LYRTIODLGIGTFRDLAHVLETA 341
Db :
287 IATNEBGNKITGLSORRLIKTWENARRFPSSLDFYLTSTLOQLKGSNPI-TIYEDQ 345
Qy 342 PIITALDIFVDRRVSAIPVNNEGQGVGLYSREFDVIHLAAQOQTYNHLDMSV-----GEALR 397
Db :
346 MLTEALKHMENERVSSLAVIDRSKTLIGNISIVDVKNVTSSKNSHLLFKSVLNFIYNLS 405
Qy 398 QRTLCLEG-----VLSQCPHSEIGEVIDRTAREQVHRLVLVDETOHLLGVVSLUS 446
Db :
406 QKGI-BEGODQPFIFHNNQTSLSGRVIAKLVAQSHRLWIVDSSROASSMSSAS 458

RESULT 11
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hypothetical protein F9UL27 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: F86287
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Pedersenpiel, N.A.; Kaul, S.; White, O.; Alonso,
ansen, N.F.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
Nature 408, 816-820, 2000
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: AB6141; MUID:21016719; PMID:11130712
A:Accession: F86287
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-352 <STO>
A:Cross-references: UNIPROT:Q9X137; UNIPARC:UIP000004825C; GB:AB005172; NID:g5103830; PT
C:Genetics:
A:Map position: 1

Query Match 7.9%; Score 189.5; DB 2; Length 352;
Best Local Similarity 23.2%; Pred. No. 2.8e-07;
Matches 81, Conservative 59; Mismatches 128; Indels 81; Gaps 13;

Qy 167 TCYDAMATSKSLVIPDTMLSIKKAFFALVANGVRAAPL-----W-----DSKKQS 211
Db | :
17 TAKDLTVRNRLRVPEVPTYATLSHAMNTLVANSIALPVAAPPGHWITGAGGSMTMESDKQT 76

C:Genetics:
A;Note: Ca41C0.01c

Query Match 8.2%; Score 197; DB 2; Length 629;
Best Local Similarity 22.4%; Pred. No. 1.6e-07;
Matches 106, Conservative 79; Mismatches 197; Indels 92; Gaps 20;

Qy 46 PPOGEGPRG--RPTAESTGLEAT-----PPK-TTPLAQADPAGVGPPTPGWDCLPSCDT 97
Db :
4 PPQPROMPKSPRLSTSTSGPSAPVNLLGSRPSPPOLQHQPSSASTSST-----TST 56
Qy 98 ASAGSTDDVEATEEPATEAW-----ECEGLELLEERPALCLSPQAPFFKLGM--- 147
Db :
57 ATTGGGIS-----ATAPGSTOYHLHHHPSRKTSIVELLSPPLPTDNDPIHQLSLRH 111
Qy 148 -----DDELAKPGAQIYMRFQEHTC-----YDMATSKGLVIFDTMLSIKKA 190
Db :
112 ASTSSNKSSQSOTAPGSTA----ITNHAFSLVDNSEIPLTETESKNLISHSHSVQSA 167
Qy 191 FFALVANGVRAAPLWSKK--QSFVGMLTI-----TDFILVLHRYRSP-----VQ 235
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168 FETLLKNTLTSVPVISKSDPHDLTNCLTPDYSDLNLYLLIMKINYSSELNVDDIGDPN 227
Qy 236 IYIEIQH-----KIETWEIYLQCFK-----PLVSISPNDLSFEAVYTILKRIRH 282
Db :
228 ISPPERHEFVTQTISKARCEEVPEVFIIKHPKNPFKEFNEDTLFSVMETL-GNGVHR 286
Qy 283 LPVLDPVSGNVLHILTHKRLKFLHFISGLLPRSP-LYRTIODLGIGTFRDLAHVLETA 341
Db :
287 IATNBEGNKITGLSORRLIKTWENARRFPSSLDFYLTSTLOQLKIGSNPI-TIYEDQ 345
Qy 342 PIITALDIFVDRRVSAIPVNECGVVGLYSREFDVIHLAAQOQTYNHLDMSV-----GEALR 397
Db :
346 MLTEALHKMFNERVSSLAVIDRSKTLIGNISIVDVKNVTSSKNSHLLFKSVLNFIYNLS 405
Qy 398 QRTLCLEG-----VLSQCPHSEIGEVIDRTAREQVHRLVLVDETOHLLGVVSL 446
Db :
406 QKGI-BEGODQPFIFHYNNQTSIGRWIAKLVAQSHRLWIVDSSROASSMSSAS 458

RESULT 11
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hypothetical protein F9U1.27 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: F86287
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Pedersen, N.A.; Kaul, S.; White, O.; Alonso,
Chen, N.F.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
Nature 408, 816-820, 2000
A:A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: AB6141; MUID:21016719; PMID:11130712
A:Accession: F86287
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-352 <STO>
A:Cross-references: UNIPROT:Q9X137; UNIPARC:UPI000004825C; GB:AB005172; NID:g5103830; PT
C:Genetics:
A:Map position: 1

Query Match 7.9%; Score 189.5; DB 2; Length 352;
Best Local Similarity 23.2%; Pred. No. 2.8e-07;
Matches 81, Conservative 59; Mismatches 128; Indels 81; Gaps 13;

Qy 167 TCYDAMATSKLVIPDTMLSIKKAFFALVANGVRAAPL-----W-----DSKQOS 211
Db | :
17 TAKDLTVNRNLRVPEVPTYATLSHAMMTLVANSIALPVAAPPGHWITGAGGSMTMESDKQT 76

Qy	202	APLWSUKQKQSFVGMLTITDFILVL---HRYRSPLOIYIEIOHKIETW-----REY	251
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Qy	252	LOGCFKPLVISPNDSLFEAVYTIKKRIHRPLVLPDVSNGVLIHLTHKRLKFLHIFGS	311
		: : : : : : : : : : : : : : : : : : : :	
Db	74	-----KPAPVVKPTDDLSHAALKLLETDLASLPVGEN-KAEILGVISDMALLE-----	120
Qy	312	LLPRSFYRIQTDLGIGCTFFDLAVLLETAPILTALDIFVDRRVKSALPVVNBGGQVVGLY	371
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Db	121	RVAAEEFGKRKVEEF---MTRKDVITLGGDDDTAKALATMRDHGIRISIPVVDDEGLGIV	177
Qy	372	SRFEDVI-----HLAAOQTYNHLMSVGE-----ALRQRTLCLEGVLSOPHESIGEVID	420
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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 24, 2006, 21:54:27 ; Search time 127.313 Seconds
(without alignments)
1601.338 Million cell updates/sec

Title: US-10-070-794A-30
Perfect score: 2403
Sequence: 1 MSFLEQENSSWSPAVTSS.....LSDILQALVLSFAGIDALGA 464

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- A_Geneseq_21.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2403	100.0	464	AAE00223	Aae00223 Human AMP
2	2403	100.0	464	ADP43223	Adp43223 Human AMP
3	2403	100.0	489	ADF50310	Adf50310 Human AMP
4	2398	99.8	489	AB47679	Aab47679 PRKAG3.1
5	2398	99.8	489	AAE32034	Aae32034 Human kin
6	2398	99.8	489	ADP87617	Adp87617 Human NOV
7	2391	99.5	489	ABP43929	Abp43929 AMP activ
8	2376	98.9	489	AAE38410	Aae38410 Human Prk
9	2376	98.9	489	ADP50314	Adf50314 Human AMP
10	2372	98.7	492	ADP87619	Adp87619 Human NOV
11	2372	98.7	492	AE69187	Aeb69187 Human mod
12	2013	83.8	464	AAE22985	Aae22985 Pig PRKAG
13	2011	83.7	464	AAE00222	Aae00222 Pig AMPK
14	2011	83.7	464	AAE22984	Aae22984 Pig wild-
15	2011	83.7	514	AAE00224	Aae00224 Sus scrof
16	2010	83.6	464	AAE22987	Aae22987 Pig PRKAG
17	2010	83.6	489	ADP43210	Adp43210 Mouse AMP
18	2007	83.5	464	AAE22988	Aae22988 Pig PRKAG
19	2005	83.4	464	AAE22986	Aae22986 Pig PRKAG
20	2000	83.2	489	ADF50312	Adf50312 Murine AM
21	1989	82.8	489	ADP87682	Adp87682 AMPK rat
22	1551	64.5	305	AAE00221	Aae00221 Human AMP
23	1550	64.5	305	AAE00329	Aae00329 Human Prk
24	1547	64.4	305	AAE00328	Aae00328 Human Prk

25	1507	62.7	305	4	AAE00220	Aae00220 Pig AMPK
26	1506	62.7	305	4	AAE00226	Aae00226 Sus scrof
27	1503	62.5	305	4	AAE00225	Aae00225 Sus scrof
28	1093	45.5	569	8	ADP43207	Adp43207 Human AMP
29	1093	45.5	569	8	ADP43217	Adp43217 Human AMP
30	1093	45.5	569	9	AE69186	Aeb69186 Human mod
31	1092	45.4	414	9	AD280782	Adz80782 Amino aci
32	1082.5	45.0	352	5	AAO18495	Aao18495 Human ins
33	1082.5	45.0	352	8	ADP43208	Adp43208 Human AMP
34	1080.5	45.0	328	2	AAW88438	Aaw88438 Disease a
35	1080.5	45.0	328	4	AAE93432	Aab93432 Human pro
36	1080.5	45.0	328	5	AAO18496	Aao18496 Human ins
37	1080.5	45.0	328	8	ADP87611	Adp87611 Human NOV
38	1080.5	45.0	328	8	ADP87613	Adp87613 Human AMP
39	1076.5	44.8	328	8	ADP87694	Adp87694 Human AMP
40	1075.5	44.8	328	8	ADP87615	Adp87615 Human NOV
41	1050	43.7	391	8	ABM83420	Abm83420 Human dia
42	1028	42.8	330	7	ADE62621	Ade62621 Rat Prote
43	1028	42.8	330	8	ADP43225	Adp43225 Rat AMPK
44	1017	42.3	331	2	AAW29817	Aaw29817 Mammalian
45	1017	42.3	331	5	AAO18497	Aao18497 Human ins

ALIGNMENTS

RESULT 1

AAE00223

ID AAE00223 standard; protein; 464 AA.

XX AC AAE00223;

XX XX

DT 13-JUN-2001 (first entry)

XX XX

DE Human AMPK gamma subunit muscle-specific isoform, complete PRKAG3.

XX XX

KW Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK;
KW PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;
KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;
KW cystathione beta synthase; CBS; cardiant; gene therapy.

XX Homo sapiens.

OS Homo sapiens.

XX Key Location/Qualifiers

XX Domain 172..225

XX /label= CBS

XX /note= "Cystathione beta synthase domain"

XX Misc-difference 200

XX /note= "RN- mutation site"

XX Domain 253..307

XX /label= CBS

XX /note= "Cystathione beta synthase domain"

XX Domain 329..382

XX /label= CBS

XX /note= "Cystathione beta synthase domain"

XX Domain 400..453

XX /label= CBS

XX /note= "Cystathione beta synthase domain"

XX WO200120003-A2.

XX 22-MAR-2001.

XX 11-SEP-2000; 2000WO-EF009896.

XX 10-SEP-1999; 99EP-00402236.

XX 18-MAY-2000; 2000EP-00401388.

XX (INRG) INRA INST NAT RECH AGRONOMIQUE.

XX (ANDE/) ANDERSSON L.

XX (LOOF/) LOOFT C.

XX (KALM/) KALM E.

XX

Db 121 ECELEGLLEERPALCLSPQAPPPKLGWDDDELKPKGAQIYMRFMQEHCTCYDAMATSSKLV 180
 Qy 181 FDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMGLTITDFILVHLHYRSPVQIYIE 240
 Db 181 FDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMGLTITDFILVHLHYRSPVQIYIE 240
 Qy 241 QHKIETWREIYLOGCFKPLVSIISPNDSLFEAVYTLIKNRHRLVLPVDPVSGNVLHILTHK 300
 Db 241 QHKIETWREIYLOGCFKPLVSIISPNDSLFEAVYTLIKNRHRLVLPVDPVSGNVLHILTHK 300
 Qy 301 RLLKFLHIFGSLPRPSFLYRTIQQDLGIGTFRDLAVVLETAPIITALDIFVDRVSALPV 360
 Db 301 RLLKFLHIFGSLPRPSFLYRTIQQDLGIGTFRDLAVVLETAPIITALDIFVDRVSALPV 360
 Qy 361 VNECGQVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQRTCLRGVLSQCPHESLGEVID 420
 Db 361 VNECGQVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQRTCLRGVLSQCPHESLGEVID 420
 Qy 421 RIAREQVHRLVLDVETQHLGWSLSLQALVLSVSPAGIDALGA 464
 Db 421 RIAREQVHRLVLDVETQHLGWSLSLQALVLSVSPAGIDALGA 464

RESULT 3

ADP50310 standard; protein; 489 AA.

XX AC ADP50310;
 XX DT 12-FEB-2004 (first entry)
 XX DE Human AMP-activated protein kinase (AMPK)-gamma 3 protein subunit.
 XX KW human; transgenic; AMP-activated protein kinase gamma 3 subunit; Prkg3;
 KW AMPK; energy metabolism; obesity; dyslipidaemia;
 KW insulin resistance syndrome; type 2 diabetes; antidiabetic; anorectic;
 KW antilipaemic.
 XX OS Homo sapiens.
 XX PN WO2003063586-A1.
 XX PD 07-AUG-2003.

31-JAN-2003; 2003WO-IB000912.

01-FEB-2002; 2002US-0353430P.

(AREX-) AREXIS AB.

Andersson L, Marklund S;

WPI; 2003-663404/62.

N-PSDB; ADF50309.

New transgenic non-human animals expressing an AMP-activated protein kinase gamma 3 subunit, useful as models for improving treatment, prevention or diagnosis of diseases related to energy metabolism, e.g. obesity or type 2 diabetes.

Claim 3; SEQ ID NO 2; 46pp; English.

This invention relates to novel transgenic non-human animals expressing an AMP-activated protein kinase (AMPK)-gamma 3 subunit. Specifically, it relates to the transgene Prkg3 gene that encodes the AMPK gamma3 subunit or a variant thereof, where the nucleic acid is operably linked to a regulatory element. AMPK is involved in the regulation of energy metabolism in eukaryotic cells, and is recognised as a major regulator of lipid biosynthetic pathways due to its role in the phosphorylation and inactivation of key enzymes such as acetyl-CoA carboxylase. The present invention describes transgenic animals expressing AMPK-gamma 3 to be used as models for energy metabolism diseases and also methods for the development of drugs for the treatment or prevention of obesity.

CC dyslipidaemia, insulin resistance syndrome or type 2 diabetes.
 CC According to the compositions of this invention have various activities including antidiabetic, anorectic and antilipaemic. This polypeptide sequence is the human AMPK-gamma3 protein subunit of the invention.
 XX
 SQ Sequence 489 AA;
 Query Match 100.0%; Score 2403; DB 7; Length 489;
 Best Local Similarity 100.0%; Pred. No. 4.2e-240;
 Matches 464; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MSFLEQNSSSWSPSPAVTSSSERIRGRRAKALRWTRQKSVGEPPGQGGSPSRPTAE 60
 Db 26 MSFLEQNSSSWSPSPAVTSSSERIRGRRAKALRWTRQKSVGEPPGQGGSPSRPTAE 85
 Qy 61 STGLEATFPKTTPLAQADPAGVTPPTGWDCLPSDCTASAGSSTDVDELATEPATEAW 120
 Db 86 STGLEATFPKTTPLAQADPAGVTPPTGWDCLPSDCTASAGSSTDVDELATEPATEAW 145
 Qy 121 ECELEGLLEERPALCLSPQAPPPKLGWDDDELKPKGAQIYMRFMQEHCTCYDAMATSSKLV 180
 Db 146 ECELEGLLEERPALCLSPQAPPPKLGWDDDELKPKGAQIYMRFMQEHCTCYDAMATSSKLV 205
 Qy 181 FDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMGLTITDFILVHLHYRSPVQIYIE 240
 Db 206 FDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGMGLTITDFILVHLHYRSPVQIYIE 265
 Qy 241 QHKIETWREIYLOGCFKPLVSIISPNDSLFEAVYTLIKNRHRLVLPVDPVSGNVLHILTHK 300
 Db 266 QHKIETWREIYLOGCFKPLVSIISPNDSLFEAVYTLIKNRHRLVLPVDPVSGNVLHILTHK 325
 Qy 301 RLLKFLHIFGSLPRPSFLYRTIQQDLGIGTFRDLAVVLETAPIITALDIFVDRVSALPV 360
 Db 326 RLLKFLHIFGSLPRPSFLYRTIQQDLGIGTFRDLAVVLETAPIITALDIFVDRVSALPV 385
 Qy 361 VNECGQVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQRTCLRGVLSQCPHESLGEVID 420
 Db 386 VNECGQVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQRTCLRGVLSQCPHESLGEVID 445
 Qy 421 RIAREQVHRLVLDVETQHLGWSLSLQALVLSVSPAGIDALGA 464
 Db 446 RIAREQVHRLVLDVETQHLGWSLSLQALVLSVSPAGIDALGA 489
 RESULT 4
 AAB47679
 ID AAB47679 standard; protein; 489 AA.
 XX AC AAB47679;
 XX DT 21-JAN-2002 (first entry)
 XX DE PRKAG3.
 XX KW Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant;
 KW metabolic disease; diabetes; obesity; substitution; ss.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT Misc-difference 71
 FT /note= "Possible variation point P71A"
 FT Misc-difference 340
 FT /note= "Possible variation point R340W"
 XX PN WO200177305-A2.
 XX PD 18-OCT-2001.
 XX PF 06-APR-2001; 2001WO-SE000765.
 XX PR 07-APR-2000; 2000US-0195665P.
 XX

CC compounds for effectiveness as agonist or antagonist of the polypeptides,
CC or in altering the expression of the target polynucleotide and compounds
CC that specifically bind to or modulate the activity of the polypeptide.
CC The microarray is useful in monitoring or measuring protein-protein
CC interactions, drug-target interactions, and gene expression profiles. KPP
CC DNA is used in gene therapy. The present sequence is human KPP protein
XX
SQ Sequence 489 AA;

Query Match 99.8%; Score 2398; DB 6; Length 489;
Best Local Similarity 99.8%; Pred. No. 1.4e-239;
Matches 463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MSFLEQNSSWSPSPAVTSSSIRIGKRAKALWTRQKSVGEPPGQEGPRSRPTAE 60
Db 26 MSFLEQNSSWSPSPAVTSSSIRIGKRAKALWTRQKSVGEPPGQEGPRSPAEE 85
Qy 61 STGLEATFPKTTPLAQAADPAGVCTPTGWDCLPSDCTASAGSSTDVELATFPATEAW 120
Db 86 STGLEATFPKTTPLAQAADPAGVCTPTGWDCLPSDCTASAGSSTDVELATFPATEAW 145
Qy 121 ECELEGLLEERPALCLSPQAPFPKLGWDDLRKPGAQIYMRFMQHTCYDAMATSSKLVI 180
Db 146 ECELEGLLEERPALCLSPQAPFPKLGWDDLRKPGAQIYMRFMQHTCYDAMATSSKLVI 205
Qy 181 FDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMLTITDFFILVHRYRSPVLQIYEIE 240
Db 206 FDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMLTITDFFILVHRYRSPVLQIYEIE 265
Qy 241 QHKIETWREIYLOQCFKPLVISPNDLSLFEAVNTLKNRTHRLPVLDPVSGNVLHILTHK 300
Db 266 QHKIETWREIYLOQCFKPLVISPNDLSLFEAVNTLKNRTHRLPVLDPVSGNVLHILTHK 325
Qy 301 RLLKFLHIFGSLPRPSFLYRTIQDLGIGTRDLAVVLETPILTALDIFVDRRVSALPV 360
Db 326 RLLKFLHIFGSLPRPSFLYRTIQDLGIGTRDLAVVLETPILTALDIFVDRRVSALPV 385
Qy 361 VNECGQVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQRTLCEGLVSLQCPHESLGEVID 420
Db 386 VNECGQVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQRTLCEGLVSLQCPHESLGEVID 445
Qy 421 RIAREQVHRLVLDVETQHLGVLVSLDILQALVLSFAGIDALGA 464
Db 446 RIAREQVHRLVLDVETQHLGVLVSLDILQALVLSFAGIDALGA 489

RESULT 6

ADP87617
ID ADP87617 standard; protein; 489 AA.
AC ADP87617;
XX

DT 23-SEP-2004 (first entry)

XX Human NOVX polypeptide, NOV10a.

XX anorectic; antidiabetic; gene therapy; vaccine; obesity; diabetes;
KW insulin resistance; hybridization probe; chromosome mapping;
KW tissue typing; preventive medicine; pharmacogenomics; NOVX; human.
XX

OS Homo sapiens.

XX W02004056961-A2.

XX 08-JUL-2004.

XX 27-OCT-2003; 2003WO-US034114.

XX 25-OCT-2002; 2002US-0421239P.

PR 28-OCT-2002; 2002US-0421700P.

PR 31-OCT-2002; 2002US-0422776P.

PR 13-NOV-2002; 2002US-0426197P.

PR 20-DEC-2002; 2002US-0435498P.

PR 20-DEC-2002; 2002US-0435510P.
PR 20-DEC-2002; 2002US-0435568P.
PR 21-MAR-2003; 2003US-0456812P.
XX
XX (CURA-) CURAGEN CORP.
XX Berghs C, Catterton E, Ellerman K, Ort T, Rieger D, Chaudhuri A;
XX WPI; 2004-500293/47.
DR N-PSDB; ADP87616.
XX
XX New NOVX nucleic acid molecules and polypeptides useful for preventing or
PT treating NOVX-associated disorders, e.g. diabetes, insulin resistance or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX
PS Claim 3; SEQ ID NO 74; 570pp; English.

CC The invention relates to a novel isolated nucleic acid molecule
CC comprising any of the nucleotide sequences (e.g. 3634, 2127 or 2120 base
CC pairs) fully defined in the specification; or encodes any of the amino
CC acid sequences (e.g. 698, 702 or 709 amino acids) fully defined in the
CC specification. The invention further comprises: an isolated polypeptide
CC comprising any of the amino acid sequences cited above; a method for
CC identifying compounds that modulate target polypeptide activity; an
CC antibody that immunospecifically binds to the target polypeptide, where
CC the target polypeptide comprises any of the above-mentioned amino acid
CC sequences, an amino acid sequence that is at least 95% identical to the
CC above amino acid sequences, an amino acid sequence of at least one domain
CC of the above-mentioned amino acid sequences, or an amino acid sequence
CC that is at least 95% identical to the domain of the above amino acid
CC sequences; a method for identifying a potential therapeutic agent for use
CC in treatment of a pathology, where the pathology is related to aberrant
CC expression or aberrant physiological interactions of a target polypeptide
CC; and a method of screening for a modulator of activity of or of latency
CC or predisposition to a pathology associated with a target polypeptide.
CC The modulating compounds have anorectic and antidiabetic activities. The
CC nucleic acid sequences of the invention may be used in gene therapy to
CC treat disorders. The proteins of the invention may be used in creating a
CC vaccine. The composition and methods of the invention may be used in identifying compounds
CC that modulate protein activity or for diagnosing, preventing or treating
CC diverse pathological conditions, such as obesity, diabetes or insulin
CC resistance. The nucleic acids are also used as hybridization probes, in
CC chromosome mapping, tissue typing, preventive medicine, and
CC pharmacogenomics. This sequence represents a NOVX polypeptide of the
CC invention.

XX Sequence 489 AA;

Query Match 99.8%; Score 2398; DB 8; Length 489;
Best Local Similarity 99.8%; Pred. No. 1.4e-239;
Matches 463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSFLEQNSSWSPSPAVTSSSIRIGKRAKALWTRQKSVGEPPGQEGPRSRPTAE 60
Db 26 MSFLEQNSSWSPSPAVTSSSIRIGKRAKALWTRQKSVGEPPGQEGPRSPAEE 85
Qy 61 STGLEATFPKTTPLAQAADPAGVCTPTGWDCLPSDCTASAGSSTDVELATFPATEAW 120
Db 86 STGLEATFPKTTPLAQAADPAGVCTPTGWDCLPSDCTASAGSSTDVELATFPATEAW 145
Qy 121 ECELEGLLEERPALCLSPQAPFPKLGWDDLRKPGAQIYMRFMQHTCYDAMATSSKLVI 180
Db 146 ECELEGLLEERPALCLSPQAPFPKLGWDDLRKPGAQIYMRFMQHTCYDAMATSSKLVI 205
Qy 181 FDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMLTITDFFILVHRYRSPVLQIYEIE 240
Db 206 FDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMLTITDFFILVHRYRSPVLQIYEIE 265
Qy 241 QHKIETWREIYLOQCFKPLVISPNDLSLFEAVNTLKNRTHRLPVLDPVSGNVLHILTHK 300
Db 266 QHKIETWREIYLOQCFKPLVISPNDLSLFEAVNTLKNRTHRLPVLDPVSGNVLHILTHK 325
Qy 301 RLLKFLHIFGSLPRPSFLYRTIQDLGIGTRDLAVVLETPILTALDIFVDRRVSALPV 360

Db 326 RLLKFLHIFGSLPRPSFLYRTIQDLGIGTRDLAVVLETPAPILTALDIFVDRVSALPV 385
Qy 361 VNECGQVVGLYSRFDVTHLAAQQTYNHLDMSVGEALRQRTLCLEGVLSQOPHESLGEVID 420
Db 386 VNECGQVVGLYSRFDVTHLAAQQTYNHLDMSVGEALRQRTLCLEGVLSQOPHESLGEVID 445
Qy 421 RIAREQVHRLVLDVDETOHLLGVWSLSDILOALVLSPPAGIDALGA 464
Db 446 RIAREQVHRLVLDVDETOHLLGVWSLSDILOALVLSPPAGIDALGA 489

RESULT 7
ABP43929
ID ABP43929 standard; protein; 489 AA.
AC ABP43929;
XX
DT 26-FEB-2003 (first entry)
XX
DE AMP activated protein kinase gamma 3 subunit.
XX
KW Neuroprotective; immunomodulator; cancer; chromosome 2; cytostatic;
KW anti-inflammatory; gene therapy; nutritional supplement; wound; burn;
KW ulcer; Alzheimer's disease; Huntington's disease;
KW amyotrophic lateral sclerosis; autoimmune disorder; inflammation;
KW vulnery.
XX
OS Homo sapiens.
XX
FN WO200231111-A2.
XX
PD 18-APR-2002.
XX
PF 11-OCT-2001; 2001WO-US027760.
XX
PR 12-OCT-2000; 2000US-00687527.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;
XX
DR WPI; 2002-426278/45.
DR N-PSDB; ABQ61173.
XX
PT New polypeptides and their encoded proteins, useful as nutritional
PT sources or supplements, or in gene therapy, particularly for treating
PT wounds, Alzheimer's disease, amyotrophic lateral sclerosis, cancer or
PT inflammation.
XX
PS Claim 20; SEQ ID # 832; 357pp + Sequence Listing; English.
XX
CC The invention relates to 446 newly isolated polynucleotide sequences. The
CC activity of polynucleotides of the invention may be described as,
CC vulnerary, neuroprotective, immunomodulator, cytostatic and anti-
CC inflammatory. Compositions comprising nucleic acids of the invention are
CC useful for treating a mammalian subject, or as nutritional sources or
CC supplements. These are useful in gene therapy, particularly for treating
CC wounds, burns or ulcers, Alzheimer's disease, Huntington's disease,
CC amyotrophic lateral sclerosis, autoimmune disorders, cancer or
CC inflammation. The nucleic acids and polypeptides are also useful in
CC diagnostic and research methods. The sequences given in records ABP43544-
CC ABP43999 represent polypeptides encoded by polynucleotides of the
CC invention. NOTE: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 489 AA;

Query Match 99.5%; Score 2391; DB 5; Length 489;
Best Local Similarity 99.4%; Pred. No. 7.4e-239;
Matches 461; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSFLEQENSSSWPSPAVTSSSRIRKRAKALRWTRQKSVESGEPGQGEGRSPRTAE 60
Db 26 MSFLEQENSSSWPSPAVTSSSRIRKRAKALRWTRQKSVESGEPGQGEGRSPRTAE 85
Qy 61 STGLEATFPKTTPLAQAADPAGVGTPTGWDCLPSCDCTASAGSSTDDVELATEFPATEAW 120
Db 86 STGLEATFPKTTPLAQAADPAGVGTPTGWDCLPSCDCTASAGSSTDDVELATEFPATEAW 145
Qy 121 ECELEGLLEERPALCLSPQAPFPKLGWDDLRKPGAQIYMRFMQHTCYDAMATSSKLVI 180
Db 146 ECELEGLLEERPALCLSPQAPFPKLGWDDLRKPGAQIYMRFMQHTCYDAMATSSKLVI 205
Qy 181 FDTMLEIKKAFPAALVANGVRAAPLWDSKKQSFVGMLTITDIFILVHRYRSPVQIYEIE 240
Db 206 FDTMLEIKKAFPAALVANGVRAAPLWDSKKQSFVGMLTITDIFILVHRYRSPVQIYEIE 265
Qy 241 QHKIETWREIYLOQCFKPLVSIISPNDSLFEAVVTLIKNRIHRLPVLDPVSGNVLHILTHK 300
Db 266 QHKIETWREIYLOQCFKPLVSIISPNDSLFEAVVTLIKNRIHRLPVLDPVSGNVLHILTHK 325
Qy 301 RLLKFLHIFGSLPRPSFLYRTIQDLGIGTRDLAVVLETPAPILTALDIFVDRVSALPV 360
Db 326 RLLKFLHIFGSLPRPSFLYRTIQDLGIGTRDLAVVLETPAPILTALDIFVDRVSALPV 385
Qy 361 VNECGQVVGLYSRFDVTHLAAQQTYNHLDMSVGEALRQRTLCLEGVLSQOPHESLGEVID 420
Db 386 VNECGQVVGLYSRFDVTHLAAQQTYNHLDMSVGEALRQRTLCLEGVLSQOPHESLGEVID 445
Qy 421 RIAREQVHRLVLDVDETOHLLGVWSLSDILOALVLSPPAGIDALGA 464
Db 446 RIAREQVHRLVLDVDETOHLLGVWSLSDILOALVLSPPAGIDALGA 489

RESULT 8
AAE38410
ID AAE38410 standard; protein; 489 AA.
XX
AC AAE38410;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human Prkag3 protein.
XX
KW Human; Prkag3; transcription; therapy; prevention; energy metabolism;
KW obesity; dyslipidaemia; insulin resistance syndrome; type II diabetes;
KW anorectic; antilipaeamic; antidiabetic.
OS
XX Homo sapiens.
XX
FN WO2003064465-A2.
XX
PD 07-AUG-2003.
XX
PF 31-JAN-2003; 2003WO-IB000762.
XX
PR 01-FEB-2002; 2002US-0353429P.
XX
PA (AREX-) AREXIS AB.
XX
PI Svensson T;
XX
DR WPI; 2003-636796/60.
DR N-PSDB; AAD58250.
XX
PT Novel isolated nucleic acid encoding human Prkag3 promoter capable of
PT directing transcription of a heterologous coding sequence, useful for
PT screening compounds which modulate human Prkag3 promoter activity.
XX
PS Disclosure; Page 52-53; 53pp; English.
XX
CC The present invention relates to novel human Prkag3 promoter capable of
CC directing transcription of a heterologous coding sequence, useful for

CC screening compounds which modulate human Prkg3 promoter activity. The
 CC invention is useful for treating or preventing diseases related to energy
 CC metabolism e.g. obesity, dyslipidaemia, insulin resistance syndrome or
 CC type II diabetes. The present sequence is human Prkg3 protein
 XX
 SQ Sequence 489 AA;

Query Match 98.9%; Score 2376; DB 7; Length 489;
 Best Local Similarity 98.9%; Pred. No. 2.7e-237;
 Matches 459; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MSFLEQENSSWSPAVTSSSERIRGKRKALRWTRQKSVEEGPPGQGGPRSRPTAE 60
 DB 26 MSFLEQENSSWSPAVTSSSERIRGKRKALRWTRQKSVEEGPPGQGGPRSRPAE 85
 QY 61 STGLEATFPKTTPLAQADPAGVGTPTGWDCLPSDCTASAAGSSTDVDELATEFPATEAW 120
 DB 86 STGLEATFPKTTPLAQADPAGVGTPTGWDCLPSDCTASAAGSSTDVDELATEFPATEAW 145
 QY 121 ECELEGLLEERPALCLSPQAPFPKLGWDELKFGAQIYMRFMQEHCTCYDAMATSSKLVI 180
 DB 146 ECELEGLLEERPALCLSPQAPFPKLGWDELKFGAQIYMRFMQEHCTCYDAMATSSKLVI 205
 QY 181 FDTMLEIKKAFVALVANGVRAAPLWDSKKQSFVGMLTITDFFILVLRHYRSPVQIYEIE 240
 DB 206 FDTMLEIKKAFVALVANGVRAAPLWDSKKQSFVGMLTITDFFILVLRHYRSPVQIYEIE 265
 QY 241 QHKIETWREIYLOGCFKPLVSIISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHK 300
 DB 266 QHKIETWREIYLOGCFKPLVSIISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHK 325
 QY 301 RLLKFLHIFGSLPRPSFLYRTIQDLGIGTRDLAVVLETAPILTALDIFVDRRVSAALPV 360
 DB 326 RLLKFLHIFGSLPRPSFLYRTIQDLGIGTRDLAVVLETAPILTALDIFVDRRVSAALPV 385
 QY 361 VNECGQVGLYSRFDVTHLAAQQTYNHLDMSVGEALRQRTLCLEGLVSCOPHESLGEVID 420
 DB 386 VNECGQVGLYSRFDVTHLAAQQTYNHLDMSVGEALRQRTLCLEGLVSCOPHESLGEVID 445
 QY 421 RIAREQVHRLVLVDVETQHLGVVSLSDILQALVLSAPAGIDALGA 464
 DB 446 RIAREQVHRLVLVDVETQHLGVVSLSDILQALVLSAPAGIDALGA 489

RESULT 9
 ADF50314
 ID ADF50314 standard; protein; 489 AA.

XX ADF50314;

XX 12-FEB-2004 (first entry)

XX Human AMPK-gamma 3 protein subunit (seqid 6).

XX human; transgenic; AMP-activated protein kinase gamma 3 subunit; Prkg3;
 KW AMPK; energy metabolism; obesity; dyslipidaemia;
 KW insulin resistance syndrome; type 2 diabetes; antidiabetic; anorectic;
 KW antilipaeamic.

OS Homo sapiens.

XX W02003063586-A1.

XX 07-AUG-2003.

XX 31-JAN-2003; 2003WO-IB0000912.

XX 01-FEB-2002; 2002US-0353430P.

XX (AREX-) AREXIS AB.

XX Anderson L, Marklund S;

XX

DR WPI; 2003-663404/62.
 DR N-PSDB; ADF50313.

PT New transgenic non-human animals expressing an AMP-activated protein
 PT kinase gamma 3 subunit, useful as models for improving treatment, e.g.
 PT prevention or diagnosis of diseases related to energy metabolism, e.g.
 PT obesity or type 2 diabetes.

XX Example 1; SEQ ID NO 6; 46pp; English.

XX This invention relates to novel transgenic non-human animals expressing
 CC an AMP-activated protein kinase (AMPK)-gamma 3 subunit. Specifically, it
 CC relates to the transgene Prkg3 gene that encodes the AMPK gamma3 subunit
 CC or a variant thereof, where the nucleic acid is operably linked to a
 CC regulatory element. AMPK is involved in the regulation of energy
 CC metabolism in eukaryotic cells, and is recognised as a major regulator of
 CC lipid biosynthetic pathways due to its role in the phosphorylation and
 CC inactivation of key enzymes such as acetyl-CoA carboxylase. The present
 CC invention describes transgenic animals expressing AMPK-gamma 3 to be used
 CC as models for energy metabolism diseases and also methods for the
 CC development of drugs for the treatment or prevention of obesity,
 CC dyslipidaemia, insulin resistance syndrome or type 2 diabetes.
 CC Accordingly, the compositions of this invention have various activities
 CC including, antidiabetic, anorectic and antilipaeamic. This polypeptide
 CC sequence is the human AMPK-gamma3 protein subunit of the invention.

XX Sequence 489 AA;

Query Match 98.9%; Score 2376; DB 7; Length 489;
 Best Local Similarity 98.9%; Pred. No. 2.7e-237;
 Matches 459; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MSFLEQENSSWSPAVTSSSERIRGKRKALRWTRQKSVEEGPPGQGGPRSRPTAE 60
 DB 26 MSFLEQENSSWSPAVTSSSERIRGKRKALRWTRQKSVEEGPPGQGGPRSRPAE 85
 QY 61 STGLEATFPKTTPLAQADPAGVGTPTGWDCLPSDCTASAAGSSTDVDELATEFPATEAW 120
 DB 86 STGLEATFPKTTPLAQADPAGVGTPTGWDCLPSDCTASAAGSSTDVDELATEFPATEAW 145
 QY 121 ECELEGLLEERPALCLSPQAPFPKLGWDELKFGAQIYMRFMQEHCTCYDAMATSSKLVI 180
 DB 146 ECELEGLLEERPALCLSPQAPFPKLGWDELKFGAQIYMRFMQEHCTCYDAMATSSKLVI 205
 QY 181 FDTMLEIKKAFVALVANGVRAAPLWDSKKQSFVGMLTITDFFILVLRHYRSPVQIYEIE 240
 DB 206 FDTMLEIKKAFVALVANGVRAAPLWDSKKQSFVGMLTITDFFILVLRHYRSPVQIYEIE 265
 QY 241 QHKIETWREIYLOGCFKPLVSIISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHK 300
 DB 266 QHKIETWREIYLOGCFKPLVSIISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHK 325
 QY 301 RLLKFLHIFGSLPRPSFLYRTIQDLGIGTRDLAVVLETAPILTALDIFVDRRVSAALPV 360
 DB 326 RLLKFLHIFGSLPRPSFLYRTIQDLGIGTRDLAVVLETAPILTALDIFVDRRVSAALPV 385
 QY 361 VNECGQVGLYSRFDVTHLAAQQTYNHLDMSVGEALRQRTLCLEGLVSCOPHESLGEVID 420
 DB 386 VNECGQVGLYSRFDVTHLAAQQTYNHLDMSVGEALRQRTLCLEGLVSCOPHESLGEVID 445
 QY 421 RIAREQVHRLVLVDVETQHLGVVSLSDILQALVLSAPAGIDALGA 464
 DB 446 RIAREQVHRLVLVDVETQHLGVVSLSDILQALVLSAPAGIDALGA 489

RESULT 10

ADP87619

ID ADP87619 standard; protein; 492 AA.

XX ADP87619;

XX 23-SEP-2004 (first entry)

XX

DE	Human NOVX polypeptide, NOV10b.	
XX	anorectic; antidiabetic; gene therapy; vaccine; obesity; diabetes;	
KW	insulin resistance; hybridization probe; chromosome mapping;	
KW	tissue typing; preventive medicine; pharmacogenomics; NOVX; human.	
XX	Homo sapiens.	
XX	WO2004056961-A2.	
XX	08-JUL-2004.	
XX	27-OCT-2003; 2003WO-US034114.	
XX	25-OCT-2002; 2002US-0421239P.	
PR	28-OCT-2002; 2002US-0421700P.	
PR	31-OCT-2002; 2002US-0422776P.	
PR	13-NOV-2002; 2002US-0426197P.	
PR	20-DEC-2002; 2002US-0435498P.	
PR	20-DEC-2002; 2002US-0435510P.	
PR	20-DEC-2002; 2002US-0435568P.	
PR	21-MAR-2003; 2003US-0456812P.	
XX	(CURA-) CURAGEN CORP.	
XX	Berghs C, Catterton E, Ellerman K, Ort T, Rieger D, Chaudhuri A;	
PI	WPI; 2004-500293/47.	
XX	N-PSDB; ADP87618.	
DR		
XX	New NOVX nucleic acid molecules and polypeptides useful for preventing or	
PT	treating NOVX-associated disorders, e.g. diabetes, insulin resistance or	
PT	obesity, and in chromosome mapping, tissue typing or pharmacogenomics.	
XX	Claim 3; SEQ ID NO 76; 570pp; English.	
PS		
XX	The invention relates to a novel isolated nucleic acid molecule	
CC	comprising any of the nucleotide sequences (e.g. 3634, 2127 or 2120 base	
CC	pairs) fully defined in the specification; or encodes any of the amino	
CC	acid sequences (e.g. 698, 702 or 709 amino acids) fully defined in the	
CC	specification. The invention further comprises: an isolated polypeptide	
CC	comprising any of the amino acid sequences cited above; a method for	
CC	identifying compounds that modulate target polypeptide activity; an	
CC	antibody that immunospecifically binds to the target polypeptide; where	
CC	the target polypeptide comprises any of the above-mentioned amino acid	
CC	sequences, an amino acid sequence that is at least 95% identical to the	
CC	above amino acid sequences, an amino acid sequence of at least one domain	
CC	of the above-mentioned amino acid sequences, or an amino acid sequence	
CC	that is at least 95% identical to the domain of the above amino acid	
CC	sequences; a method for identifying a potential therapeutic agent for use	
CC	in treatment of a pathology, where the pathology is related to aberrant	
CC	expression or aberrant physiological interactions of a target polypeptide	
CC	; and a method of screening for a modulator of activity of or of latency	
CC	or predisposition to a pathology associated with a target polypeptide.	
CC	The modulating compounds have anorectic and antidiabetic activities. The	
CC	nucleic acid sequences of the invention may be used in gene therapy to	
CC	treat disorders. The proteins of the invention may be used in creating a	
CC	vaccine. The composition and methods are useful for identifying compounds	
CC	that modulate protein activity or for diagnosing, preventing or treating	
CC	diverse pathological conditions, such as obesity, diabetes or insulin	
CC	resistance. The nucleic acids are also used as hybridization probes, in	
CC	chromosome mapping, tissue typing, preventive medicine, and	
CC	pharmacogenomics. This sequence represents a NOVX polypeptide of the	
XX	invention.	
SQ	Sequence 492 AA;	
	Query Match 98.7%; Score 2372; DB 8; Length 492;	
	Best Local Similarity 98.7%; Pred. No. 7.1e-237;	
	Matches 457; Conservative 3; Mismatches 3; Indels 0; Gaps 0;	
QY	1 MSFLEQENSSWPSPAVTSSSRIRGKRRAKALRWTRQKSVGEPPGQEGGPRSRPAE 60	

CC growth factor receptor (IGFR) pathway modulating agent comprising
 CC screening for agents that modulate the activity of a modifier of IGFR
 CC (MIGFR). The method comprises providing an assay system comprising an
 CC MIGFR polypeptide or polynucleotide, contacting the assay system with a
 CC test agent under conditions where, but for the presence of the test
 CC agent, the system provides a reference activity and detecting a test
 CC agent-biased activity of the assay system, where a difference between the
 CC test agent-biased activity and the reference activity identifies the test
 CC agent as a candidate IGFR pathway modulating agent. The invention also
 CC relates to methods for modulating an IGFR pathway of a cell or in a
 CC mammalian cell and a method for diagnosing or treating a disease in a patient. The
 CC methods are useful for diagnosing or treating cancer or for identifying
 CC modulators of an IGFR pathway, which may be utilized as therapeutic
 CC targets for disorders associated with defective IGFR function, such as
 CC cancer. This sequence represents a human modulator of IGFR pathway
 CC polypeptide of the invention.

XX SQ Sequence 492 AA;

Query Match 98.7%; Score 2372; DB 9; Length 492;
 Best Local Similarity 98.7%; Pred. No. 7.1e-237;
 Matches 457; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MSFLEQENSSWSPSPAVTSSERIRGKRRAKALRWTRQKSVGECEPQGEGPESRTAE 60
 DB 26 MSFLEQENSSWSPSPAVTSSERIRGKRRAKALRWTRQKSVGECEPQGEGPESRTAE 85
 QY 61 STGLEATFPKTTPLAQADPAGVTPPTGWDCLPDSCTASAGSSTDVDELATEPPEAW 120
 DB 86 STGLEATFPKTTPLAQADPAGVTPPTGWDCLPDSCTASAGSSTDVDELATEPPEAW 145
 QY 121 ECELEGLLEERPALCLSPQAPPFKLGDWDELKPKGAQIYMRFMQEHCTCYDAMATSSKLVI 180
 DB 146 ECELEGLLEERPALCLSPQAPPFKLGDWDELKPKGAQIYMRFMQEHCTCYDAMATSSKLVI 205
 QY 181 FDTMLEIKKAPFALVANGVRAAPLWDSKQSFVGMLTITDILVLRHYRSPVQIYEIE 240
 DB 206 FDTMLEIKKAPFALVANGVRAAPLWDSKQSFVGMLTITDILVLRHYRSPVQIYEIE 265
 QY 241 QHKIETWREIYLOQCFKPLVSIISPNDSLFAVYTLIKNRIHRLPVLDPVSGNVLHITHK 300
 DB 266 QHKIETWREIYLOQCFKPLVSIISPNDSLFAVYTLIKNRIHRLPVLDPVSGNVLHITHK 325
 QY 301 RLLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSAIPV 360
 DB 326 RLLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSAIPV 385
 QY 361 VNECGQVGLYSRFDVTHLAAQQTYNHLDMSVGEALRQRTLCLEGLVSCOPHESLGEVID 420
 DB 386 VNECGQVGLYSRFDVTHLAAQQTYNHLDMSVGEALRQRTLCLEGLVSCOPHESLGEVID 445
 QY 421 RIAREQVHRLVLDVDETQHLLGVVSLSDILQALVLSPPAGIDALG 463
 DB 446 RIAREQVHRLVLDVDETQHLLGVVSLSDILQALVLSPPAGIDPSG 488

RESULT 12
 AAE22985
 ID AAE22985 standard; protein; 464 AA.
 XX AC AAE22985;
 XX DT 09-AUG-2002 (first entry)
 XX DE Pig PRKAG3 polymorphic variant (PRKAG3-30).
 XX KW AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene;
 XX KW screening; meat quality; single nucleotide polymorphism; SNP; pig;
 XX KW variant.
 XX OS Sus scrofa.
 XX PH Key Location/Qualifiers

FT Misc-difference 30
 FT /note= "Wild type An is substituted with Thr due to
 FT single nucleotide polymorphism (SNP)"
 XX W0200220850-A2.
 XX 14-MAR-2002.
 XX 10-SEP-2001; 2001WO-US028283.
 XX 08-SEP-2000; 2000US-0231045P.
 XX 08-JAN-2001; 2001US-0260239P.
 XX 18-JUN-2001; 2001US-029911P.
 XX (IOWA) UNIV IOWA STATE RES FOUND INC.
 XX Rothechild MF, Ciobanu DC, Malek M, Plastow G;
 XX WPI; 2002-393850/42.
 XX N-PSDB; AAD36457.
 XX Screening animals to determine those likely to produce larger litters and
 XX improved meat quality traits involves assaying for the presence of
 XX polymorphisms in the AMP activated protein kinase regulatory gamma
 XX subunit gene.
 XX Disclosure; Page 91-93; 109pp; English.
 XX The invention relates to a method for screening animals to determine
 XX those more likely to produce large litters and improved meat quality
 XX traits. The method involves assaying for the presence of a genotype in
 XX the sample of genetic material obtained from animal. The genotype is
 XX characterised by polymorphism(s) in the AMP activated protein kinase
 XX regulatory gamma subunit (PRKAG3) gene. The method is used for screening
 XX animals e.g., pigs to determine those most likely to exhibit improved
 XX meat quality traits and to produce larger litters. The present sequence
 XX is pig PRKAG3 polymorphic variant (PRKAG3-30)
 XX SQ Sequence 464 AA;

Query Match 83.8%; Score 2013; DB 5; Length 464;
 Best Local Similarity 86.0%; Pred. No. 1.3e-199;
 Matches 400; Conservative 19; Mismatches 44; Indels 2; Gaps 2;
 QY 1 MSFLEQENSSWSPSPAVTSSERIRGKRRAKALRWTRQKSVGECEPQGEGPESRTAE 60
 DB 1 MSFLEQENSSWSPSPAVTSSERIRGKRRAKALRWTRQKSVGECEPQGEGPESRTAE 60
 QY 61 STGLEATFPKTTPLAQADP--AGVGTPTTGDCLPDSCTASAGSSTDVDELATEPPEATEA 119
 DB 61 STGLEATFPKTTPLAQADP--AGVGTPTTGDCLPDSCTASAGSSTDVDELATEPPEATEA 120
 QY 120 WECELEGLLEERPALCLSPQAPPFKLGDWDELKPKGAQIYMRFMQEHCTCYDAMATSSKLVI 179
 DB 121 SGDEL--GLVEEKPAFCPSPEVLPRLGWDELQKGAQVYMHFMQEHCTCYDAMATSSKLVI 179
 QY 180 IFDTMLEIKKAPFALVANGVRAAPLWDSKQSFVGMLTITDILVLRHYRSPVQIYEIE 239
 DB 180 IFDTMLEIKKAPFALVANGVRAAPLWDSKQSFVGMLTITDILVLRHYRSPVQIYEIE 239
 QY 240 EOHKIETWREIYLOQCFKPLVSIISPNDSLFAVYTLIKNRIHRLPVLDPVSGNVLHITHK 299
 DB 240 EOHKIETWREIYLOQCFKPLVSIISPNDSLFAVYTLIKNRIHRLPVLDPVSGNVLHITHK 299
 QY 300 KRLLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSAIPV 359
 DB 300 KRLLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSAIPV 359
 QY 360 VNECGQVGLYSRFDVTHLAAQQTYNHLDMSVGEALRQRTLCLEGLVSCOPHESLGEVID 419
 DB 360 VNECGQVGLYSRFDVTHLAAQQTYNHLDMSVGEALRQRTLCLEGLVSCOPHESLGEVID 419
 QY 420 RIAREQVHRLVLDVDETQHLLGVVSLSDILQALVLSPPAGIDALGA 464

Db 420 DRIVEQVHRLVLDVDETHLGLGVVSLSDILQALVLSGAGIDALGA 464

RESULT 13

AAE00222 ID AAE00222 standard; protein; 464 AA.

AC AAE00222;

XX 13-JUN-2001 (first entry)

XX Pig AMPK gamma subunit muscle-specific isoform, complete PRKAG3.

XX Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK;
KW PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;
KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;
KW cystathione beta synthase; CBS; cardiant; gene therapy; RN locus;
KW chromosome 15.

XX Sus scrofa.

XX Key Location/Qualifiers

FF Domain 172..225

FF /label= CBS

FF /note= "Cystathione beta synthase domain"

FF Misc-difference 200

FF /note= "RN- mutation site"

FF Domain 253..307

FF /label= CBS

FF /note= "Cystathione beta synthase domain"

FF Domain 329..382

FF /label= CBS

FF /note= "Cystathione beta synthase domain"

FF Domain 400..453

FF /label= CBS

FF /note= "Cystathione beta synthase domain"

XX WO200120003-A2.

XX 22-MAR-2001.

XX 11-SEP-2000; 2000WO-EP009896.

XX 10-SEP-1999; 99EP-00402236.

XX 18-MAY-2000; 2000EP-00401388.

XX (INRG) INRA INST NAT RECH AGRONOMIQUE.

XX (ANDE/) ANDERSSON L.

XX (LOOF/) LOOFT C.

XX (KALM/) KALM E.

XX Andersson L, Loof C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;

XX Iannuccelli N, Gellin J, Le Roy P, Chardon P;

XX WPI; 2001-244810/25.

XX DR N-PSDB; AAD03319.

XX New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and myopathy.

XX Claim 5; Fig 3; 7lpp; English.

CC mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3. Transgenic animal and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a PRKAG3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy

XX SQ Sequence 464 AA;

Query Match 83.7%; Score 2011; DB 4; Length 464;
Best Local Similarity 86.0%; Pred. No. 2.2e-199;
Matches 400; Conservative 19; Mismatches 44; Indels 2; Gaps 2;
Qy 1 MSFLEQENSSWPSPAVTSSSRIRKRAKALRWTRQKSVEEGEPGQGGPRSRPTAE 60
Db 1 MSFLEQGESRWSFSAVTTSERSHGDQGNKASRWTFQEDVEEGPFGREGPQSRPVAE 60
Qy 61 STGLEATFPKTTPLAQADP-AGVGTPTGWDCLPSPDCTSAAGSSTDDELATFPATEA 119
Db 61 STGQEAATPKATPLAQAAPLAEVDNPPPTERDILPSCDAASASDNTDHLDIGIEFSAA 120
Qy 120 WECELEGLLEERPALCLSPQAPPKLGWDDDELKPGAGLYMRFMQEHCTCYDAMATSSKLV 179
Db 121 SGDEL-GLVEEKAPCPSPPEVLLPRLGWDDDELKPGAGLYMRFMQEHCTCYDAMATSSKLV 179
Qy 180 IFDTMLEIKKFAFFALVANGVRAAPLWDSKKQSFVGMLTITDFFILVHRYRSPVLQIYEI 239
Db 180 IFDTMLEIKKFAFFALVANGVRAAPLWDSKKQSFVGMLTITDFFILVHRYRSPVLQIYEI 239
Qy 240 EOHKIETWREIYLCQCFKPLVSPNDLSLFEAVTYLKNRIHRPLVLDVPSGVNHLIUTH 299
Db 240 EEHKIETWREIYLCQCFKPLVSPNDLSLFEAVTYLKNRIHRPLVLDVPSGVNHLIUTH 299
Qy 300 KRLKFLHIFGSLPRPSFLYRTTODLGIGTFRDLAVVLETPILTALDIFVDRRVSAIP 359
Db 300 KRLKFLHIFGTLPRPSFLYRTTODLGIGTFRDLAVVLETPILTALDIFVDRRVSAIP 359
Qy 360 VVNECGOVVGLYSRFDVHLLAAQOTYNHLDMSVGEALRQRTLCLEGLVSCOPHESLGEVI 419
Db 360 VVNETGVVGLYSRFDVHLLAAQOTYNHLDNMGVGEALRQRTLCLEGLVSCOPHETLGEVI 419
Qy 420 DRIAREQVHRLVLDVDETHLGLGVVSLSDILQALVLSGAGIDALGA 464
Db 420 DRIVEQVHRLVLDVDETHLGLGVVSLSDILQALVLSGAGIDALGA 464

RESULT 14

AAE22984 ID AAE22984 standard; protein; 464 AA.

AC AAE22984;

XX 09-AUG-2002 (first entry)

XX Pig wild-type PRKAG3 protein.

XX AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene;
KW screening; meat quality; single nucleotide polymorphism; SNP; pig.

XX Sus scrofa.

XX Key Location/Qualifiers

FF Misc-difference 30

FF /note= "Wild type Asn is replaced with Thr during single nucleotide polymorphism (SNP)"

FF Misc-difference 52

FF /note= "Wild type Gly is replaced with Ser during single nucleotide polymorphism (SNP)"

FF FT

Query Match 83.7%; Score 2011; DB 4; Length 514;
Best Local Similarity 86.0%; Pred. No. 2.5e-199;
Matches 400; Conservative 19; Mismatches 44; Indels 2; Gaps 2;

Qy	1	MSFLEQENSSSWPSPAVTSSSERIRGKRRAKALRWTRQKSVEEGEPGQGEGRSRPTAE	60
Db	51	MSFLEQESRWPSRAVTTSSERHGDGKNKASRWTRQEDVEEGEPGPGREGQSRPVAE	110
Qy	61	STGLEATFPKTTPLAQADP-AGVCTPPTGWDCLPSCDCTASAGSSTDDELATEFPATEA	119
Db	111	STGQEAFFPKATPLAQAPLAENVNPTTDRILPSCDAASASDNTDHLDLGIEFSASA	170
Qy	120	WECLEGLLEERPALCLSPQAPFKLGWDDDELKKGAGIYMRFMQEHCTCYDAMATSSKLV	179
Db	171	SGDEL-GLVEEKPAFCPSPEVLLPRLGWDDDELQKGAQVYMHFMQEHCTCYDAMATSSKLV	229
Qy	180	IFDTWLETKKAPFALVANGVRAAPLWDSKKQSFVGMLTITDFILVLRHYRSPLVQIYEI	239
Db	230	IFDTWLETKKAPFALVANGVRAAPLWDSKKQSFVGMLTITDFILVLRHYRSPLVQIYEI	289
Qy	240	EOHKIETWREIYLGQCFKPLVSI SPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVHLHILTH	299
Db	290	EEHKIETWREIYLGQCFKPLVSI SPNDSLFEAVYTLIKNRIHRLPVLDPVSGAVLHILTH	349
Qy	300	KRLKFLHIFGSLIPRPSFLYRTIQDLGIGTFRDLAVVLETPAPILTALDIFVDRRVSAIP	359
Db	350	KRLKFLHIFGTLIPRPSFLYRTIQDLGIGTFRDLAVVLETPAPILTALDIFVDRRVSAIP	409
Qy	360	VVNECGQVGLYSRFDVIHLAAQOQTYNHLDMSVGEALRQRTLCLEGLVSCOPHESLGEVI	419
Db	410	VVNETGVVGLYSRFDVIHLAAQOQTYNHLDNMGVGEALRQRTLCLEGLVSCOPHETLGEVI	469
Qy	420	DRIAREQVHRLVLDVDETQHLLGWVSLSDILOALVLSPAGIDALGA	464
Db	470	DRIVEQVHRLVLDVDETQHLLGWVSLSDILOALVLSPAGIDALGA	514

Search completed: January 24, 2006, 22:08:49
Job time : 128.313 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 26, 2006, 03:26:13 ; Search time 709.948 Seconds
(without alignments)
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Title: US-10-070-794A-4

Perfect score: 1551

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
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Deiop 6.0 , Delext 7.0

Searched: 6059551 seqs, 415333918 residues

Total number of hits satisfying chosen parameters: 12119102

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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6: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:
7: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:
8: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:
9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:
10: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:
11: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1002	64.6	1628	8	US-11-136-527-2210
2	500.5	32.3	1321	7	Sequence 2210, Ap
3	500.5	32.3	1321	7	Sequence 28770, A
4	461.5	29.8	568	8	Sequence 28770, A
5	461.5	29.8	568	8	Sequence 330, App
6	461.5	29.8	568	8	Sequence 3972, App
7	461.5	29.8	568	8	Sequence 330, App
					Sequence 3972, App

8	229.5	14.8	1500	8	US-11-041-776-79	Sequence 79, Appl
9	107.5	6.9	1494	7	US-10-467-657-5005	Sequence 5005, Ap
c 10	95.5	6.2	170837	8	US-11-121-086-97	Sequence 97, Appl
c 11	91.5	5.9	3061	7	US-10-793-626-4134	Sequence 4134, Ap
c 12	89.5	5.8	1467	7	US-10-793-626-2307	Sequence 2307, Ap
c 13	89.5	5.8	2980	7	US-10-793-626-4242	Sequence 4242, Ap
c 14	89.5	5.8	3840	7	US-10-793-626-4013	Sequence 4013, Ap
c 15	87	5.6	2862	8	US-11-156-953-6	Sequence 6, Appli
c 16	86.5	5.6	1641	8	US-11-055-822-945	Sequence 945, App
c 17	86.5	5.6	5100	8	US-11-136-527-4000	Sequence 4000, App
c 18	86	5.5	1400	8	US-11-136-527-4370	Sequence 4370, Ap
c 19	86	5.5	6021	8	US-11-136-527-274	Sequence 274, App
c 20	85.5	5.5	574	8	US-11-055-822-947	Sequence 947, App
c 21	85.5	5.5	1131	7	US-10-467-657-8227	Sequence 8227, Ap
c 22	85.5	5.5	1431	8	US-11-143-980-17	Sequence 17, Appl
c 23	85.5	5.5	1662	7	US-10-467-657-8239	Sequence 8239, Ap
c 24	85.5	5.5	116856	8	US-11-143-980-1	Sequence 1, Appli
c 25	84.5	5.4	4716	8	US-11-156-953-4	Sequence 4, Appli
c 26	83.5	5.4	1832	8	US-11-136-527-3815	Sequence 3815, Ap
c 27	83	5.4	1400	8	US-11-128-061-6939	Sequence 6939, Ap
c 28	83	5.4	3030	8	US-11-128-061-3297	Sequence 3297, Ap
c 29	83	5.4	3030	8	US-11-128-049-3297	Sequence 3297, Ap
c 30	83	5.4	3030	8	US-11-128-049-3297	Sequence 3297, Ap
c 31	82.5	5.3	1212	7	US-10-821-234-638	Sequence 638, App
c 32	82.5	5.3	1311	8	US-11-000-688-494	Sequence 494, App
c 33	82.5	5.3	1677	7	US-10-750-185-60961	Sequence 60961, A
c 34	82.5	5.3	1677	7	US-10-750-623-60961	Sequence 60961, A
c 35	82.5	5.3	35997	7	US-10-895-561-13301	Sequence 13301, A
c 36	81.5	5.3	7396	8	US-11-136-527-2724	Sequence 2724, Ap
c 37	80.5	5.2	960	7	US-10-873-528-275	Sequence 275, App
c 38	80.5	5.2	1963	8	US-11-038-981A-28	Sequence 28, Appl
c 39	80.5	5.2	6406	7	US-10-821-234-311	Sequence 311, App
c 40	80	5.2	4914	7	US-10-947-249-163	Sequence 163, App
c 41	80	5.2	5270	8	US-11-136-527-2161	Sequence 2161, Ap
c 42	80	5.2	160170	8	US-11-121-086-32	Sequence 32, Appl
c 43	79.5	5.1	2147	7	US-10-750-185-32313	Sequence 32313, A
c 44	79.5	5.1	2147	7	US-10-750-623-32313	Sequence 32313, A
c 45	79	5.1	987	8	US-11-128-061-971	Sequence 971, App

ALIGNMENTS

RESULT 1

US-11-136-527-2210
; Sequence 2210, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136, 527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574, 294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2210
; TYPE: DNA
; LENGTH: 1628
; ORGANISM: Rattus norvegicus
US-11-136-527-2210

Alignment Scores:	Pred. No.:	2.59e-107	Length:	1628
Score:		1002.00	Matches:	191
Percent Similarity:		82.65%	Conservative:	52
Best Local Similarity:		64.97%	Mismatches:	51
Query Match:		64.60%	Indels:	0
DB:		8	Gaps:	0

US-10-070-794A-4 (1-305) x US-11-136-527-2210 (1-1628)


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Db 760 GCAGAGACACACAGTGGGTTACCATTTCTCTTCAGTGTATTCATCCATCAGGACGCA 819
Qy 223 GlnGlnThrTyAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThrLeu 242
Db 820 TAAAGATCTACACACACACACAGTGGTGTAGTCAAGCCCTGAAATTCATCCAG 879
Qy 243 CysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGluValIleAspArg 262
Db 880 TACTTTAAATGTAGCTTCAAGTGGACCTGCATGAGGCTCTGGAGACCTTTCTCAGCAGG 939
Qy 263 IleAlaArgGluGlnValHisArgLeuValValAspGluThrGlnHisLeuGly 282
Db 940 CTAGTGAACAGGAGTACACGACTCGTGTGGTGGATGAGATGATGTGATCAAGGGA 999
Qy 283 ValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSer 296
Db 1000 ACTGTATCACCATCTGTCTCTCTGTAGACCTGTGTCTCACA 1041

RESULT 3
US-10-750-623-28770
; Sequence 28770, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750, 623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437, 482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28770
; TYPE: DNA
; ORGANISM: Bovine 19865880603844
US-10-750-623-28770

Alignment Scores:
Pred. No.: 2,42e-48 Length: 1321
Score: 500.50 Matches: 136
Percent Similarity: 53.27% Conservative: 43
Best Local Similarity: 40.48% Mismatches: 89
Query Match: 32.27% Indels: 69
DB: 7 Gaps: 5

US-10-070-794A-4 (1-305) x US-10-750-623-28770 (1-1321)
Qy 9 CyteTyAspAlaMetAlaThrSerSerLysLeuValIlePheAspThrMetLeuGluIle 28
Db 101 TGCTATGACCTGAGTCTCAACAGCTCCAAATTTGGTTGTTATTTGCTACTTCCCTGCAGTA 160
Qy 29 LysLysAlaPhePheAlaLeuValAlaAsnGlyValArgAlaAlaProLeu-TrpAsp 48
Db 161 TACAAG-----TTGCCCTTCTCGATAC 184
Qy 48 rLysLysGlnSerPheValGlyMetLeuThrIleThrAspPheIleLeuValLeuHisAr 68
Db 185 TAAAGACAGGACTTGTGGCATGTGGATATACCAATTCATCAATATCTCTGACTA 244
Qy 68 gTyTyArgSerProLeuVal-GlnIleTyGluIleGluGlnHisLysIleGluThr 88
Db 245 TTACTATATGACCTTGGTTCCAGAGCTATGAGTGGGAAGATACAAATAAGAACTT 304
Qy 88 rPargGluIleTyLeuGlnGlyCysPheLysProLeuValSerIleSerProAsnAspS 108
Db 305 GAAAGGAGGTGTATATACAGGACTTCTTTAAACCACTTGTCTCATTTCTTAAATGCCA 364
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Qy 108 erLeuPheGluAlaValTyThrLeuIleLysAsnArgIleHisArgLeuProValLeuA 128
Db 365 ACTTGTTTAATGCTGTCTTTTCAATTAATTCAGAACAGATCCACAGGCTGCCAGTTGTTG 424
Qy 128 spProValSerGlyAnValLeuHisIleLeuThrHisLysArgLeuLeuLysPheLeuH 148
Db 425 ACCAAGATCAAGCAACATCTTGTACACCTTCACCCCAAGTCATTTCTCATGTTCTCTCA 484
Qy 148 isIlePheGlySerLeuProArgProSerPheLeuTyArgThr-IleGlnAspLeu 167
Db 485 AGTGTTTATCACTGAGCTCTT-AAAGCCAGAAATTCATGTCTAAGTCTAATAGAAGAT--- 540
Qy 168 GlyIleGlyThrPheArgAspLeuAlaValValLeuGluThrAlaProIleLeuThrAla 187
Db 541 -----TAGCTTCTATGCCAGCATTTGCCATTTCTGCACCTATGACCCCATGACAGGCT 594
Qy 188 LeuAspIlePheValAspArgValSerAlaLeuProValValAsnGluCysGlyGln 207
Db 595 CTGGGCATC-----TCTGTACAGGATCTGCCA---GTGAATGAGGAAGGTCAG 639
Qy 208 ValValGlyLeuTySerArgPhe----- 215
Db 640 GTGGTGAACATCTATTCACATTTGATGTATCTGTGTAACTCACTTCACTCAGTCACGTC 699
Qy 215 ----- 215
Db 700 ACTCTTTGGGATCCTCTGACCTGTAGCCGTCAGGCTTCTCTCTCCATGGGACTTCCAG 759
Qy 216 -----AspValIleHisLeuAlaAala 222
Db 760 GCAGAACACTAGAGTGGGTACCATTTCTTCTCAGTGTATTTATCCATCAGGCAGCA 819
Qy 223 GlnGlnThrTyAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThrLeu 242
Db 820 TAAAGATCTACCAACCTAGATGTGCTGTAGTCAAGCCCTGAAATTCATCATCAG 879
Qy 243 CysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAspArg 262
Db 880 TACTTTAAATGTAGCTTCAAGTGGACCTGTGAGGCTCTGGAGACCTTTCTCAGCAGG 939
Qy 263 IleAlaArgGluGlnValHisArgLeuValValAspGluThrGlnHisLeuGly 282
Db 940 CTAGTGAAGACAGGAGTCAACGACTCTGTGTGGTGGATGAGAAATGATGTGATCAAGGGA 999
Qy 283 ValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSer 296
Db 1000 ACTGTATCACCATCTGTCTCTCTGTAGACCTGTGTCTCACA 1041

RESULT 4
US-11-128-061-330
; Sequence 330, Application US/111128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
; TITLE OF INVENTION: TO MONITOR GENE EXPRESSION
; FILE REFERENCE: 01997.027701
; CURRENT APPLICATION NUMBER: US/11/128, 061
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 330
; LENGTH: 568
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; TYPE: DNA
; ORGANISM: Cricetus griseus
US-11-128-061-330

Alignment Scores:
Pred. No.: 2,69e-44 Length: 568
Score: 461.50 Matches: 104
Percent Similarity: 59.32% Conservative: 36
Best Local Similarity: 44.07% Mismatches: 40
Query Match: 29.75% Indels: 57
DB: 8 Gaps: 2

US-10-070-794A-4 (1-305) x US-11-128-061-330 (1-568)
Qy 62 PheileLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGlu 81
Db 3 TTTATCAACATCTCTGCCCGCATATATAAGTCGGCCTTGGTGACAGATCTATGAAGTGA 62
Qy 82 GlnHisIleGluThrTyrArgGluIleTyrLeuGlnGlyCysPheLysProLeuVal 101
Db 63 GAACACAAAGATAGAACTTGGAGAGGTATACCTACAGGACTCTTTAAGCCCTTGTC 122
Qy 102 SerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIle 121
Db 123 TGCATTCTCCAAATGC-CAGATCACTGAG----- 151
Qy 122 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 141
Db 151 ----- 151
Qy 142 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 161
Db 152 -----TTCCCAAGCCAGCAATTCATGCT 175
Qy 162 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGluThr 181
Db 176 AAGTCTCTGGAGAGCTACAGATTGGCACCTATGCCAATTCATGCTCGTACTACC 235
Qy 182 AlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProVal 201
Db 236 ACACCTGTCTATGTGGCTCTAGGCATCTTTGTACAGCACCGAGTCTCTGCCCTCGCTGTG 295
Qy 202 ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIle-HisLeuAl 221
Db 296 GTGGATGAG-----AAGAATTGGC 316
Qy 221 aAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgTh 241
Db 317 AGCAGAAAGACCTATATAACACCTGGATATATCTGTGACAAAGCTCTACACACCGGTC 376
Qy 241 rLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAs 261
Db 377 TCACACTTTGAGGGTGTCTCAAGTGTCTATCTACAGGAGACTCTGGAGACTATCATTA 436
Qy 261 pArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLe 281
Db 437 TAGACTGTGGAGACGAGAGGTTCACCGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 496
Qy 281 uGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSer 296
Db 497 GGGCATCGTATGCTGTCCGATATCTCTGCAGGCTCTGTGTGTGTGTGTGTGTGTGTGT 542

RESULT 5
US-11-128-061-3972
; Sequence 3972, Application US/11128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
```

Db 497 GGGCATCGTATCGCTGTCCGATATCTGTCAGGCTCTGGTGTCTACA 542

RESULT 6

US-11-128-049-330

Sequence 330, Application US/11128049

Publication No. US20060010513A1

GENERAL INFORMATION:

APPLICANT: Melville, Mark W.

APPLICANT: Charlebois, Timothy S.

APPLICANT: Mounts, William M.

APPLICANT: Hann, Louane E.

APPLICANT: Sinacore, Martin S.

APPLICANT: Leonard, Mark W.

APPLICANT: Brown, Eugene L.

APPLICANT: Miller, Christopher P.

TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR

FILE REFERENCE: 01997.027700

CURRENT APPLICATION NUMBER: US/11/128,049

CURRENT FILING DATE: 2005-05-11

PRIOR FILING DATE: 2004-05-11

NUMBER OF SEQ ID NOS: 7285

SOFTWARE: PatentIn version 3.3

SEQ ID NO 330

LENGTH: 568

TYPE: DNA

ORGANISM: Cricetulus griseus

US-11-128-049-330

Alignment Scores:

Pred. No.:	2.69e-44	Length:	568
Score:	461.50	Matches:	104
Percent Similarity:	59.32%	Conservative:	36
Best Local Similarity:	44.07%	Mismatches:	40
Query Match:	29.75%	Indels:	57
DB:	8	Gaps:	2

US-10-070-794A-4 (1-305) x US-11-128-049-330 (1-568)

Qy 62 PheileuValLeuHisArgTyrArgSerProleuValGlnIleTyrGluileGlu 81

Db 3 TTTATCAACATCTCGCACCAGATATCTAAGTCGCCCTTGGTGCAGATCTAAGACTGGA 62

Qy 82 GlnHisIleGluThrTrpArgGluileTyrLeuGlnGlyCysPheLysProLeuVal 101

Db 63 GAACACAGATAGAACTTGGAGAGGTATACCTACAGACTCTTTAGCCCTTGTCTC 122

Qy 102 SerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgile 121

Db 123 TGCATTTCTCCAAATGC-CAGATCACTGAG----- 151

Qy 122 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 141

Db 151 ----- 151

Qy 142 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 161

Db 152 -----TTCCCAAGCCAGATTCATGTCT 175

Qy 162 ArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGluThr 181

Db 176 AAGTCTCGGAAGAGCTACAGATTGGCACCTTATGCCAACATTGTATGTCGCTACTACC 235

Qy 182 AlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProVal 201

Db 236 ACACCTGTCTATGTGGCTTAGGCATCTTTGTACAGACCCAGTCTCTGCCCTGCCCTGTG 295

Qy 202 ValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIle-HisLeuAl 221

Db 296 GTGGATGAG-----AAAGATTTGGC 316

Qy 221 aAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyAlaLeuArgGlnArgTh 241

Db 317 AGCAGAAAGACCTATAACAACTGGATATATCTGTGACAAAGCTCTACAACACCCGTC 376

Qy 241 xLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAs 261

Db 377 TCACTACTTTGAGGGTGTCTCAAGTCTATCTACAGGAGACTCTGGAGACTATCATAA 436

Qy 261 pArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLe 281

Db 437 TAGACTGGTGGAAAGCAGAGGTTTCCCGTCTGGTGGTGGATGAGAACGACGTTGGTCAA 496

Qy 281 uGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSer 296

Db 497 GGGCATCGTATCGCTGTCCGATATCTGTCAGGCTCTGGTGTCTACA 542

RESULT 7

US-11-128-049-3972

Sequence 3972, Application US/11128049

Publication No. US20060010513A1

GENERAL INFORMATION:

APPLICANT: Melville, Mark W.

APPLICANT: Charlebois, Timothy S.

APPLICANT: Mounts, William M.

APPLICANT: Hann, Louane E.

APPLICANT: Sinacore, Martin S.

APPLICANT: Leonard, Mark W.

APPLICANT: Brown, Eugene L.

APPLICANT: Miller, Christopher P.

TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR

FILE REFERENCE: 01997.027700

CURRENT APPLICATION NUMBER: US/11/128,049

CURRENT FILING DATE: 2005-05-11

PRIOR FILING DATE: 2004-05-11

NUMBER OF SEQ ID NOS: 7285

SOFTWARE: PatentIn version 3.3

SEQ ID NO 3972

LENGTH: 568

TYPE: DNA

ORGANISM: Cricetulus griseus

US-11-128-049-3972

Alignment Scores:

Pred. No.:	2.69e-44	Length:	568
Score:	461.50	Matches:	104
Percent Similarity:	59.32%	Conservative:	36
Best Local Similarity:	44.07%	Mismatches:	40
Query Match:	29.75%	Indels:	57
DB:	8	Gaps:	2

US-10-070-794A-4 (1-305) x US-11-128-049-3972 (1-568)

Qy 62 PheileuValLeuHisArgTyrArgSerProleuValGlnIleTyrGluileGlu 81

Db 3 TTTATCAACATCTCGCACCAGATATCTAAGTCGCCCTTGGTGCAGATCTAAGACTGGA 62

Qy 82 GlnHisIleGluThrTrpArgGluileTyrLeuGlnGlyCysPheLysProLeuVal 101

Db 63 GAACACAGATAGAACTTGGAGAGGTATACCTACAGACTCTTTAGCCCTTGTCTC 122

Qy 102 SerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgile 121

Db 123 TGCATTTCTCCAAATGC-CAGATCACTGAG----- 151

Qy 122 HisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLys 141

Db 151 ----- 151

Qy 142 ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyr 161

Db 152 -----TTCCCAAGCCAGATTCATGTCT 175


```

US-10-793-626-4134/c
; Sequence 4134, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4134
; LENGTH: 3061
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-4134

Alignment Scores:
Pred. No.: 13.8 Length: 3061
Score: 91.50 Matches: 52
Percent Similarity: 41.08% Conservative: 24
Best Local Similarity: 28.11% Mismatches: 70
Query Match: 5.90% Indels: 40
DB: 7 Gaps: 10

US-10-070-794A-4 (1-305) x US-10-793-626-4134 (1-3061)
Qy 61 AspPheLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80
Db 2401 AATCTCAATTTGGTAATCCATCGTCAATAC-----ATTCTATTGGTAGAGATG 2354
Qy 81 GluGlnHisLysIleGluThrTyrArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100
Db 2353 CACGCAATAT-CTTGATCAGTCAGTCGTGACAGTTGACAA-----TTG 2310
Qy 101 ValSerIleSerProAsnAspSerLeuPhe-----GluAlaValTyrThr 115
Db 2309 TTGGAGCGAATCCGATGAAGTAATATTACAGTGTGTGCACAGATCGAATAACACT 2250
Qy 116 LeuLysAsnArgIleHisArgLeuProValLeuAspProValSerGlyAsnValLeu 135
Db 2249 GCTATTAAAGGATTAGTGAAGCGGAATGAACAATTA-----GGTAAT- 2208
Qy 136 HisIleLeuThrHisLys---ArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeu 154
Db 2207 CATATTATTACTACCAAAATTTGAACACCATTCAGTATTACACGATATATGACAACTTGA 2148
Qy 155 ProArgPro---SerPheLeuTyrArgThrIleGlnAspLeuGlyIleGlyThrPheArg 173
Db 2147 AAAGAAGTTATGATGTTACGTATCTAGATGATGATGATGATGATGATGATGATGATGAT 2097
Qy 174 AspLeuAlaValValLeuGluThrAlaProIleLeuThrAlaLeuAspIlePheValAsp 193
Db 2096 GATTTAGACCAATTAAGAAACAAATTAATGATAGACAAATTTTA----- 2052
Qy 194 ArgArgValSerAlaLeuProValValAenGluCysGlyGlnValValGlyLeuTyrSer 213
Db 2051 -----GATCAATTTATGTTGTAATAATGATGATGATGATGATGATGATGATGATGAT 1998
Qy 214 ArgPheAspValIle-----HisLeuAlaAlaGlnGlnThrTyr 226
Db 1997 ATTGAAGATATTATTGGAGACACTCATGCTTATTCATGTTGATGCTGTTCAACCAATT 1938
Qy 227 AsnHisLeuAspMet 231
Db 1937 GCACATTTAGATTTA 1923

, RESULT 12

```

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US-10-793-626-2307
; Sequence 2307, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2307
; LENGTH: 1467
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-2307

Alignment Scores:
Pred. No.: 7.84 Length: 1467
Score: 89.50 Matches: 71
Percent Similarity: 40.75% Conservative: 59
Best Local Similarity: 22.26% Mismatches: 122
Query Match: 5.77% Indels: 67
DB: 7 Gaps: 15

US-10-070-794A-4 (1-305) x US-10-793-626-2307 (1-1467)
Qy 22 PheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyValArg 41
Db 37 TTCAGCAGCTGTACTCATTCAGCTGCATCAGATGTTTACCAGCGATGTTGACTTA 96
Qy 42 AlaAlaProLeuTyrAspSerLysLysGlnSerPhe-----ValGlyMetLeu 57
Db 97 AGTGTCAATATTCAGATAGATCAAGTTAAACATTCCTGTTATCTCAGCAGGTTATGAT 156
Qy 58 ThrIleThrAspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIle 77
Db 157 ACAGTAACGAATCAAAATGCAATGCTATGCTCGACAAAGCGGTTTAGGTGTTATT 216
Qy 78 TyrGlu-----IleGluGlnHisLysIleGluThrTyrArg---GluIleTyrLeu 93
Db 217 CATAGAATATGGCGTCGAAGACAGCTGATGAGGTACAAAGGTTTAAAGCTTCAGAA 276
Qy 94 GlnGlyCysPheLysProLeuValSerIleSerProAsnAspSerLeuPheGluAlaVal 113
Db 277 AATGGTGTATTTCTAACCCGTTCTTCTTAACCGGAGAAAGTGTGTATGAGGCTGAA 336
Qy 114 TyrThrLeuLysAsnArgIleHisArgLeuProValLeuAsp---ProValSerGly 132
Db 337 GCATTAAATGGTAAATACCGTATCTCTGCTGATCCCATTTGCGATAATCAAGAGGATCGC 396
Qy 133 AsnValLeuHisIleLeuThrHisLysArgLeuLeuLysPheLeuHisIlePheGlySer 152
Db 397 AAGTTGATGGGATTTTAAACAAATTCGTGATTTA----- 429
Qy 153 LeuLeuProArgProSerPheLeuTyrArgThrIleGlnAspLeuGlyIleGlyThrPhe 172
Db 430 -----CGTTTTATGAAGATTTTCAATT---AAAATA 459
Qy 173 ArgAspLeuAlaValVal-----LeuGluThrAlaProIleLeuThrAlaLeuAsp--- 189
Db 460 TCAGATGAATGACGAAAGATAAATTAATAACAGCTCCAGTTGGTACGACTTTAGATGAA 519
Qy 190 -----IlePheValAspArgValSerAlaLeuProValValAsnGlyCysGly 206
Db 520 GCCGAGGCTATTCTTCAAAAACATAAGATTGAGAAACTTCCATTAGTA---GAAATGGT 576
Qy 207 GlnValValGlyLeuTyrSerArgPheAspVal-----IleHisLeuAla 221

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Db 577 GGTITAGAGGAGTAATCACTATTAAAGATATTGAAAAAGTACTTGAATTCCTCCATATGCA 636
 Qy 222 AlaGlnGlnThrTyrAsnHisLeu-
 Db 637 GCTAAAGATCAACATGCGAGATCTTACTGCGCGCAGCAATCGTACGTCTAAAGATACT 696
 Qy 236 AlaLeuArgGlnArgThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSer 255
 Db 697 GAAATTCGTGCACAAAACTAGTTGAAGCTGGCGTA-----GATGCA 738
 Qy 256 LeuGlyGluValIleAspArgIleAlaArgGluGlnValHisArgLeuValLeuValAsp 275
 Db 739 TTA-----ATTATTGAT-----ACAGCTCATGTCATCTTAAAGCGTTTATTAAAT 783
 Qy 276 GluThrGlnHisLeu-----LeuGlyValValSer 285
 Db 784 CAAGTTAAACACATCAAGAAACATATCTCTGAATTAATCTGTCGCTGCTGTAAGTAGCG 843
 Qy 286 LeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAspAlaLeuGly 304
 Db 844 ACTGCAGAGGCAACACGCTGCTTTATTTCAGAGCGGTGCGATGTTGTTAAAGTAGGT 900

RESULT 13

US-10-793-626-4242
 ; Sequence 4242, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KIMMERLY, WILLIAM JOHN
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PU3480US
 ; CURRENT APPLICATION NUMBER: US/10/793,626
 ; PRIOR FILING DATE: 2004-03-04
 ; PRIOR APPLICATION NUMBER: 60/164,258
 ; PRIOR FILING DATE: 1999-11-09
 ; NUMBER OF SEQ ID NOS: 4472
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 4242
 ; LENGTH: 2980
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 ; OTHER INFORMATION: nucleic acid sequence
 US-10-793-626-4242

Alignment Scores:
 Pred. No.: 22.8 Length: 2980
 Score: 89.50 Matches: 71
 Percent Similarity: 40.75% Conservative: 59
 Best Local Similarity: 22.26% Mismatches: 122
 Query Match: 5.77% Indels: 67
 DB: 7 Gaps: 15

US-10-070-794A-4 (1-305) x US-10-793-626-4242 (1-2980)

Qy 22 PheAspThrMetLeuGluIleLysLysAlaPheAlaLeuValAlaAsnGlyValArg 41
 Db 653 TTCGACGACGTGTACTCTTCACGCTGCATCAGATGTTTACCAGCGATGTGACTTA 712
 Qy 42 AlaAlaProLeuTrpAspSerLysLysGlnSerPhe-----ValGlyMetLeu 57
 Db 713 AGTGCAATATATCAGATAAGATCAAGTTAAACATCTCTGTTATCTCAGCAGGTATGGAT 772
 Qy 58 ThrIleThrAspPheIleLeuValLeuValHisArgTyrTyrArgSerProLeuValGlnIle 77
 Db 773 ACAGTAATCACTCAAAATGGCAATTCGATGCTCGACAGCGGTGTTAGGTGTTATT 832
 Qy 78 TyrGlu-----IleGluGlnHisLysIleGluThrTrpArg---GluIleTyrLeu 93
 Db 833 CATAGAATATGGCGCTCGAGAGCAAGCTGATGAGGTACAAAAGGTAAACGTTACAGAA 892
 Qy 94 GlnGlyCysPheLysProLeuValSerIleSerProAsnAspSerLeuPheGluAlaVal 113

Db 893 AATGGTGTATTATTCTTAACCGTCTTCTTAAACCGGAAGAAAGTGTGTATGAGGCTGAA 952
 Qy 114 TyrThrLeuIleLysAsnArgIleHisArgLeuProValLeuAsp---ProValSerGly 132
 Db 953 GCATTAAATGGTAAATACCGTATCTCTGGGTATCCCATTCGATTCGATATCAAGAGGATCGC 1012
 Qy 133 AsnValLeuHisIleLeuThrHisLysArgLeuLeuLysPheLeuHisIlePheGlySer 152
 Db 1013 AAGTTGATTGGGATTTTAACAAACTCGTATTAA----- 1045
 Qy 153 LeuLeuProArgProSerPheLeuTyrArgThrIleGlnAspLeuGlyIleGlyThrPhe 172
 Db 1046 -----CGTTTATTGAAGATTTTTCAAATT---AAAATA 1075
 Qy 173 ArgAspLeuAlaValVal-----LeuGluThrAlaProIleLeuThrAlaLeuAsp--- 189
 Db 1076 TCAGATGTAATGACGAAGATAATTTAATAACAGCTCCAGTTGGTAGACACTTATAGATGAA 1135
 Qy 190 -----IlePheValAspArgValSerAlaLeuProValValAsnGluCysGly 206
 Db 1136 GCCGAGGCTATTCTTCAAAAACATAAGATTGAGAAACTTCCATTAGTA---GAAAATGGT 1192
 Qy 207 GlnValValGlyLeuTyrSerArgPheAspVal-----IleHisLeuAla 221
 Db 1193 CGTTTGAAGGATTAATCACTATTAAAGATATTGAAAAAGTACTTGAATTCCTCCATATGCA 1252
 Qy 222 AlaGlnGlnThrTyrAsnHisLeu-----AspMetSerValGlyGlu 235
 Db 1253 GCTAAGATGAACATGCGCAGATTTAGCTGCGCAGCAATCGTACGTCTTAAAGATACT 1312
 Qy 236 AlaLeuArgGlnArgThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSer 255
 Db 1313 GAAATTCGTGCACAAAACTAGTTGAAGCTGGCGTA-----GATGCA 1354
 Qy 256 LeuGlyGluValIleAspArgIleAlaArgGluGlnValHisArgLeuValLeuValAsp 275
 Db 1355 TTA-----ATTATTGAT-----ACAGCTCATGTCATTTCTAAAGCGGTATTAAAT 1399
 Qy 276 GluThrGlnHisLeu-----LeuGlyValValSer 285
 Db 1400 CAAGTTAAACACATCAAGGAACATATCTCGAAATTAATCTGTCGCTGCTGTAAGTAGCG 1459
 Qy 286 LeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAspAlaLeuGly 304
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RESULT 14

US-10-793-626-4013
 ; Sequence 4013, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KIMMERLY, WILLIAM JOHN
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PU3480US
 ; CURRENT APPLICATION NUMBER: US/10/793,626
 ; PRIOR FILING DATE: 2004-03-04
 ; PRIOR APPLICATION NUMBER: 60/164,258
 ; PRIOR FILING DATE: 1999-11-09
 ; NUMBER OF SEQ ID NOS: 4472
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 4013
 ; LENGTH: 3840
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 ; OTHER INFORMATION: nucleic acid sequence
 US-10-793-626-4013

Alignment Scores:
 Pred. No.: 33.3 Length: 3840
 Score: 89.50 Matches: 71


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Db 984 GAGCGCGAGCACGTCCATCTCTCCCGCATCAGGTCGATGAGGGCAG----- 937
Qy 283 ValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIleAspAla 302
Db 936 -----GAACAGCTGGCGGTTGAGCCCGTCCTTGTAGAGATC 901
Qy 303 LeuGly 304
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Search completed: January 26, 2006, 08:30:07
Job time : 767.948 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 25, 2006, 21:43:01 ; Search time 4086.76 Seconds
(without alignments)
4242.296 Million cell updates/sec

Title: US-10-070-794A-4

Perfect score: 1551
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Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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SUMMARIES

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1	1551	100.0	1470	6	AX814738 Sequence
2	1551	100.0	1597	8	BC098255 Homo sapi
3	1551	100.0	1597	8	BC098277 Homo sapi

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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5	1551	100.0	1599	8	BC098102	Homo sapi
6	1551	100.0	1647	6	AX281582	Sequence
7	1551	100.0	2109	6	AX099776	Sequence
8	1551	100.0	2115	6	AX099802	Sequence
9	1551	100.0	2115	8	AF214519	Homo sapi
10	1525	98.3	2290	8	HS249977	
11	1507	97.2	1867	6	AX099774	Sequence
12	1507	97.2	1873	6	AX099800	Sequence
13	1507	97.2	1873	6	AX398331	Sequence
14	1507	97.2	1873	6	AX398333	Sequence
15	1507	97.2	1873	6	AX398335	Sequence
16	1507	97.2	2022	6	AX099804	Sequence
17	1507	97.2	2023	4	AF214520	Sus scrofa
18	1507	97.2	2256	4	AY264345	Sus scrofa
19	1506	97.1	1873	6	AX398337	Sequence
20	1503	96.9	1873	6	AX398339	Sequence
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23	1479	95.4	1518	6	AX814740	Sequence
24	1376	88.7	1322	4	AY376689	Equus cab
25	1275	82.2	1570	6	CQ714782	Sequence
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30	1068	68.9	2192	9	AY348864	Mus muscu
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33	1067	68.8	3132	9	BC015283	Mus muscu
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37	1064	68.6	1167	6	CS129185	Sequence
38	1064	68.6	1167	8	AB025580	Homo sapi
39	1064	68.6	1435	6	AR139104	Sequence
40	1064	68.6	1846	6	CS084094	Sequence
41	1064	68.6	2062	8	HS249976	Homo sapi
42	1064	68.6	2194	8	AF087875	Homo sapi
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ALIGNMENTS

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LOCUS	AX814738					
DEFINITION	Sequence 1 from Patent WO03063586.					
ACCESSION	AX814738					
VERSION	AX814738.1	GI:39103937				
KEYWORDS						
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;					
	Hominidae; Homo.					
REFERENCE	1					
AUTHORS	Andersson, L. and Marklund, S.					
TITLE	Transgenic animals expressing prkag3					
JOURNAL	Patent: WO 03063586-A 1 07-AUG-2003;					
	Arexis AB (SE)					
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ORIGIN

Alignment Scores: 1.63e-131 Length: 1470
Pred. No.: 1551.00 Matches: 305
Score: 1551.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 6

US-10-070-794A-4 (1-305) x AX814738 (1-1470)

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Qy	21	IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal	40
Db	613	ATCTTCGACACCATGCTGGAGATCAAGAAGCCCTCTTTGCTGCTGGTGGCAACGGTGTG	672
Qy	41	ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr	60
Db	673	CGGGCAGCCCTCTATGGGACGACGACGAGCTTTGTGGGAGATGCTGACCATCACT	732
Qy	61	AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle	80
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Qy	81	GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu	100
Db	793	GAACAACATAAGATTGACACCTGGAGGAGATCTACTTGCAGAGGTGCTTCAAGCCTCTG	852
Qy	101	ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg	120
Db	853	GTCTCCATCTCTCTTAATGATAGCTGTGTGAAGCTGTCTACCCCTCATCAAGAACCGG	912
Qy	121	IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis	140
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Qy	141	LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu	160
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Qy	181	ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuPro	200
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Qy	221	AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg	240
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Qy	301	AspAlaLeuGlyAla	305
Db	1453	GATGCCCTCGGGGCC	1467

RESULT 2

BC098255

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 1597)

Klausner,R.L., Collins,F.S., Wagner,L., Shermen,C.M., Schuler,G.D.,

Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,

Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Haieh,F.,

Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,

Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,

Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,

Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,

Abramson,R.D., Mullaly,S.J., Bosak,S.A., McEwan,P.J.,

McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,

Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,

Vallalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,

Fahy,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S.,

Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,

Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,

Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,

Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,

Schmerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

Mammalian Gene Collection Program Team

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

2 (bases 1 to 1597)

NIH MGC Project

Direct Submission

Submitted (10-JUN-2005) National Institutes of Health, Mammalian

Gene Collection (MGC), Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapbs-remail.nih.gov

Tissue Procurement: Baylor Human Genome Sequencing Center

cDNA Library Preparation: Baylor Human Genome Sequencing Center

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC),

Gaithersburg, Maryland;

Web site: <http://www.nisc.nih.gov/>

Contact: nisc_mgc@hgri.nih.gov

Akter,N., Ayale,K., Beckstrom-Sternberg,S.M., Benjamin,B.,

Blakesley,R.W., Bouffard,G., Breen,K., Brinkley,C., Brooks,S.,

Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,

Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Latic,P., Legaspi,R.,

Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,

McDowell,J., Pearson,R., Stantropop,S., Thomas,P.J., Touchman,J.W.,

Turgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,

Young, A., Zhang, J.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.llnl.gov>
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LVANGRAAPLWDSKKQSFYGMILTIDFVLVHRYRSPVQIYEIQHKIETWRBIY
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gene

CDS

ORIGIN

Alignment Scores:
Pred. No.: 1.81e-131 Length: 1597
Score: 1551.00 Matches: 305
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0
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Qy 41 ArgAlaAlaProLeuTyrAspSerLysLysLysLysLysLysLysLysLysLysLysLys 60
Db 692 CGGGCAGCCCTCTATGGGACAGCAAGACAGCAGCTTTTGTGGGATGCTGACCATCACT 751
Qy 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80
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Qy 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValIle 260
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Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300
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Qy 301 AspAlaLeuGlyAla 305
Db 1472 GATGCTGCTGGGGCC 1486
RESULT 3
BC098277
LOCUS
DEFINITION
Homo sapiens protein kinase, AMP-activated, gamma 3 non-catalytic subunit, mRNA (cdna clone MGC:119344 IMAGE:40005886), complete cds.
ACCESSION
BC098277
VERSION
BC098277.1 GI:67514270
KEYWORDS
MGC.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 1597)
AUTHORS
Straussberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Schetz, T.E., Brownstein, M.J., Ustin, T.B., Toshikiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallos, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Mammalian Gene Collection Program Team

CONSRMT

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED 12477932
REFERENCE 2 (bases 1 to 1597)
AUTHORS NTH MGC Project
CONSTRM Direct Submission
TITLE Submitted (10-JUN-2005) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA
JOURNAL NTH-MGC Project URL: http://mgc.nci.nih.gov
REMARK Contact: MGC help desk
COMMENT Email: cgaps@email.nih.gov
 Tissue Procurement: Baylor Human Genome Sequencing Center
 cDNA Library Preparation: Baylor Human Genome Sequencing Center
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland.
 Web site: http://www.nisc.nih.gov/
 Contact: nisc_mgc@nhgri.nih.gov
 Akhter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsurgeson, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 Series: IRAM Plate: 4 Row: f Column: 1.
 Location/Qualifiers

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ORIGIN

Alignment Scores:
 Pred. No.: 1..81e-131 Length: 1597
 Score: 1551.00 Matches: 305
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0

DB: 8 Gaps: 0
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 Qy 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValle 260
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 Qy 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280
 Db 1352 GACAGGATGTCTGGAGCAGGTACACAGGCTGGTGTAGTGGACGAGACCACCACTCTC 1411
 Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyle 300
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 DEFINITION Homo sapiens protein kinase, AMP-activated, gamma 3 non-catalytic subunit, mRNA (CDNA clone MGC:119342 IMAGE:40005880), complete cds.
 ACCESSION BC098102
 VERSION BC098102.1 GI:66990059
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Strausberg,R.L., Feingold,B.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,J., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,K.H., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusich,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Schetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzyzanski,M.I., Skalska,U., Smalilus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
 Mammalian Gene Collection Program Team
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 12477932
 2 (bases 1 to 1599)

CONSRM
 TITLE Mammalian Gene Collection Project
 JOURNAL NIH MGC Project
 PUBMED Direct Submission
 REFERENCE Submitted (03-JUN-2005) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA
 AUTHORS NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT Contact: MGC help desk
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Baylor Human Genome Sequencing Center
 cDNA Library Preparation: Baylor Human Genome Sequencing Center
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC),
 Gaithersburg, Maryland:
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc_mgc@nigri.nih.gov
 Akhter,N., Ayale,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Green,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsugeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
 Series: IRAM Plate: 4 Row: e Column: 1.

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gene

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ORIGIN

Alignment Scores:
 Pred. No.: 1.81e-131 Length: 1599
 Score: 1551.00 Matches: 305
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 8 Gaps: 0

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DEFINITION Sequence 5 from Patent WO0177305.
ACCESSION AX281582
VERSION AX281582.1 GI:16608833
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Andersson, L., Luthman, H. and Marklund, S.
TITLE Variants of the human amp-activated protein kinase gamma 3 subunit.
JOURNAL Patent: WO 0177305-A 5 18-OCT-2001;
Aresis AB (SE)
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Alignment Scores:
Pred. No.: 1.88e-131 Length: 1647
Score: 1551.00 Matches: 305
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

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US-10-070-794A-4 (1-305) x AX281582 (1-1647)

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Db 632 ATCTTGACACCATCTGCGAGATCAAGAAGCGCTTCTTCTGCTGGTGGCCACGGTGTG 691
Qy 41 ArgAlaAlaProLeuTyrAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 60
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RESULT 7
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DEFINITION Sequence 3 from Patent WO0120003.
ACCESSION AX099776
VERSION    AX099776.1 GI:13538810
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE  1
AUTHORS    Andersson, L., Looft, C., Kalm, E., Milan, D., Robic, A.,
            Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., le Roy, P. and
            Chardon, P.
TITLE      Variants of the gamma chain of ampk, dna sequences encoding the
            same, and uses thereof
JOURNAL    Patent: WO 0120003-A 3 22-MAR-2001;
            INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
            Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)
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ORIGIN
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Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
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Db      1312  TTGGCGTGTGCTCCCTCTCGACATCTTCAGGCACTGCTGAGCCCTGCTGCGGCATC 1371
Qy      301  AspAlaLeuGlyAla 305
Db      1372  GATGCCCTCGGGGCC 1386

RESULT 8
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DEFINITION Sequence 29 from Patent WO0120003.
ACCESSION AX099802
VERSION    AX099802.1 GI:13538836
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
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            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE  1
AUTHORS    Andersson, L., Looft, C., Kalm, E., Milan, D., Robic, A.,
            Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., le Roy, P. and
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Chardon, P.
 Variants of the gamma chain of ampk, dna sequences encoding the same, and uses thereof
 Patent: WO 0120003-A 29 22-MAR-2001;
 INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
 Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)
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 LOCUS Homo sapiens AMP-activated protein kinase gamma subunit (PRKAG3)
 DEFINITION mRNA, complete cds.
 ACCESSION AF214519
 VERSION AF214519.1 GI:8215681
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 REFERENCE 1 (bases 1 to 2115)
 AUTHORS Milan, D., Jeon, J.T., Looft, C., Amarger, V., Robic, A., Thelander, M.,
 Rogel-Gaillard, C., Paul, S., Iannuccelli, N., Rask, L., Ronne, H.,
 Lundstrom, K., Reinsch, N., Gellin, J., Kalm, E., Roy, P.L., Chardon, P.
 and Andersson, L.
 TITLE A mutation in PRKAG3 associated with excess glycogen content in pig
 skeletal muscle
 JOURNAL Science 288 (5469), 1248-1251 (2000)
 PUBMED 10818001
 REFERENCE 2 (bases 1 to 2115)
 AUTHORS Milan, D., Jeon, J.T., Looft, C., Amarger, V., Robic, A.,
 Rogel-Gaillard, C., Paul, S., Gellin, J., Lundstrom, K., Reinsch, N.,
 Kalm, E., Le Roy, P., Chardon, P. and Andersson, L.
 TITLE Direct Submission
 JOURNAL Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish
 University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
 Sweden
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ORIGIN

Alignment Scores:

Pred. No.: 2,54e-131 Length: 2115
Score: 1551.00 Matches: 305
Percent Similarity: 100.00% Conservativity: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-070-794A-4 (1-305) x AF214519 (1-2115)

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Db	538	ATCTTCGACACCATGCTGGAGATCAAGAAGCCCTCTTTGCTCTGTTGGCCCAACGGGTG	597
Qy	41	ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr	60
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Qy	81	GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu	100
Db	718	GAACACATAGATTGACACCTGGAGGGAGATCTACCTGCAAGCTGCTTCAAGCCCTG	777
Qy	101	ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg	120
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RESULT 10

HSA249977

LOCUS

HSA249977

DEFINITION

Homo sapiens mRNA for AMP-activated protein kinase gamma 3 subunit

(AMPK gamma 3 gene).

ACCESSION

AJ249977.1

GI:6688200

VERSION

AMP-activated protein kinase; AMPK gamma 3 gene; gamma 3 subunit.

KEYWORDS

Homo sapiens (human)

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE

1

Cheung, P.C., Salt, I.P., Davies, S.P., Hardie, D.G. and Carling, D.

Characterization of AMP-activated protein kinase gamma-subunit

isoforms and their role in AMP binding

Biochem. J. 346 Pt 3, 659-669 (2000)

JOURNAL

PUBMED

10698692

REFERENCE

2 (bases 1 to 2290)

Carling, D.

AUTHORS

Direct Submission

Submitted (12-OCT-1999) Carling D., Cellular Stress Group, MRC

Clinical Sciences Centre, Hammersmith Hospital, DuCane Road,

London, W12 0NN, UNITED KINGDOM

FEATURES

Location/Qualifiers

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ORIGIN

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Pred. No.: 6,53e-129 Length: 2290

Score: 1525.00 Matches: 299

Percent Similarity: 99.34% Conservativity: 3

Best Local Similarity: 98.36% Mismatches: 2

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Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300
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Qy 301 AspAlaLeuGlyAla 305
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RESULT 12
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LOCUS AX099800
DEFINITION Sequence 27 from Patent WO0120003.
ACCESSION AX099800
VERSION AX099800.1 GI:13538834
KEYWORDS
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.

REFERENCE 1
AUTHORS Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A.,
Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy,P. and
Chardon,P.
TITLE Variants of the gamma chain of ampk, dna sequences encoding the
same, and uses thereof
JOURNAL Patent: WO 0120003-A 27 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)
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Alignment Scores:
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Score: 1507.00 Matches: 296
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Query Match: 97.16% Indels: 0
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Db 538 ATCTTCGACACCATGCTGGAGATCAAGAAGCCCTTCTTTGCCCTGTGGTGGCCACGCGGTC 597
Qy 41 ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 60
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 LOCUS AX398331 1873 bp DNA linear PAT 27-MAY-2002
 DEFINITION Sequence 1 from Patent WO0220850.
 ACCESSION AX398331
 VERSION AX398331.1 GI:21261106
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 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa

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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
 Sus.

REFERENCE

1.
 Rothschild, M.F., Ciobanu, D.C., Malek, M. and Plastow, G.
 Novel prkag3 alleles and use of the same as genetic markers for
 reproductive and meat quality traits
 JOURNAL Patent: WO 0220850-A 1 14-MAR-2002;
 Iowa State University Research Foundation, Inc. (US)

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ORIGIN

Alignment Scores:
 Pred. No.: 2.23e-127 Length: 1873
 Score: 1507.00 Matches: 296
 Percent Similarity: 98.36% Conservative: 4
 Best Local Similarity: 97.05% Mismatches: 5
 Query Match: 97.16% Indels: 0
 DB: 6 Gaps: 0

US-10-070-794A-4 (1-305) x AX398331 (1-1873)

Qy 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 20
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 Qy 21 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 40
 Db 538 ATCTTCGACACCATGCTGGAGATCAGAAGCCCTTCTTCCCTCGGTGGCCAAACGGCGTC 597
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 DEFINITION Sequence 3 from Patent WO0220850.
 ACCESSION AX398333
 VERSION AX398333.1 GI:21261108
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 ORGANISM Sus scrofa
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 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
 Sus.
 1.
 Rothschild, M.F., Ciobanu, D.C., Malek, M. and Plastow, G.
 Novel prkag3 alleles and use of the same as genetic markers for
 reproductive and meat quality traits
 JOURNAL Patent: WO 0220850-A 3 14-MAR-2002;
 Iowa State University Research Foundation, Inc. (US)
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Job time : 4102.76 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 25, 2006, 20:40:11 ; Search time 469.2 Seconds
(without alignments)
4332.332 Million cell updates/sec

Title: US-10-070-794A-4

Perfect score: 1551

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Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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14: geneseqn2005s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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9	1525	98.3	2290	12	ADP87618	Adp87618 Human NOV
10	1525	98.3	2290	14	AE869127	Aeb869127 Human mod
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15	1507	97.2	1873	6	AAD36456	Aad36456 Pig wild-
16	1507	97.2	2022	4	AAD03321	Aad03321 Sus scrofa
17	1506	97.1	1873	6	AAD36459	Aad36459 Pig PRKAG
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ALIGNMENTS

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AC ADF50309;
XX
DT 12-FEB-2004 (first entry)
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XX human; gene; ss; transgenic;
KW AMP-activated protein kinase gamma 3 subunit; Prkag3; AMPK;
KW energy metabolism; obesity; dyslipidaemia; insulin resistance syndrome;
KW type 2 diabetes; antidiabetic; anorectic; antilipaemic.
XX Homo sapiens.
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FT /product= "AMPK-gamma 3 protein"
XX
XX W02003063586-A1.
XX
PD 07-AUG-2003.
XX
PF 31-JAN-2003; 2003WO-IB000912.
XX

PA	07-APR-2000; 2000US-0195665P.	161	TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu	180
XX	(AREX-) AREXIS AB.	1052	TACCGCACTATCCAAAGATTGGGGCATCGGCACATTCGAGACTTGGCTGTGTGGAG	1111
XX	Andersson L, Luthman H, Marklund S;	181	ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro	200
XX	WPI; 2001-657170/75.	1112	ACAGACCCATCTGACTGCATCTGGACATCTTTGGACCGCGTGTCTGCATGCT	1171
XX	P-PSDB; Q0847679.	201	ValValAsnGluCysGlyGlnValValIleGlyLeuTyrSerArgPheAspValIleHisLeu	220
XX	New variants of human AMP-activated protein kinase gamma3 subunit	1172	GTGGTCAACGAATGTGTGAGTGTGGGCTCTATTCCCGCTTTGATGTGATTCACCTG	1231
PT	associated with a metabolic disease e.g. diabetes or obesity and method	221	AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg	240
PT	for determining a risk estimate of diseases in subject by detecting the	1232	GCTGCCAGCAAACTACAACCACTGGACATGATGTGGGAGAAGCCCTGAGGCAGAGG	1291
XX	variant.	241	ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyValIle	260
XX	Disclosure; Fig 5; 25pp; English.	1292	ACATATGTCTGGAGGAGTCTTCTTCTGCCAGCCCAACGAGAGCTTGGGGAAAGTATC	1351
XX	This sequence represents the full length cDNA encoding the human AMP-	261	AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu	280
CC	activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence	1352	GACAGGATTGCTCGGAGCAGGTACACAGGCTGTGTGTAGTGGACGAGACCAGCATCTC	1411
CC	of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate	281	LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle	300
CC	of a metabolic disease, such as diabetes or obesity, in a subject. The	1412	TTGGCGTGTGTCTCCCTCTCCGACATCTTCAGGCACTGTGTCTCAGCCCTGCTGGCATC	1471
CC	variation may occur in exons 3, 4 or 10. In exon 3 variation may be a	301	AspAlaLeuGlyAla	305
CC	substitution of a G for a C at nucleotide 320, resulting in the amino	1472	GATGCCCTCGGGGCC	1486
CC	acid substitution P71A; in exon 4 variation may be a substitution	RESULT 3		
CC	for a C at nucleotide 550; and in exon 10 variation may be a substitution	ID	ADP87616 standard; DNA; 1647 BP.	
CC	of a T for a C at nucleotide 1037, resulting in the amino acid	XX	ADP87616;	
CC	substitution R340W. There may also be nucleotide variation in intron 6.	XX	23-SEP-2004 (first entry)	
CC	The numbering of these variations is based on the full length cDNA as	XX	Human NOVX polypeptide encoding DNA, NOV10a.	
CC	given, rather than on position 1 of the open reading frame	XX	anorectic; antidiabetic; gene therapy; vaccine; obesity; diabetes;	
XX	Sequence 1647 BP; 346 A; 502 C; 462 G; 337 T; 0 U; 0 Other;	XX	insulin resistance; hybridization probe; chromosome mapping;	
		XX	tissue typing; preventive medicine; pharmacogenomics; NOVX; human; gene;	
		XX	ds.	
		XX	Homo sapiens.	
		XX	WO2004056961-A2.	
		XX	08-JUL-2004.	
		XX	27-OCT-2003; 2003WO-US034114.	
		XX	25-OCT-2002; 2002US-0421239P.	
		XX	28-OCT-2002; 2002US-0421700P.	
		XX	31-OCT-2002; 2002US-0422776P.	
		XX	13-NOV-2002; 2002US-0426197P.	
		XX	20-DEC-2002; 2002US-0435498P.	
		XX	20-DEC-2002; 2002US-0435510P.	
		XX	20-DEC-2002; 2002US-0435568P.	
		XX	21-MAR-2003; 2003US-0456812P.	
		XX	(CURA-) CURAGEN CORP.	
		XX	Berghs C, Catterton E, Ellerman K, Ort T, Rieger D, Chaudhuri A;	
		XX	WPI; 2004-500293/47.	
		XX	P-PSDB; ADP87617.	
		XX	New NOVX nucleic acid molecules and polypeptides useful for preventing or	
		XX	treating NOVX-associated disorders, e.g. diabetes, insulin resistance or	

PA	07-APR-2000; 2000US-0195665P.	161	TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu	180
XX	(AREX-) AREXIS AB.	1052	TACCGCACTATCCAAAGATTGGGGCATCGGCACATTCGAGACTTGGCTGTGTGGAG	1111
XX	Andersson L, Luthman H, Marklund S;	181	ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro	200
XX	WPI; 2001-657170/75.	1112	ACAGACCCATCTGACTGCATCTGGACATCTTTGGACCGCGTGTCTGCATGCT	1171
XX	P-PSDB; Q0847679.	201	ValValAsnGluCysGlyGlnValValIleGlyLeuTyrSerArgPheAspValIleHisLeu	220
XX	New variants of human AMP-activated protein kinase gamma3 subunit	1172	GTGGTCAACGAATGTGTGAGTGTGGGCTCTATTCCCGCTTTGATGTGATTCACCTG	1231
PT	associated with a metabolic disease e.g. diabetes or obesity and method	221	AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg	240
PT	for determining a risk estimate of diseases in subject by detecting the	1232	GCTGCCAGCAAACTACAACCACTGGACATGATGTGGGAGAAGCCCTGAGGCAGAGG	1291
XX	variant.	241	ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyValIle	260
XX	Disclosure; Fig 5; 25pp; English.	1292	ACATATGTCTGGAGGAGTCTTCTTCTGCCAGCCCAACGAGAGCTTGGGGAAAGTATC	1351
XX	This sequence represents the full length cDNA encoding the human AMP-	261	AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu	280
CC	activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence	1352	GACAGGATTGCTCGGAGCAGGTACACAGGCTGTGTGTAGTGGACGAGACCAGCATCTC	1411
CC	of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate	281	LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle	300
CC	of a metabolic disease, such as diabetes or obesity, in a subject. The	1412	TTGGCGTGTGTCTCCCTCTCCGACATCTTCAGGCACTGTGTCTCAGCCCTGCTGGCATC	1471
CC	variation may occur in exons 3, 4 or 10. In exon 3 variation may be a	301	AspAlaLeuGlyAla	305
CC	substitution of a G for a C at nucleotide 320, resulting in the amino	1472	GATGCCCTCGGGGCC	1486
CC	acid substitution P71A; in exon 4 variation may be a substitution	RESULT 3		
CC	for a C at nucleotide 550; and in exon 10 variation may be a substitution	ID	ADP87616 standard; DNA; 1647 BP.	
CC	of a T for a C at nucleotide 1037, resulting in the amino acid	XX	ADP87616;	
CC	substitution R340W. There may also be nucleotide variation in intron 6.	XX	23-SEP-2004 (first entry)	
CC	The numbering of these variations is based on the full length cDNA as	XX	Human NOVX polypeptide encoding DNA, NOV10a.	
CC	given, rather than on position 1 of the open reading frame	XX	anorectic; antidiabetic; gene therapy; vaccine; obesity; diabetes;	
XX	Sequence 1647 BP; 346 A; 502 C; 462 G; 337 T; 0 U; 0 Other;	XX	insulin resistance; hybridization probe; chromosome mapping;	
		XX	tissue typing; preventive medicine; pharmacogenomics; NOVX; human; gene;	
		XX	ds.	
		XX	Homo sapiens.	
		XX	WO2004056961-A2.	
		XX	08-JUL-2004.	
		XX	27-OCT-2003; 2003WO-US034114.	
		XX	25-OCT-2002; 2002US-0421239P.	
		XX	28-OCT-2002; 2002US-0421700P.	
		XX	31-OCT-2002; 2002US-0422776P.	
		XX	13-NOV-2002; 2002US-0426197P.	
		XX	20-DEC-2002; 2002US-0435498P.	
		XX	20-DEC-2002; 2002US-0435510P.	
		XX	20-DEC-2002; 2002US-0435568P.	
		XX	21-MAR-2003; 2003US-0456812P.	
		XX	(CURA-) CURAGEN CORP.	
		XX	Berghs C, Catterton E, Ellerman K, Ort T, Rieger D, Chaudhuri A;	
		XX	WPI; 2004-500293/47.	
		XX	P-PSDB; ADP87617.	
		XX	New NOVX nucleic acid molecules and polypeptides useful for preventing or	
		XX	treating NOVX-associated disorders, e.g. diabetes, insulin resistance or	

Alignment Scores:
 Pred. NO.: 4.15e-171 Length: 1647
 Score: 1551.00 Matches: 305
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 5 Gaps: 0

US-10-070-794A-4 (1-305) x AAH43685 (1-1647)

Qy	1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal	20
Db	572 ATGGCTTTCATGCGAGGACACCTGCTACATGCCATGCGAAGTCTCAAGCTAGTC	631
Qy	21 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal	40
Db	632 ATCTTCGACCACTGCTGGAGATCAAGAGCCCTTCTTGTCTGTGGCCACGGTGTG	691
Qy	41 ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr	60
Db	692 CGGGCAGCCCTCTATGGGACAGCAAGCAGAGCTTTGTGGGATGTGACCATCACT	751
Qy	61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle	80
Db	752 GACTTCATCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	811
Qy	81 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu	100
Db	812 GAACAAATAGATTGAGCTGAGGGAGATCTACTCTGAGGCTGCTTCAAGCTCTG	871
Qy	101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg	120
Db	872 GTCTCCATCTCTCTTAATGATAGCTGTTTGAAGCTGTCTACACCTCATCAAGACCGG	931
Qy	121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisLeuThrHis	140
Db	932 ATCCATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	991
Qy	141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu	160
Db	992 AAACGCTGCTCAAGTTCCTGACATCTTGTGTTCTGCTGCTGCTGCTGCTGCTGCTGCT	1051

PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
 XX Claim 1; SEQ ID NO 73; 570pp; English.

XX The invention relates to a novel isolated nucleic acid molecule
 CC comprising any of the nucleotide sequences (e.g. 3634, 2127 or 2120 base
 CC pairs) fully defined in the specification; or encodes any of the amino
 CC acid sequences (e.g. 698, 702 or 709 amino acids) fully defined in the
 CC specification. The invention further comprises: an isolated polypeptide
 CC comprising any of the amino acid sequences cited above; a method for
 CC identifying compounds that modulate target polypeptide activity; an
 CC antibody that immunospecifically binds to the target polypeptide, where
 CC the target polypeptide comprises any of the above-mentioned amino acid
 CC sequences, an amino acid sequence that is at least 95% identical to the
 CC above amino acid sequences, an amino acid sequence of at least one domain
 CC that is at least 95% identical to the domain of the above amino acid
 CC sequences; a method for identifying a potential therapeutic agent for use
 CC in treatment of a pathology, where the pathology is related to aberrant
 CC expression or aberrant physiological interactions of a target polypeptide
 CC ; and a method of screening for a modulator of activity of or of latency
 CC or predisposition to a pathology associated with a target polypeptide.
 CC The modulating compounds have anorectic and antidiabetic activities. The
 CC nucleic acid sequences of the invention may be used in gene therapy to
 CC treat disorders. The proteins of the invention may be used in creating a
 CC vaccine. The composition and methods are useful for identifying compounds
 CC that modulate protein activity or for diagnosing, preventing or treating
 CC diverse pathological conditions, such as obesity, diabetes or insulin
 CC resistance. The nucleic acids are also used as hybridization probes, in
 CC chromosome mapping, tissue typing, preventive medicine, and
 CC pharmacogenomics. This polynucleotide sequence represents the DNA
 CC encoding a NOVX polypeptide of the invention.

XX SQ Sequence 1647 BP; 346 A; 502 C; 462 G; 337 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 4,15e-171 Length: 1647
 Score: 1551.00 Matches: 305
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 12 Gaps: 0

US-10-070-794A-4 (1-305) x ADP87616 (1-1647)

Qy 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 20
 Db 572 ATGGGCTTCATGCGAGGACACACCTGCTACCATGCGATGCGCACTAGCTCCAAAGCTAGTC 631
 Qy 21 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 40
 Db 632 ATCTTCGACACCATGCTGGAGATCAAGAGGCTCTTTTGTCTGTGGTGGCAACGGTGTG 691
 Qy 41 ArgAlaAlaProLeuTyrAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 60
 Db 692 CGGGCAGGCCCTCTATGGACACGACGAGCGAGCTTTTGTGGGATGCTGACCATCACT 751
 Qy 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80
 Db 752 GACTTCATCTCGTGTGCTGCTACTACAGTCCCTCCCTGCTCCAGATCTATGAGATT 811
 Qy 81 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysPProLeu 100
 Db 812 GAACAACATAAGATTGAGACCTGGAGGAGATCTACCTGCAAGGCTGCTTCAAGCTCTG 871
 Qy 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuLysAsnArg 120
 Db 872 GTCTCCATCTCTCTTAATGATAGCTGTTGAGGTGTCTACACCTCATCNAGAACCGG 931
 Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140
 Db 932 ATCCATCGCTGCTGCTGTTCTTGACCCGGTGTGAGCAACGCTACTCCACATCTCCACAC 991

Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160
 Db 992 AAGCGCTGCTCAAGTTCTTCCGACATCTTTGGTTCCCTGCTGCCCGGCCCTCTCTCTC 1051
 Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 180
 Db 1052 TACCGCACTATCCAAAGTTGGGCACTCGGCACATTCGAGACTTGGCTGTGGTCTGGAG 1111
 Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuPro 200
 Db 1112 ACAGCACCCATCTGACTGCACTGCACTGCACTCTTTGTGGACCGCGTGTCTGCACTGCCT 1171
 Qy 201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220
 Db 1172 GTGGTCAACGAATGTGTGAGTGTGGGCTCTATTCCCGCTTTGATGTGATTCACCTG 1231
 Qy 221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240
 Db 1232 GCTGCCCGACCAACCTACACCACTGACATGATGATGTGGAGAAGCCCTGAGGCAGAGG 1291
 Qy 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValIle 260
 Db 1292 ACATATGTCTGGAGGAGTCTCTTCTGTCAGCCGCCACGAGAGCTTTGGGGAAAGTGA 1351
 Qy 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280
 Db 1352 GACAGGATGCTCGGAGCAGGTACACAGGCTGGTGTGTAGTGGACGAGACCAGCATCTC 1411
 Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300
 Db 1412 TTGGGCGTGGTCTCCCTCTCCGACATCTTCAGGCACTGGTGTCTCAGCCCTGCTGGCATC 1471
 Qy 301 AspAlaLeuGlyAla 305
 Db 1472 GATGCCCTCGGGGCC 1486

RESULT 4
 AAD03296
 ID AAD03296 standard; DNA; 2109 BP.
 XX
 AC AAD03296;
 XX
 DT 13-JUN-2001 (first entry)
 XX
 DE Human AMPK gamma subunit muscle-specific isoform, PRKAG3 CDNA.
 XX
 KW Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK;
 KW PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;
 KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;
 KW cystathione beta synthase; CBS; cardiant; gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 5'UTR 1..471
 FT /*tag= a
 FT CDS 472..1389
 FT /*tag= b
 FT /product= "Human Prkag3 protein"
 FT 3'UTR 1390..2109
 FT /*tag= c
 XX
 PN WO200120003-A2.
 XX
 PD 22-MAR-2001.
 XX
 PF 11-SEP-2000; 2000WO-EP009896.
 XX
 PR 10-SEP-1999; 99EP-00402236.
 PR 18-MAY-2000; 2000EP-00401388.
 XX
 PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
 PA (ANDE/) ANDERSSON L.

comprises contacting a polypeptide at least 85% identical to e.g., alpha adenosine monophosphate-activated protein kinase (AMPK) subunit with a test compound.

Disclosure; SEQ ID NO 50; 160pp; English.

The invention relates to a method of evaluating a compound by contacting a polypeptide comprising a sequence at least 85% identical to alpha, beta or gamma adenosine monophosphate-activated protein kinase (AMPK) subunit or a functional domain *in vitro* with a test compound, evaluating interaction between compound and polypeptide, contacting a cell or organism that produces the polypeptide with test compound, and evaluating a rate of aging of the cell or organism. A method comprising providing a modulator of the AMPK pathway to the subject is useful for treating or preventing a disease or disorder in a subject, preferably a cardiovascular disorder, a neurological disorder, a metabolic disorder, a dermatological disorder, a neoplastic disorder, an age-associated disorder, or a geriatric disorder. A compound that alters the expression or activity of an AMPK pathway component is useful for altering lifespan regulation in a cell or organism. This sequence represent the DNA sequence encoding one of the AMPK protein subunits.

Sequence 2115 BP; 460 A; 622 C; 562 G; 471 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.05e-171	Length:	2115
Score:	1551.00	Matches:	305
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	12	Gaps:	0

US-10-070-794A-4 (1-305) x ADP43247 (1-2115)

Qy	1	MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal	20
Db	478	ATGGCTTTCATGAGGAGCACACCTGCTACCATGCCATGGCAACTAGCTCCAAAGCTAGTC	537
Qy	21	IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal	40
Db	538	ATCTTCGACACCATGCTGGAGATCAAGAAGGCCCTTCTTGCTCTGGTGGCCACCGGTGTG	597
Qy	41	ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr	60
Db	598	CGGGCAGCCCTCTATGGGACAGCAAGACGAGACTTTGTGGGGATGCTGACCATCACT	657
Qy	61	AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle	80
Db	658	GACTTCATCTGGTGTGTCATCGCTACTACAGTCCCCCTGGTCCAGATCTATGAGATT	717
Qy	81	GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu	100
Db	718	GAACAAATAGATTGAGACTGGAGGGAGATCTACCTGCAAGGCTGCTTCAGCCCTCTG	777
Qy	101	ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg	120
Db	778	GTCTCCATCTCTCTAATAGTGGCTGTTGAAGCTGCTACACCTCATCAGAACCGG	837
Qy	121	IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis	140
Db	838	ATCCATCGCTCGCTGTCTTTGACCCGGTGTGAGGCAACGTACTTCCACATCTCTCACAC	897
Qy	141	LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu	160
Db	898	AAACGCTTGCTCAAGTTCCTGCACATCTTTGGTTCCTGTGCCCCCGGCCCTCTCTCCTC	957
Qy	161	TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu	180
Db	958	TACGGCACTATCCAAGATTGGGCATTCGGCACATTCGGAGACTTGGCTGTGTGTGGAG	1017
Qy	181	ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro	200
Db	1018	ACAGACCCATCTTGACTGCACTGGACATCTTTGTGACCGGGTGTGTGCACTGCTCT	1077

Qy	201	valValIaenGluCysGlyGlnValValGlyLeuTy-SerArgPheaspValIleHisLeu	220
Db	1078	GTGGTCAACGAATGTGGTCAGAGTCGTGGGCCTCTATTCCCGCTTTGATGTGATTCACCTG	1137
Qy	221	AlaAlaGlnGlnThrTyrsenHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg	240
Db	1138	GCTGCCCAGCAACCTTACCAACCACTTGGACATGAGTGTGGAGAGACCCCTTGAGGCAGAGG	1197
Qy	241	ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIle	260
Db	1198	ACACTATGTCTCGAGGAGTCTTTCTCTCCAGCCCAACGAGAGCTTGGGGGAAGTGATC	1257
Qy	261	AspArgIleAlaArgGlnGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu	280
Db	1258	GACAGGATTCTCTGGGAGCAGGTACACAGCTGTGTCTAGTGGACGAGACCCAGCATCTC	1317
Qy	281	LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle	300
Db	1318	TTGGGCGTGTCTCTCTCCGACATCTTCCAGCATCTTCCAGGCACTGGTGTCTGACCCCTGCTGGCANTC	1377
Qy	301	AspAlaLeuGlyAla 305	
Db	1378	GATGCCCTCGGGGCC 1392	
RESULT 7			
AAD49456			
ID	AAD49456 standard; cDNA; 2781 BP.		
XX			
AC	AAD49456;		
XX			
DT	24-MAR-2003 (first entry)		
XX			
DE	Human kinase and phosphatase (KPP)-15 cDNA.		
XX			
KW	Human; kinase and phosphatase; KPP; cardiovascular; hypertension;		
KW	myocardial infarction; angina pectoris; Alzheimer's disease; epilepsy;		
KW	acquired immune deficiency syndrome; AIDS; Grave's disease; diabetes;		
KW	neurological; Parkinson's disease; cirrhosis; psoriasis; gene therapy;		
KW	hypercholesterolemia; anticonvulsant; hepatotropic; lipid myopathy;		
KW	cell proliferative disorder; cancer; cardiac; neuroprotective; enzyme;		
KW	nootropic; ophthalmological; anorectic; cytostatic; cataract; obesity;		
KW	gene; 5s.		
OS	Homo sapiens.		
XX			
FH	Location/Qualifiers		
FT	21..1500		
FT	/*tag= a		
FT	/product= "Human KPP protein"		
XX			
FN	W0200283709-A2.		
XX			
PD	24-OCT-2002.		
XX			
PF	05-APR-2002; 2002WQ-US010818.		
XX			
PR	06-APR-2001; 2001US-0282119P.		
PR	13-APR-2001; 2001US-0283588P.		
PR	13-APR-2001; 2001US-0283759P.		
PR	20-APR-2001; 2001US-0285589P.		
PR	27-APR-2001; 2001US-0287036P.		
PR	27-APR-2001; 2001US-0287037P.		
PR	04-MAY-2001; 2001US-0286608P.		
PR	04-MAY-2001; 2001US-0288712P.		
PR	09-MAY-2001; 2001US-0289909P.		
PR	17-MAY-2001; 2001US-0292246P.		
XX			
PA	(INCY-) INCYTE GENOMICS INC.		
XX			
PI	Recipon SA, Burrill JD, Marcus GA, Zingler KA, Tang YT;		
PI	Thornton M, Borowsky ML, Baughn MR, Burford N, Lee SY, Bandman O;		
PI	Hafalia AJA, Yao MG, Ramkumar J.		
PI	Waliala NK, Lai DAM, Arvizu CS;		

PI Ison CH, Ding L, Lu Y, Gururajan R, Walsh RT, Gandhi AR;
PI Swarnakar A, Forsythe IJ, Yue H, Au-Young JK, Elliott VS, Lee S;
XX WPI; 2003-092995/08.
XX P-PSDB; AAE32034.
XX New human kinases and phosphatases (KPP), useful for diagnosing, treating
PT and preventing diseases or conditions associated with the aberrant KPP
PT expression, e.g. hypertension, cancer, AIDS, diabetes, cataract,
PT psoriasis, obesity.
XX Claim 5; Page 195-196; 195pp; English.
XX The invention relates to human kinases and phosphatases (KPP), and their
CC corresponding nucleic acids. The polypeptides and polynucleotides of the
CC invention are useful in diagnosing, treating and preventing diseases or
CC conditions associated with the decreased expression or overexpression of
CC KPP, such as cardiovascular (e.g. hypertension, myocardial infarction,
CC angina pectoris), immune (e.g. acquired immune deficiency syndrome
CC (AIDS), Grave's disease, diabetes), neurological (e.g. Parkinson's
CC disease, Alzheimer's disease, epilepsy), disorders affecting growth and
CC development (e.g. cirrhosis, psoriasis, cataract), lipid (e.g.
CC hypercholesterolemia, obesity, lipid myopathies), cell proliferative
CC disorders, or cancer. They are also useful in assessing the effects of
CC exogenous compounds on the expression of nucleic acid and amino acid
CC sequences of KPP. The KPP or its fragments are useful in screening
CC compounds for effectiveness as agonist or antagonist of the polypeptides,
CC or in altering the expression of the target polynucleotide and compounds
CC that specifically bind to or modulate the activity of the polypeptide.
CC The microarray is useful in monitoring or measuring protein-protein
CC interactions, drug-target interactions, and gene expression profiles. KPP
CC DNA is used in gene therapy. The present sequence is human KPP CDNA
XX
SQ Sequence 2781 BP; 628 A; 795 C; 714 G; 644 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9,14e-171 Length: 2781
Score: 1551.00 Matches: 305
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-070-794A-4 (1-305) x AAD49456 (1-2781)

QY 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 20
Db 573 ATGGCTTTCATGTCAGGAGCACACCTGCTACGATGCATGGCACTAGCTCCAAGCTAGTC 632

QY 21 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 40
Db 633 ATCTTCGACACCATCTCGAGATCAAGAGGCTCTTTTGTCTGTGGTGGCAACGGTGTG 692

QY 41 ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 60
Db 693 CGGGCAGGCCCTCTATGGACACGACGACGAGCTTTGGGGATGCTGACCATCACT 752

QY 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80
Db 753 GACTTCATCTGGTGTGTCATCGCTACTACAGGTCCCGCTGCTCCAGATCTATGAGATT 812

QY 81 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100
Db 813 GAACAACATAAGATTGAGACCTGGAGGGGAGATCTACCTGCAAGGCTGCTTCAAGCTCTG 872

QY 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120
Db 873 GTCTCATCTCTCTTAAATGATAGCTGTGTTGAAGCTGTCTACACCTCATCAAGAACGG 932

QY 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140
Db 933 ATCCATCGCGCTGCTGCTTCTTGAACCGGGTGTGAGGCAACGCTACTCCACATCTCCACAC 992

QY 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160
Db 993 AAAGCTGTCTCAAGTTCCTGACATCTTTGGTTCCTGCTGCCCGCCCTCTCTCTC 1052

QY 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 180
Db 1053 TACGCACACTATCAAGATTGGGCATCGGCACATTCGAGACTTGGCTGTGGTCTGGAG 1112

QY 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 200
Db 1113 ACAGCACCATCTGACTGACATGACATCTTTGTGACCGCGGTGTCTGCACTGCCT 1172

QY 201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220
Db 1173 GTGGTCAACGAAATGTGTGAGTCTGGGCTCTATTCCCGCTTGTATGTGATTCACCTG 1232

QY 221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240
Db 1233 GCTGCCCAGCAACCTACCAACCATGATGATGTGGAGAAAGCCCTGAGGCAGAGG 1292

QY 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValIle 260
Db 1293 ACATATGTCTGGAGGAGTCTTCTTCTGCCAGCCCCCAGAGACTTGGGGAAAGTGATC 1352

QY 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280
Db 1353 GACAGGATTGCTCGGAGCAGGTACACAGGCTGGTGTGTAGTGACAGAGACCCAGCATCTC 1412

QY 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300
Db 1413 TTGGCGTGGTCTCCCTCTCCGACATCTTCAGGCACTGGTGTCTCAGCCCTGTGGCATC 1472

QY 301 AspAlaLeuGlyAla 305
Db 1473 GATGCCCTCGGGGCC 1487

RESULT 8
ABQ61173
ID ABQ61173 standard; cDNA; 2314 BP.
XX
AC ABQ61173;
XX
DT 26-FEB-2003 (first entry)
XX
DE AMP kinase gamma 3 subunit encoding sequence.
XX
KW Neuroprotective; immunomodulator; cancer; chromosome 2; cytostatic;
KW anti-inflammation; gene therapy; nutritional supplement; wound; burn;
KW ulcer; Alzheimer's disease; Huntington's disease;
KW amyotrophic lateral sclerosis; autoimmune disorder; inflammation;
KW vulnery; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200231111-A2.
XX
PD 18-APR-2002.
XX
PF 11-OCT-2001; 2001WO-US027760.
XX
PR 12-OCT-2000; 2000US-00687527.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;
XX
DR WPI; 2002-426278/45.
DR N-PSDB; ABP43929.
XX
PT New polypeptides and their encoded proteins, useful as nutritional
PT sources or supplements, or in gene therapy, particularly for treating
PT wounds, Alzheimer's disease, amyotrophic lateral sclerosis, cancer or

PT inflammation.

PS Claim 1; SEQ ID # 386; 357pp + Sequence Listing; English.

The invention relates to 446 newly isolated polynucleotide sequences. The activity of polynucleotides of the invention may be described as, CC vulnary, neuroprotective, immunomodulator, cytostatic and anti- CC inflammatory. Compositions comprising nucleic acids of the invention are CC useful for treating a mammalian subject, or as nutritional sources or CC supplements. These are useful in gene therapy, particularly for treating CC wounds, burns or ulcers, Alzheimer's disease, Huntington's disease, CC amyotrophic lateral sclerosis, autoimmune disorders, cancer or CC inflammation. The nucleic acids and polypeptides are also useful in CC diagnostic and research methods. The sequences given in records AB060788- CC AB061233 represent polynucleotides of the invention. NOTE: The sequence CC data for this patent did not form part of the printed specification, but CC was obtained in electronic format directly from WIPO at CC [ftp.wipo.int/pub/published/pct](http://pub.int/pub/published/pct) sequences

Sequence 2314 BP; 513 A; 677 C; 618 G; 506 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4.586-170	Length:	2114
Argument Scores:	Score:	Matches:	303
	Percent Similarity:	Conservative:	2
	Best Local Similarity:	Mismatches:	0
	Query Match:	Indels:	0
DB:		Gaps:	0
			6

US-10-070-794A-4 (1-305) x ABO61173 (1-2314)

Qy	1	MetArgPheMetGlnGluHisThrCysTrpAspAlaMetAlaThrSerSerIysLeuVal	20
Db	574	ATCGGCTTCAAGGAGGACACCTGCTACGATGCATGGCAACTAGCTCCAAGCTAGTC	633
Qy	21	IlePheAspThrMetLeuGluIleIysIysAlaPhePheAlaLeuValAlaAsnGlyVal	40
Db	634	ATCTTCACACCATGCTGGAGATCAAGAAGGCTTCTTTGCTCTGGTGGCCACGGGTGG	693
Qy	41	ArgAlaAlaProLeuTrpAspSerIysIysGlnSerPheValGlyMetLeuThrIleThr	60
Db	694	CGGCGAGCCCTCTATATGGGACAGCAAGAAGCAGAGCTTTGTGGGGATGCTGACCATCACT	753
Qy	61	AspPheIleLeuValLeuHisArgTyrTrpArgSerProLeuValGlnIleTyrGluIle	80
Db	754	GACTTCATCTCGTGTGCTGATCGCTATACAGTCCCCCTGGTCCAGATCATAGAGATT	813
Qy	81	GluGlnHisIysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheIysProLeu	100
Db	814	GAACAAATAGAATTGAGACCTGGAGGGAGATCTACTGTCAAGGCTGCTTCAAGGCTCTG	873
Qy	101	ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleIysAsnArg	120
Db	874	GTCTCCATCTCTCTAATGATAGCTGTATTGAGCTGTCTACACCTCATCAAGAACCGG	933
Qy	121	IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis	140
Db	934	ATCCATCGCTCGCTGTTCTTTGACCCGGTGTGAGCAACGTACTCCACATCTCCACAC	993
Qy	141	LysArgLeuLeuIysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu	160
Db	994	AAACGGCTGTCTCAAGTTCTCTGCACATCTTTGGTTCCTGCTGCCCCGGCCCTCTCTCTC	1053
Qy	161	TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu	180
Db	1054	TACCGCACTATCCAAGATTTGGGCATCTCCGACACTTTGGCTGTGGTGTGGTGAG	1113
Qy	181	ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuPro	200
Db	1114	ACAGACCCATCTCTGACTGTCACTGGACATCTTTGTGGACCGCGGTGTCTGSCACTGGCT	1173
Qy	201	ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu	220

CC identifying compounds that modulate target polypeptide activity; an
 CC antibody that immunospecifically binds to the target polypeptide, where
 CC the target polypeptide comprises any of the above-mentioned amino acid
 CC sequences, an amino acid sequence that is at least 95% identical to the
 CC above amino acid sequences, an amino acid sequence of at least one domain
 CC of the above-mentioned amino acid sequences, or an amino acid sequence
 CC that is at least 95% identical to the domain of the above amino acid
 CC sequences; a method for identifying a potential therapeutic agent for use
 CC in treatment of a pathology, where the pathology is related to aberrant
 CC expression or aberrant physiological interactions of a target polypeptide
 CC ; and a method of screening for a modulator of activity of or of latency
 CC or predisposition to a pathology associated with a target polypeptide.
 CC The modulating compounds have anorectic and antidiabetic activities. The
 CC nucleic acid sequences of the invention may be used in gene therapy to
 CC treat disorders. The proteins of the invention may be used in creating a
 CC vaccine. The composition and methods are useful for identifying compounds
 CC that modulate protein activity or for diagnosing, preventing or treating
 CC diverse pathological conditions, such as obesity, diabetes or insulin
 CC resistance. The nucleic acids are also used as hybridization probes, in
 CC chromosome mapping, tissue typing, preventive medicine, and
 CC pharmacogenomics. This polynucleotide sequence represents the DNA
 CC encoding a NOVX polypeptide of the invention.

XX Sequence 2290 BP; 501 A; 674 C; 617 G; 498 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 7,62e-168 Length: 2290
 Score: 1525.00 Matches: 299
 Percent Similarity: 99.34% Conservative: 3
 Best Local Similarity: 98.36% Mismatches: 2
 Query Match: 98.32% Indels: 0
 DB: 12 Gaps: 0

US-10-070-794A-4 (1-305) x ADP87618 (1-2290)

QY 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 20
 Db 574 ATGGCGTTCATCGAGGAGACACCTCGTACCATGCGACTAGCTCCAGCTAGTC 633
 QY 21 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 40
 Db 634 ATCTTCGACACCATGCTGAGATCAAGAAGGCTTCTTTGCTGTTGGTGGCCCAACGGTGTG 693
 QY 41 ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 60
 Db 694 CGGGCAGCCCTCTATGGGACAGCAAGAAAGCAGAGCTTTGTGGGATGCTGACCATCACT 753
 QY 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80
 Db 754 GACTTCATCTCGTGTGCTGCATCGCTACTACAGGTCCCCCTGGTCCAGATCTATGAGATT 813
 QY 81 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100
 Db 814 GAACAACATAGATTGAGACCTGGAGGAGATCTACCTGCAAGGCTGTTCAAGCCTCTG 873
 QY 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrIleLysAsnArg 120
 Db 874 GTCTCCATCTCTCTAATGATAGCTGTGTGAAGCTGTCTACACCTCATCAAGAACCGG 933
 QY 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140
 Db 934 ATCCATCGCTGCCCTGTTCTTGACCCGGTGTGTCAGCAAGTACTCCATCTCCACAC 993
 QY 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160
 Db 994 AAACGCCCTGCTCAAGTTCCTGCACATCTTTGGTTCCTGCTGCCCGCCCTCTCTC 1053
 QY 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGlu 180
 Db 1054 TACCGCACTATCAAGATTGGGCAATCCGACATTCGAGACTTGGCTGTGGTGTGGAG 1113
 QY 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 200

Db 1114 ACAGCACCCTCTGACTGCTGACATCTTTGTGTGACCGGCTGTGTGTGCACTGCCT 1173
 QY 201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220
 Db 1174 GTGGTCAACGAATGTGTGTCAGGTGCGTGGGCTCTATTCCCGCTTTGATGTGATTCACCTG 1233
 QY 221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240
 Db 1234 GCTGCCCAAGCAACCTTACACCACTGGACATGATGTTGGAGAGAGCCCTGAGGAAGAGG 1293
 QY 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValIle 260
 Db 1294 ACACTATGTCTGGAGGAGTCTTCTTCTGCGAGCCCCCAGAGAGCTTTGGGGGAAGTGATC 1353
 QY 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280
 Db 1354 GACAGGATTCCTCGGGAGCAGGTACACAGGCTGTGTGTGTGACGACGAGACCCAGCATCTC 1413
 QY 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300
 Db 1414 TTGGGCGTGTCTCCCTCTCGACATCTTCAGGCACTTGGTGTGCTCAGCCCTGCTGGCATC 1473
 QY 301 AspAlaLeuGly 304
 Db 1474 GATCCCTCGGGG 1485

RESULT 10

AEB69127

ID AEB69127 standard; DNA; 2290 BP.

XX AEB69127;

DT 20-OCT-2005 (first entry)

DE Human modulator of IGFR pathway polynucleotide #4.

KW Screening; insulin growth factor receptor; IGFR; diagnosis; cancer;
 KW neoplasm; cytostatic; gene; ds.

OS Homo sapiens.

PN WO2005073723-A1.

XX 11-AUG-2005.

PF 27-JAN-2005; 2005WO-US002638.

XX 28-JAN-2004; 2004US-0539837P.

PR 12-MAR-2004; 2004US-0552634P.

PR 21-JUN-2004; 2004US-0581696P.

XX (EXEL-) EXELIXIS INC.

PA (NICO)/ NICOLL M.

PI Nicoll M, Friedman L, Francis-Lang H, Parks A, Shaw KJ, Zhang H;

PI Bjerke LM, Adamkiewicz J, Hitz BC, Lickteig K, Jin Y;

XX WPI; 2005-582573/59.

DR P-PSDB; AEB69187.

XX Identifying a candidate insulin growth factor receptor (IGFR) pathway
 PT modulating agents useful for diagnosing or treating, for e.g. cancer,
 PT comprises screening for agents that modulate the activity of a modifier
 PT of IGFR (MIGFR).

PS Example; SEQ ID NO 4; 334pp; English.

XX The invention relates to a method of identifying a candidate insulin
 CC growth factor receptor (IGFR) pathway modulating agent comprising
 CC screening for agents that modulate the activity of a modifier of IGFR
 CC (MIGFR). The method comprises providing an assay system comprising an
 CC MIGFR polypeptide or polynucleotide, contacting the assay system with a
 CC test agent under conditions where, but for the presence of the test

CC agent, the system provides a reference activity and detecting a test
 CC agent-biased activity of the assay system, where a difference between the
 CC test agent-biased activity and the reference activity identifies the test
 CC agent as a candidate IGRF pathway modulating agent. The invention also
 CC relates to methods for modulating an IGRF pathway of a cell or in a
 CC mammalian cell and a method for diagnosing a disease in a patient. The
 CC methods are useful for diagnosing or treating cancer or for identifying
 CC modulators of an IGRF pathway, which may be utilized as therapeutic
 CC targets for disorders associated with defective IGRF function, such as
 CC cancer. This sequence represents a human modulator of IGRF pathway
 CC polynucleotide of the invention.

SQ Sequence 2290 BP; 501 A; 674 C; 617 G; 498 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 7.62e-168 Length: 2290
 Score: 1525.00 Matches: 299
 Percent Similarity: 99.34% Conservative: 3
 Best Local Similarity: 98.36% Mismatches: 2
 Query Match: 98.32% Indels: 0
 DB: 14 Gaps: 0

US-10-070-794A-4 (1-305) x AEB69127 (1-2290)

Qy 1 MetArgPheMetGlnGluHisThrCysTyAspAlaMetAlaThrSerSerLysLeuVal 20
 Db 574 ATGGCTTCATCGAGGAGCACACCTGTACGATGCCATGCGCACTAGCTCAAGCTAGTC 633
 Qy 21 IlePheAspThrMetLeuGluLeuValLeuValPheAlaLeuValAlaAenGlyVal 40
 Db 634 ATCTTCGACACCATGCTGGAGATCAAGAGCGCTTCTTGTCTGTGGCCAAACGGTGTG 693
 Qy 41 ArgAlaAlaProLeuTrpAspSerLysGlnSerPheValGlyMetLeuThrIleThr 60
 Db 694 CGGCGACCCCTCTATCGGACAGCAGACAGACAGCTTGTGGGATGCTGACCATCACT 793
 Qy 61 AspPheIleLeuValLeuHisArgTyTyArgSerProLeuValGlnIleTyrgluile 80
 Db 754 GACTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 813
 Qy 81 GluGlnHisValIleGluThrTrpArgGluLeuLeuGlnGlyCysPheLysProLeu 100
 Db 814 GAACACATAGATTGAGACTTGAGGAGGAGATCTACCTGCAAGCGCTCTCAAGCCCTCTG 873
 Qy 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyThrLeuIleLysAsnArg 120
 Db 874 GTCTCCATCTCTCTATGATGCTCTTTGAGAGCTGTCTACACCTCATCAAGACCGG 933
 Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140
 Db 934 ATCCATCGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 993
 Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160
 Db 994 AAAGCGCTGCTCAAGTTCCTGCGACATCTTGGTTCCTGCTGCTGCTGCTGCTGCTGCT 1053
 Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGlu 180
 Db 1054 TACCGCACTATCCAGATTGGGATCGGCACATCCGACACTTGGCTGTGTGGAG 1113
 Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 200
 Db 1114 ACAGCACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1173
 Qy 201 ValValAsnGluCysGlyGlnValValGlyLeuTySerArgPheAspValIleHisLeu 220
 Db 1174 GTGGTCAACGAATGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1233
 Qy 221 AlaAlaGlnGlnThrTyAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240
 Db 1234 GCTGCCCGGCAACCTTCAACACCTGAGATGATGATGATGATGATGATGATGATGATG 1293
 Qy 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIle 260

Db 1294 ACATATGTCTGGAGGAGTCTTTCCTGTCAGCCACGAGAGCTTGGGGGAAGTATC 1353
 Qy 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValLeuValLeuValLeu 280
 Db 1354 GACAGGATTCTCGGAGCAGGTACACAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 1413
 Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300
 Db 1414 TTGGGCGTGTCTCTCCCTCTCCGACATCTTTCAGGCACTGTGTGTGTGTGTGTGTGT 1473
 Qy 301 AspAlaLeuGly 304
 Db 1474 GATCCCTCGGGG 1485
 RESULT 11
 AAD03295
 ID AAD03295 standard; cDNA; 1867 BP.
 XX
 AC AAD03295;
 XX
 DT 13-JUN-2001 (first entry)
 XX
 DE Pig AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA.
 XX
 KW Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK;
 KW PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;
 KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;
 KW cystathione beta synthase; CBS; cardiac; gene therapy; RN locus;
 KW chromosome 15; ss.
 XX
 OS Sus scrofa.
 XX
 FH Key Location/Qualifiers
 FT 5'UTR 1..471
 FT CDS /tag= a
 FT 472..1389
 FT /tag= b
 FT /product= "Sus scrofa PRKAG3 protein"
 FT 3'UTR 1390..1867
 FT /tag= c
 XX
 PN WO200120003-A2.
 XX
 PD 22-MAR-2001.
 XX
 PF 11-SEP-2000; 2000WO-EP009896.
 XX
 PR 10-SEP-1999; 99EP-00402236.
 PR 18-MAY-2000; 2000EP-00401388.
 XX
 PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
 PA (ANDE/) ANDERSSON L.
 PA (LOOF/) LOOFT C.
 PA (KALM/) KALM E.
 XX
 PI Andersson L, Loof C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;
 PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;
 XX
 DR WPI; 2001-244810/25.
 DR P-PSDB; AAE00220.
 XX
 PT New variants of the gamma subunit of vertebrate adenosine monophosphate-
 PT activated kinase for diagnosis or treatment of disorders associated with
 PT energy metabolism such as diabetes, obesity, and myopathy.
 XX
 PS Claim 12; Fig 2; 71pp; English.
 XX
 CC The present sequence is a cDNA encoding pig adenosine monophosphate (AMP)
 CC -activated kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3.
 CC Prkag3 gene is located in the RN locus of chromosome 15. Mutation in
 CC Prkag3 results in an altered regulation of carbohydrate metabolism,
 CC particularly in skeletal muscle. PRKAG3 is useful as therapeutic for

CC treating carbohydrate metabolism disorders such as diabetes, obesity, and
 CC disorders associated with muscle metabolism such as myopathy and
 CC cardiovascular diseases, to modulate AMPK activity, and for restoring a
 CC normal AMPK function. PRKAG3 sequence and its functionally altered
 CC mutants are useful for the diagnostic evaluation, genetic testing and
 CC prognosis of a metabolic disorder, preferably a carbohydrate metabolism
 CC disorder. Primers that can detect a genetic polymorphic marker linked to
 CC a sequence encoding PRKAG3, are useful for detecting a dysfunction of
 CC carbohydrate metabolism resulting from the expression of a functionally
 CC altered allele of PRKAG3. Transgenic animal and host cell transformed
 CC with PRKAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant,
 CC are useful for screening compounds able to modulate AMPK activity.
 CC Nucleic acid encoding PRKAG3 is useful for detecting mutations in a
 CC Prkag3 gene, or in a sequence encoding the first cystathione beta
 CC synthase (CBS) domain of PRKAG3 and is useful in gene therapy
 XX
 SQ Sequence 1867 BP; 380 A; 583 C; 529 G; 375 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 7,21e-166 Length: 1867
 Score: 1507.00 Matches: 296
 Percent Similarity: 98.36% Conservative: 4
 Best Local Similarity: 97.05% Mismatches: 5
 Query Match: 97.16% Indels: 0
 DB: 4 Gaps: 0

US-10-070-794A-4 (1-305) x AAD03295 (1-1867)

QY 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 20
 DB 472 ATGCACCTTCATGCGAGGACACACCTGCTACGATGCCATGGCGACGAGCTCCAAACTGGTC 531
 QY 21 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 40
 DB 532 ATCTTCGACACCATGCTCGAGATCAAGAAGCGCTCTTTGGCCCTGGTGGCCCAAGCGGCTC 591
 QY 41 ArgAlaAlaProLeuThrAspSerLysGlnSerPheValGlyMetLeuThrIleThr 60
 DB 592 CGAGCGGCACCTTTGTGGGACGACGAAGACAGAGCTTCGTGGGATGCTGACCATACACA 651
 QY 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80
 DB 652 GACTTCATCTGGTGTGCTGACCGCTATTACAGGTCCCGCTGGTCCAGATCTACGAGATT 711
 QY 81 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheIleProLeu 100
 DB 712 GAAGAACATCAAGATTGAGACCTGGAGGAGATCTACCTTCAAGGCTGCTTCAAGCCTCTG 771
 QY 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120
 DB 772 GTCTCCATCTCTCCCAATGACAGCCTGTTCGAAGCTGTCTAGCCCTCATCAAGAACCGG 831
 QY 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140
 DB 832 ATCCACCGGCTCCCGGCTCTGGACCTGTCTCCGGGGCTGTGCTCCACATCTCACACAT 891
 QY 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160
 DB 892 AAGCGGCTTCTCAAGTTCCTGCACATCTTTGGCACCTGTGCGCCCGCCCTCCCTTCCTC 951
 QY 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 180
 DB 952 TACCGCACCATCCAGATTGGGACATTCGGACATTCCTGGGAGCTTGGCGGTGGTGTGGAA 1011
 QY 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuPro 200
 DB 1012 ACGGGGCCCATCTCCGCCACTCGACATCTTCGTGGACCGGCGGTGTCTGCGCTGCT 1071
 QY 201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220
 DB 1072 GTGGTCAACGAACCTGGACAGGTAGTGGGCTCTACTCTCGCTTTGTGTATCCACCTG 1131
 QY 221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240

DB 1132 GCTGCCCAACAACATACACCACTGGACATGAATGTGGGAGAAAGCCCTGAGCGCGG 1191
 QY 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValle 260
 DB 1192 ACATGTGTCTGGAAGCGTCCTTTCTCTGCCAGCCCCACGAGACCTTTGGGGGAAGTCATT 1251
 QY 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280
 DB 1252 GACCGGATTTCGGGAACAGGTGCACCGCTGGTGTCTCGTGGATGAGACCCAGCACCTT 1311
 QY 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300
 DB 1312 CTGGCGGTGTGTCCCTCTCTGACATCTTTCAGGCTCTGTGTCTCAGCCCTCTGTGGAATT 1371
 QY 301 AspalaleuGlyAla 305
 DB 1372 GATGCCCTCGGGGCC 1386
 RESULT 12
 AAD03319
 ID AAD03319 standard; cDNA; 1873 BP.
 XX
 AC AAD03319;
 XX
 DT 13-JUN-2001 (first entry)
 XX
 DE Pig AMPK gamma subunit muscle-specific isoform, complete PRKAG3 cDNA.
 XX
 KW Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK;
 KW PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;
 KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;
 KW cystathione beta synthase; CBS; cardiant; gene therapy; RN locus;
 KW chromosome 15; ss.
 XX
 OS Sus scrofa.
 XX
 EH Location/Qualifiers
 FT CDS 1..1395
 FT /*tag= a
 FT /product= "Sus scrofa complete Prkag3 protein"
 XX
 PN WO200120003-A2.
 XX
 PD 22-MAR-2001.
 XX
 PF 11-SEP-2000; 2000MO-EP009896.
 XX
 PR 10-SEP-1999; 99EP-00402236.
 PR 18-MAY-2000; 2000EP-00401388.
 XX
 PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
 PA (ANDE/) ANDERSSON L.
 PA (LOOF/) LOOFT C.
 PA (KALM/) KALM E.
 XX
 PI Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;
 PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;
 XX
 DR WPI; 2001-244810/25.
 DR P-PSDB; AAE00222.
 XX
 PT New variants of the gamma subunit of vertebrate adenosine monophosphate-
 PT activated kinase for diagnosis or treatment of disorders associated with
 PT energy metabolism such as diabetes, obesity, and myopathy.
 XX
 PS Claim 12; Page 62-64; 71pp; English.
 CC The present sequence is a cDNA encoding pig adenosine monophosphate (AMP)
 CC -activated kinase (AMPK) gamma subunit muscle-specific isoform, complete
 CC PRKAG3. Prkag3 gene is located in the RN locus of chromosome 15. Mutation
 CC in Prkag3 results in an altered regulation of carbohydrate metabolism,
 CC particularly in skeletal muscle. PRKAG3 is useful as therapeutic for

CC treating carbohydrate metabolism disorders such as diabetes, obesity, and
 CC disorders associated with muscle metabolism such as myopathy and
 CC cardiovascular diseases, to modulate AMPK activity, and for restoring a
 CC normal AMPK function. PRKAG3 sequence and its functionally altered
 CC mutants are useful for the diagnostic evaluation, genetic testing and
 CC prognosis of a metabolic disorder, preferably a carbohydrate metabolism
 CC disorder. Primers that can detect a genetic polymorphic marker linked to
 CC a sequence encoding PRKAG3, are useful for detecting a dysfunction of
 CC carbohydrate metabolism resulting from the expression of a functionally
 CC altered allele of PRKAG3. Transgenic animal and host cell transformed
 CC with PRKAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant,
 CC are useful for screening compounds able to modulate AMPK activity.
 CC Nucleic acid encoding PRKAG3 is useful for detecting mutations in a
 CC PRKag3 gene, or in a sequence encoding the first cystathione beta
 CC synthase (CBS) domain of PRKAG3 and is useful in gene therapy
 XX
 SQ Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 7,24e-166 Length: 1873
 Score: 1507.00 Matches: 296
 Percent Similarity: 98.36% Conservative: 4
 Best Local Similarity: 97.05% Mismatches: 5
 Query Match: 97.16% Indels: 0
 DB: 4 Gaps: 0

US-10-070-794A-4 (1-305) x AAD03319 (1-1873)

Qy 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 20
 Db 478 ATGCATTTCATGAGGAGCACCTCTACATGCCATGGGACAGCTCCAAACTGGTC 537
 Qy 21 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 40
 Db 538 ATCTTCGACACCATGCTGGAGATCAAGAGGCGCTTCTTGGCCCTGGTGGCAACGGGTC 597
 Qy 41 ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 60
 Db 598 CGAGCGGCACCTTTGTGGGACAGCAAGAGCAGAGCTTCGTGGGATGCTGACCATCACA 657
 Qy 61 AspPheIleLeuValLeuHisAspTyrTyrArgSerProLeuValGlnIleTyrGluile 80
 Db 658 GACTTCATCTGTGGTGTGACCGCTATTTACAGGTCCCTGCTGTCAGATCTACGAGATT 717
 Qy 81 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100
 Db 718 GAACAACATAAGATTGAGACCTGGAGGAGATCTACCTTCAAGGCTGCTTCAAGCCTCTG 777
 Qy 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120
 Db 778 GTCTCCATCTCTCCCAATGACAGCTGTTTGAAGCTGTCTACGCCCTCATCAAGAACCGG 837
 Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140
 Db 838 ATCCACCGCTTCCCGGTCTGGACCTGTCTCCGGGGCTGTGCTCCACATCCTCACACAT 897
 Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160
 Db 898 AAGCGGCTTCTCAAGTTCTCGACATCTTTGGCACCTCTGCTGCCCGGCTCTCTCTCTC 957
 Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGlu 180
 Db 958 TACCGCACCATCCCAAGATTTGGGATCGGCACATTCGAGACTTGGCGGTGGTCTGGAA 1017
 Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuPro 200
 Db 1018 ACGCGGCCATCTTCGACCGACCTGGACATCTTCTGGACCGGCTGTGCTGGCGCTGCT 1077
 Qy 201 ValValAsnGluCysGlyGlnValValIcLysLeuTyrSerArgPheAspValIleHisLeu 220
 Db 1078 GTGGTCAACGAACTGCACAGTAGTGGGCTCTACTCTGCTTTGATGTGATCCACCTG 1137
 Qy 221 AlaAlaGlnInThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240

Db 1138 GCTGCCCAACAAACATACACACCTGACATGAATGTGGAGAACGCTTGAGCAGCGG 1197
 Qy 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyValIle 260
 Db 1198 ACACCTGTGTGGAGGCGTCTTCTCTGCAGGCCCCACGAGACTTGGGGGAAGTCATT 1257
 Qy 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280
 Db 1258 GACCGGATTGTCGGGGAACAGGTGCACCGCTGGTGTCTCGTGGATGAGACCCAGCACCTT 1317
 Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300
 Db 1318 CTGGCGCTGTGTGCTCTCTGACATCTTCAGGCTCTGTGTGCTGAGCCCTGCTGGAATT 1377
 Qy 301 AspAlaLeuGlyAla 305
 Db 1378 GATGCCCTCGGGGCC 1392
 RESULT 13
 AAD36458
 ID AAD36458 standard; DNA; 1873 BP.
 XX
 AC AAD36458;
 XX
 DT 09-AUG-2002 (first entry)
 XX
 DE Pig PRKAG3 polymorphic variant DNA (PRKAG3-52).
 XX
 KW AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene;
 KW screening; meat quality; single nucleotide polymorphism; SNP; pig; gene;
 KW variant; ds.
 XX
 OS Sus scrofa.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1395
 FT /tag= a
 FT /product= "Pig PRKAG3 polymorphic variant (PRKAG3-52)"
 FT variation replace(154, A)
 FT /tag= b
 FT /standard_name= "Single nucleotide polymorphism (SNP)"
 XX
 PN WO200220850-A2.
 XX
 PD 14-MAR-2002.
 XX
 PF 10-SEP-2001; 2001WO-US028283.
 XX
 PR 08-SEP-2000; 2000US-0231045P.
 PR 08-JAN-2001; 2001US-0260239P.
 PR 18-JUN-2001; 2001US-0299111P.
 XX
 PA (TOWA) UNIV IOWA STATE RES FOUND INC.
 XX
 PI Rothschild MF, Ciobanu DC, Malek M, Plastow G;
 XX
 DR WPI; 2002-393850/42.
 DR P-PSDB; AAE22986.
 XX
 PT Screening animals to determine those likely to produce larger litters and
 PT improved meat quality traits involves assaying for the presence of
 PT polymorphisms in the AMP activated protein kinase regulatory gamma
 PT subunit gene.
 XX
 PS Claim 34; Page 93-95; 109pp; English.
 XX
 CC The invention relates to a method for screening animals to determine
 CC those more likely to produce large litters and improved meat quality
 CC traits. The method involves assaying for the presence of a genotype in
 CC the sample of genetic material obtained from animal. The genotype is
 CC characterised by polymorphism(s) in the AMP activated protein kinase
 CC regulatory gamma subunit (PRKAG3) gene. The method is used for screening

CC animals e.g., pigs to determine those most likely to exhibit improved
 CC meat quality traits and to produce larger litters. The present sequence
 CC is pig PRKAG3 polymorphic variant DNA (PRKAG3-52)
 XX
 SQ Sequence 1873 BP; 383 A; 580 C; 534 G; 376 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 7.24e-166 Length: 1873
 Score: 1507.00 Matches: 296
 Percent Similarity: 98.36% Conservatives: 4
 Best Local Similarity: 97.05% Mismatches: 5
 Query Match: 97.16% Indels: 0
 DB: 6 Gaps: 0
 US-10-070-794A-4 (1-305) x AAD36458 (1-1873)
 QY 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 20
 DB 478 ATGCATTCATGCAGGACACACTGTACGATGCCATGGGACACAGCTCCAAACTGGTC 537
 QY 21 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 40
 DB 538 ATCTTCGACACCATGCTGGAGATCAAGAAGGCTTCTTTGGCCTGGTGGCCAAAGGGTC 597
 QY 41 ArgAlaAlaProLeuTrpAspSerLysGlnSerPheValGlyMetLeuThrIleThr 60
 DB 598 CGAGCGGCACCTTTGTGGGACAGCAAGAGAGCTTCGTGGGGATGCTGACCATCACA 657
 QY 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80
 DB 658 GACTTCATCTTGGTGTGTCACCGCTATTACAGGTCCCTGGTCCAGATCTACGAGATT 717
 QY 81 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100
 DB 718 GAAGAACATAAGATTGAGACCTGGAGGAGATCTACCTTCAAGGCTGCTTCAAGCCTCTG 777
 QY 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120
 DB 778 GTCTCCATCTCTCCAAATGACAGCCTGTTCGAAGCTGTCTACGCCCTCTCATCAAGACCGG 837
 QY 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140
 DB 838 ATCCACCCCTGCGGCTCTGGACCTGTCTCCGGGGCTGTCTCCACATCTCTCACAT 897
 QY 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160
 DB 898 AAGCGCTTCTCAAGTCTCTGCACATCTTTGGACCCCTGCTGCCCGGCCCTCTCTTCCTC 957
 QY 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 180
 DB 958 TACCGCACCATCCAAGATTGGGCATCGGCACATTCGAGACCTTGGCCGTGTGTCTGGAA 1017
 QY 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuPro 200
 DB 1018 ACGGCGCCCAATCTGACCGCCTGACATCTTCGTGGACCGGGTGTCTCTGGCGTGGCT 1077
 QY 201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220
 DB 1078 GTGGTCAACGAACCTGGACAGGTAGTGGGCTCTACTCTCGCTTTGATGTGATCCACCTG 1137
 QY 221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240
 DB 1138 GCTGCCCAACAACATACAAACCATCGCATGATGTGGGAGAGCCCTGAGGACGGG 1197
 QY 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIle 260
 DB 1198 ACACGTGTCTGGAAGGGCTCTTCTTCCTGCACGCCACGACCTTGGGGGAATCAT 1257
 QY 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280
 DB 1258 GACCGGATTTGCCGGGAACAGGTGCACCGCTGGTGTCTGTGATGAGACCCAGCACCTT 1317
 QY 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300

DB 1318 CTGGGGTGTGTCCCTCTCTGATCATCTTCAGGCTCTGTGTCTCAGCCCTGCTGGAATT 1377
 QY 301 AspAlaLeuGlyAla 305
 DB 1378 GATGCCCTCGGGGCC 1392
 RESULT 14
 AAD36457
 ID AAD36457 standard; DNA; 1873 BP.
 XX
 AC AAD36457;
 XX
 DT 09-AUG-2002 (first entry)
 XX
 DE Pig PRKAG3 polymorphic variant DNA (PRKAG3-30).
 XX
 KW AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene;
 KW screening; meat quality; single nucleotide polymorphism; SNP; pig; gene;
 KW variant; ds.
 XX
 OS Sus scrofa.
 XX
 FH Location/Qualifiers
 CDS 1..1395
 FT /*tag= a
 FT /product= "Pig PRKAG3 polymorphic variant (PRKAG3-30)"
 FT /replace= b
 FT /*tag= b
 FT /standard_name= "Single nucleotide polymorphism (SNP)"
 XX
 PN WO200220850-A2.
 XX
 PD 14-MAR-2002.
 XX
 PF 10-SEP-2001; 2001WO-US028283.
 XX
 PR 08-SEP-2000; 2000US-0231045P.
 PR 08-JAN-2001; 2001US-0260239P.
 PR 18-JUN-2001; 2001US-0299111P.
 XX
 PA (IOWA) UNIV IOWA STATE RES FOUND INC.
 XX
 PI Rothschild MF, Ciobanu DC, Malek M, Plastow G;
 XX
 DR WPI; 2002-393850/42.
 DR P-PSDB; RAE22985.
 XX
 PT Screening animals to determine those likely to produce larger litters and
 PT improved meat quality traits involves assaying for the presence of
 PT polymorphisms in the AMP activated protein kinase regulatory gamma
 PT subunit gene.
 XX
 PS Disclosure; Page 89-91; 109pp; English.
 XX
 CC The invention relates to a method for screening animals to determine
 CC those more likely to produce large litters and improved meat quality
 CC traits. The method involves assaying for the presence of a genotype in
 CC the sample of genetic material obtained from animal. The genotype is
 CC characterised by polymorphism(s) in the AMP activated protein kinase
 CC regulatory gamma subunit (PRKAG3) gene. The method is used for screening
 CC animals e.g., pigs to determine those most likely to exhibit improved
 CC meat quality traits and to produce larger litters. The present sequence
 CC is pig PRKAG3 polymorphic variant DNA (PRKAG3-30)
 XX
 SQ Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 7.24e-166 Length: 1873
 Score: 1507.00 Matches: 296
 Percent Similarity: 98.36% Conservatives: 4
 Best Local Similarity: 97.05% Mismatches: 5
 Query Match: 97.16% Indels: 0

DB: 6 Gaps: 0
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QY 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 20
DB 478 ATGCACCTTCAGGAGCAGCAGCTGTACGATGCCATGGCCAGCAGCTCCAACTGGTC 537
QY 21 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 40
DB 538 ATCTTCGACACCATGCTGGAGATCAAGAAGCCCTTTTGGCCCTGGTGGCCACAGCGGTC 597
QY 41 ArgAlaAlaProLeuThrPheSerLysLysGlnSerPheValGlyMetLeuThrIleThr 60
DB 598 CGAGCGGACCTTTGTGGGACAGCAAGAGCAGAGCTTCGTGGGAGTCTGACCATCACA 657
QY 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80
DB 658 GACTTCATCTGTGTGCTGCACCGCTATTACAGGTCCCTCCCTGGTCCAGATCTACGAGTT 717
QY 81 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100
DB 718 GAAGAACAATAGATTGAGACCTCGAGGAGATCTACCTTCAAGGCTGCTTCAAGCCTCTG 777
QY 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120
DB 778 GTCTCCATCTCTCCCAATGACAGCCTGTTCGAAGCTGTCTACGCCCTCATCAAGAACCGG 837
QY 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140
DB 838 ATCCACCGCTTCGCGGCTCTGGACCTGTCTCCGGGGCTGTGTCCACATCTCTCACAT 897
QY 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160
DB 898 AAGCGGCTTCTCAAGTCTCTGCACATCTTTGGCACCTGTGCGCCGCTCTCTTCTC 957
QY 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGlu 180
DB 958 TACCGCACCATCCCAAGATTGGGCAATCGGCATCGCACATTCGAGACTTGGCGGTGCTG 1017
QY 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 200
DB 1018 ACGGGCGCCATCTGACCGCAGCTGGACATCTTGTGGACCGGCTGTCTGCGCTGCCT 1077
QY 201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220
DB 1078 GTGGTCAACGAAACTGACAGGAGTAGTGGCTCTACTCTCTGCTTTGATGTATACACTG 1137
QY 221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240
DB 1138 GCTGCCCAACAAACATACACACCTGACATGAATGTGGAGAAAGCCCTGAGCGAGCGG 1197
QY 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIle 260
DB 1198 AACTGTGTCTGAAGCGGCTTCTTCTGCGAGCCCGCAGACCTTGGGGAGTCAATT 1257
QY 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280
DB 1258 GACCGGATTCTCGGGAACAGGTGACCGCTGGTGTCTGTGATGATGACCCAGCACCTT 1317
QY 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300
DB 1318 CTGGGCGTGTGTCTCTCTGACATCTTTCAGGCTCTGTGTCTGACCCCTGTGGAATT 1377
QY 301 AspAlaLeuGlyAla 305
DB 1378 GATGCCCTCGGGGCC 1392
RESULT 15
ID AAD36456 standard; DNA; 1873 BP.
XX
AC AAD36456;

XX 09-AUG-2002 (first entry)
DT Pig wild-type PRKAG3 gene.
XX
DB
XX
KW AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene;
KW screening; meat quality; single nucleotide polymorphism; SNP; pig; gene;
KW ds.
XX
OS Sus scrofa.
XX
XX Location/Qualifiers
FH i.1395
FT /*tag= a
FT /product= "pig PRKAG3 wild-type protein"
FT variation
FT /*tag= b
FT /*tag= c
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT replace(154,A)
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FT replace(599,A)
FT /*tag= e
FT /standard_name= "Single nucleotide polymorphism (SNP)"
XX
XX WO200220850-A2.
XX 14-MAR-2002.
XX 10-SEP-2001; 2001WO-US028283.
XX PF
XX 08-SEP-2000; 2000US-0231045P.
PR 08-JAN-2001; 2001US-0260239P.
PR 18-JUN-2001; 2001US-0299111P.
XX
XX (IOWA) UNIV IOWA STATE RES FOUND INC.
XX
XX Rothschild MF, Ciobanu DC, Malek M, Plastow G;
XX WPI; 2002-393850/42.
DR P-PSDB; AAE22984.
XX
XX Screening animals to determine those likely to produce larger litters and
XX improved meat quality traits involves assaying for the presence of
XX polymorphisms in the AMP activated protein kinase regulatory gamma
XX subunit gene.
XX
XX Claim 17; Fig 1; 109pp; English.
XX
XX The invention relates to a method for screening animals to determine
XX those more likely to produce large litters and improved meat quality
XX traits. The method involves assaying for the presence of a genotype in
XX the sample of genetic material obtained from animal. The genotype is
XX characterised by polymorphism(s) in the AMP activated protein kinase
XX regulatory gamma subunit (PRKAG3) gene. The method is used for screening
XX animals e.g., pigs to determine those most likely to exhibit improved
XX meat quality traits and to produce larger litters. The present sequence
XX is pig wild-type PRKAG3 gene
XX
XX Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 7,24e-166 Length: 1873
XX Score: 1507.00 Matches: 296
XX Percent Similarity: 98.36% Conservatives: 4
XX Best Local Similarity: 97.05% Mismatches: 5
XX Query Match: 97.16% Indels: 0
XX DB: Gaps: 6
XX
XX US-10-070-794A-4 (1-305) x AAD36456 (1-1873)

QY	1	MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal	20
Db	478	ATGCACCTTCATGCGAGGACACCTGCTACGATGCCATGGCAGCCAGCTCCAAACTGGTC	537
QY	21	IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAenGlyVal	40
Db	538	ATCTTCGACACCATGCTGGAGATCAAGAAGCCCTTCTTGCCTTGGTGGCCAAACGGCGTC	597
QY	41	ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr	60
Db	598	CGAGCGGCACCTTTGTGGGACAGACAGACAGCTTCCTGGGATGCTGACCATCACA	657
QY	61	AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle	80
Db	658	GACTTCATCTGGTGTGTCACCGCTATTACAGGTCCGCCCTGGTCCAGATCTACGAGATT	717
QY	81	GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu	100
Db	718	GAAGAACATTAAGATTGAGACCTGGAGGGAGATCTACCTTCAAGGCTGCTTCAAGCCTCTG	777
QY	101	ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg	120
Db	778	GTCTCCATCTCTCCATGACAGCCTGTTCGAAGCTGTCTACGCCCTCATCAAGAACCGG	837
QY	121	IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis	140
Db	838	ATCCACCGCCTGCCGCTCTGACCCCTGTCTCCGGGCTGTGCTCCACATCTCCACACAT	897
QY	141	LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu	160
Db	898	AAGCGGCTTCTCAAGTTCTCTGCACATCTTTGGCACCTTGTGGCCCTGTGCCCGGCCCTCCTTCCCTC	957
QY	161	TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu	180
Db	958	TACCGCCACCATCCAAAGATTGGGCATCGGCACATTCGAGACTTGGCCGTGGTGTGGAA	1017
QY	181	ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro	200
Db	1018	ACGGCGCCCATCTGACCGCACCTGGACATCTTCGTGGACCGCGGTGTGTCTGCGCTGCT	1077
QY	201	ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu	220
Db	1078	GTGGTCAACGAACTGGACAGGTAGTGGCCCTCTACTCTCGCTTTGATGTGATCCACCTG	1137
QY	221	AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg	240
Db	1138	GCTGCCCAACAAACATACACCACTTGACATGATGTGGAGAGCCCTGAGGCAGCGG	1197
QY	241	ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIle	260
Db	1198	ACACTGTGCTGGAAAGGGTCTCTTTCTGCCAGCCGCCAGACCTTGGGGGAAAGTCATT	1257
QY	261	AspArgIleAlaArgGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu	280
Db	1258	GACCGGATGTCCGGGAACAGGTGACCGCCTGGTGTCTCGTGGATGAGACCCAGCACCTT	1317
QY	281	LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle	300
Db	1318	CTGGGCGGTGGTCTCTCTCTGACATCTTCAAGGCTCTGGTGTCTCAGGCCCTGCTGGAATT	1377
QY	301	AspAlaLeuGlyAla	305
Db	1378	GATGCCCTCGGGGCC	1392

Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Hiraoka, T., Hirozane, T., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
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JOURNAL PUBMED REFERENCE

4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
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Nature 409, 685-690 (2001)

JOURNAL REFERENCE AUTHORS

5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

JOURNAL REFERENCE AUTHORS

6 (bases 1 to 2256)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Oheato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.
Direct Submission

TITLE JOURNAL

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp).
URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216

COMMENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: <http://genome.gsc.riken.jp/>
URL: <http://fantom.gsc.riken.jp/>.

FEATURES

source

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ORIGIN

Alignment Scores: 5,23e-160 Length: 2256
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 Best Local Similarity: 96.07% Mismatches: 7
 Query Match: 96.00% Indels: 0
 DB: 4 Gaps: 0

US-10-070-794A-4 (1-305) x AK036595 (1-2256)

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 QY 41 ArgAlaAlaProLeuThrPheSerLysLysLysLysLysLysLysLysLysLysLysLysLys 60
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 QY 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80
 DB 839 GACTTTATCTCGTGGTGCACCGGTACTACAGATCCCGCTGGTCCAGATCTATGAGATT 898
 QY 81 GluGlnHisLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 100
 DB 899 GAAGAACATAAGATGAGACCTTGGAGGAGATCTACCTACAGAGCTGCTTCAAGCCCTCTA 958
 QY 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuLysLysAsnArg 120
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 QY 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisLysLysLysLysLys 140
 DB 1019 ATCCACCGCTCGCGGTCCTGGACCCGCTCTCGCAGCTGTGCTTACATACATCACTCACAC 1078
 QY 141 LysArgLeuLeuLysPheLeuHisLysLysLysLysLysLysLysLysLysLysLysLysLys 160
 DB 1079 AAGCGGCTACTCAAAGTTCTCTGCATATATTTGGTGCCTGTGTCCTCCGCGCTCTCTCTC 1138
 QY 161 TyrArgThrIleGlnAspLeuGlyLysLysLysLysLysLysLysLysLysLysLysLysLys 180
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 QY 221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240
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Qy 281 LeuGlyValValSerLeuSerAspIleuGlnAlaLeuValLeuSerProAlaGlyLe 300
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Qy 301 AspAlaLeuGlyAla 305
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RESULT 2
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LOCUS DQ030935 1470 bp DNA linear GSS 02-JUN-2005
DEFINITION Homo sapiens PRKAG3 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION DQ030935
VERSION DQ030935.1 GI:66882139
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1470)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civello,D.,
White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
JOURNAL (er) PLOS Biol. 3 (6), E170 (2005)
PUBMED 15869325
REFERENCE 2 (bases 1 to 1470)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civello,D.,
White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.
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Score: 1434.00 Matches: 285
Percent Similarity: 93.44% Conservative: 0
Best Local Similarity: 93.44% Mismatches: 20
Query Match: 92.46% Indels: 0
DB: 11 Gaps: 0

US-10-070-794a-4 (1-305) x DQ030935 (1-1470)

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Db 553 ATGGCGTTTCATGCGAGGACACACCTGCTACGATGCCATGCACTAGCTCCAAGCTAGTC 612

Qy 21 IlePheAspThrMetLeuGluIleLysLysAlaPheAlaLeuValAlaAsnGlyVal 40
Db 613 ATCTTCACACCACTGCTGGAGATCAAGAAGCCCTCTTTGCTCTGGTGGCCACAGGCTG 672

Qy 41 ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 60
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Db 793 GAACACATTAAGATTGAGACCTGGAGGAGATCTACCTGCAGAGCTGCTTCAAGCCTCTG 852
Qy 101 ValSerIleSerProLeuAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120
Db 853 GTCTCCATCTCTCTAATGATAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 912
Qy 121 IleHisArgLeuProValLeuAspProValSerClyAsnValLeuHisIleLeuThrHis 140
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Qy 301 AspAlaLeuGlyAla 305
Db 1453 GATGCCCTCAGCGCC 1467

RESULT 3
DQ030936 1470 bp DNA linear GSS 02-JUN-2005
LOCUS DQ030936
DEFINITION Pan troglodytes PRKAG3 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION DQ030936
VERSION DQ030936.1 GI:66882140
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Pan.
REFERENCE 1 (bases 1 to 1470)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civello,D.,
White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
JOURNAL (er) PLOS Biol. 3 (6), E170 (2005)
PUBMED 15869325
REFERENCE 2 (bases 1 to 1470)

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AUTHORS Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B., Rubisz, M.J., Fiedel-Alon, A., Tanenbaum, D.M., Civello, D., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

TITLE Direct Submission

JOURNAL Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.

FEATURES

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ORIGIN

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US-10-070-794A-4 (1-305) x DQ030936 (1-1470)

Qy 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 20
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Qy 21 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 40
Db 613 ATCTTCGACACCATGCTGGAGATCAAGAAGCGCTCTTTGCTCTGGTGGCCAAAGCGTGTG 672

Qy 41 ArgAlaProLeuTrpAspSerLysGlnSerPheValGlyMetLeuThrIleThr 60
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Qy 201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220
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Qy 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValIle 260
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Qy 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280
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Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300
Db 1393 TTGGGGTGTGCTCTCTCTCCGACATCTTCAGGCACCTGGTGTCTGAGCCCTGCTGGCATC 1452

Qy 301 AspAlaLeuGlyAla 305
Db 1453 GATGCCCTCGGGGCC 1467

RESULT 4

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LOCUS Rattus norvegicus cDNA clone IMAGE:7113709, containing frame-shift errors.

DEFINITION

BC079017
Rattus norvegicus (Norway rat)

ACCESSION

BC079017.1 GI:50927344

VERSION

HTC.

KEYWORDS

Rattus norvegicus

SOURCE

Rattus norvegicus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Murinae; Rattus.

REFERENCE

1 (bases 1 to 2058)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haiech, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Scapleton, M., Soares, M.B., Bonaldo, M.P., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalek, U., Smailus, D.E., Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

TITLE

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL

12477932

PUBMED

2 (bases 1 to 2058)

REFERENCE

Director MGC Project.

AUTHORS

Direct Submission

TITLE

Submitted (02-AUG-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT

Contact: MGC help desk
Email: cgabbs-remail.nih.gov
Tissue Procurement: Howard Jacobs
cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILN)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcd@paxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, J., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAP Plate: 182 Row: m Column: 20
 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, similarity but not identity to protein
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FEATURES

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 Query Match: 68.86% Indels: 0
 DB: 4 Gaps: 0

US-10-070-794A-4 (1-305) x BC079017 (1-2058)

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 Qy 21 IlePheAspThrMetLeuGluIleLysAlaPhePheAlaLeuValAlaAsnGlyVal 40
 Db 898 GTCTTCGACACTACGTTGCAAGTTAAAGAGCCCTCTTGTGTTGGTAGGCAACGGAGTC 957
 Qy 41 ArgAlaAlaProLeuTrpAspSerLysValGlnSerPheValGlyMetLeuThrIleThr 60
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 Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140
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 Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160
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 Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGlu 180
 Db 1318 AAGCAGAACTCGATGAGCTCGGAATAGGAACATATCACAAATATGCTTCATTCACCCG 1377
 Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 200
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Db 1438 GTGCTGATGAGTCAGGAAAGTTGTAGATATTTACTCCAGTTTGTATGTAATTAATCTT 1497
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 Db 1558 TCACAGTATTTTGGAGGTGTGTCAGTGCAGTAAGCTGGAACACCTGGAGACCATGTG 1617
 Qy 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280
 Db 1618 GACAGAATAGTAGAGCGGAGGTCATCGGTGCTGTGTAGTGAATGAAGCAGATAGTATT 1677
 Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGly 299
 Db 1678 GTGGTATATATCTCCCTGTGACATCTCGAGCCCTGTATCTTCACACGAGGCT 1734

RESULT 5

AK032238

LOCUS

DEFINITION

2839 bp mRNA linear HTC 03-APR-2004

Mus musculus adult male olfactory brain cDNA, RIKEN full-length

enriched library, clone:6430509K05 product:similar to AMP ACTIVATED

PROTEIN KINASE GAMMA 1 (FRAGMENT) [Mus musculus], full insert

sequence.

AK032238

VERSION

AK032238.1 GI:26328068

KEYWORDS

HTC; CAP trapper.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning

Meth. Enzymol. 303, 19-44 (1999)

10349636

REFERENCE

2

Authors

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

11042159

REFERENCE

3

Authors

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,

Konno, H., Akiyama, J., Nishi, K., Kitsuunai, T., Tashiro, H., Itoh, M.,

Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,

Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,

Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M.,

Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,

Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer

Genome Res. 10 (11), 1757-1771 (2000)

11076861

REFERENCE

4

Authors

The RIKEN Genome Exploration Research Group Phase II Team and the

FANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection

Nature 409, 685-690 (2001)

REFERENCE

5

Authors

The FANTOM Consortium and the RIKEN Genome Exploration Research

Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 2839)

REFERENCE

Authors

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,

Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,

Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,

Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katon, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saichoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayaishizaki, Y.

TITLE

JOURNAL

Submitted (16-JUL-2001) Yoshihide Hayaishizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@ec.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT

CNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/

URL: http://fantom.gsc.riken.jp/.

FEATURES

source

1. 2839

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="FANTOM_DB:6430509K05"

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/sex="male"

/tissue_type="olfactory brain"

/clone_lib="RIKEN full-length enriched mouse cDNA library"

/dev_stage="adult"

400. 1731

/note="unnamed protein product; putative

similar to AMP ACTIVATED PROTEIN KINASE GAMMA 1 (FRAGMENT)

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96.8%length, match=182)"

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KIETWREDLYQETPLVNTISPDASLFDVSLTKNKHRLPVIDIPISGNALYILTHK

RILFLQLQMSDMPKPFAMQKNDLDELIGTYHNIATFHPDTPPIIKALNI FVERISAL

PVVDSEGVVDIYSGFDVINLAETKYNLNDITVTOALQHSQYFEGVVKSKLETLE

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2815. 2821

/note="putative"

2839

/note="putative"

ORIGIN

polyA_signal

polyA_site

ORIGIN

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

Length:

Matches:

Conservative:

Mismatches:

Indels:

Gaps:

US-10-070-794A-4 (1-305) x AK032238 (1-2839)

Qy 1 MetArgPheMetGluGlnHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 20

Db 805 ATGCGATTTCATGAGGTGCACAAAGTGTATGACATCGTTCACCAACGATTCGTTGTT 864

Qy 21 IlePheAspThrMetLeuGluIleValLysAlaPhePheAlaLeuValAlaAsnGlyVal 40
Db 865 GTCTTCGACACTACGTTGCAAGTCAAAAGGCTCTTTTCCTTGTGAGCAACGGAGTC 924
Qy 41 ArgAlaAlaProLeuThrPheSerLysLysGlnSerPheValGlyMetLeuThrIleThr 60
Db 925 CGTGACGCGCGCTGTGGGAAAGTAAAAAGCAGACGCTTTGTAGGATGCTCAGCATACA 984
Qy 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80
Db 985 GATTTCATAAATATCTTACACAGATACATAAATACCCCATGGTACAGATTTATGAATG 1044
Qy 81 GluGlnHisLysIleGluThrTrpAspGluIleTyrLeuGlnGlyCysPheLysProLeu 100
Db 1045 GAGAACATGAAGATTGAACGTTGGAGGAGTGTACTTACAGAAACCTTCAGACCTTTG 1104
Qy 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120
Db 1105 GTGAACATCTCTCAGATGCGAGCCTCTTCGATGCTGTATCTCGTTGATCAAAATAAA 1164
Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140
Db 1165 ATCCACAGATTGCGAGTTATTGACCTTATCAGTGGGAAACGACCTTTATATATCTTACCAC 1224
Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160
Db 1225 AAAAGAAATCTCAAGTTCCTCCAGCTTTTATGCTGCATGCGCAAGCTTCGCTTCATG 1284
Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 180
Db 1285 AAGCAGAACCTGGATGAGCTTGGAAATCGGAACGTACCAATAATTGCTTCATTCACCCA 1344
Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 200
Db 1345 GACACTCCCATCATCAAAGCTTTGAACATCTTCGTGGAGAGACGATATCGCATTCGCT 1404
Qy 201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220
Db 1405 GTGTGTGATGAGTCAGAGAAAGTTGTAGATATTATTTCCAGTTTGTATGATTAATCTT 1464
Qy 221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240
Db 1465 GCTGCTGAGAAAACGTACAATAACTTGGACATCAGTGCACGCCAGCGCCTCGACACCGC 1524
Qy 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyValIle 260
Db 1525 TCGCAGTATTTTGAGGCTGTGGTGAAGTCAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1584
Qy 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280
Db 1585 GACAGGATAGTGAGCGGAGGTCCATCGGCTGGTTGTAGTATGATGAGCAGATAGCAT 1644
Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGly 299
Db 1645 GTGGGTATTATCTCCCTGTCAGACATCTGCAAGCCCTGATCCTCACACACGACGAGT 1701

RESULT 6

CD628192/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

EXTENSION

JOURNAL

CD628192 56028554H1 FLP Homo sapiens cDNA, mRNA sequence. EST 12-JAN-2004

CD628192 56028554H1 FLP Homo sapiens cDNA, mRNA sequence. EST 12-JAN-2004

CD628192.1 GI:40276458

EST. Homo sapiens (human)

Source: Homo sapiens

Organism: Homo sapiens

Reference: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo

1 (bases 1 to 796)

Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.

Circular rapid amplification of cDNA ends for high-throughput

extension cloning of partial genes

Genomics 84 (1), 205-210 (2004)

PUBMED 15203218
 COMMENT Contact: Fu GK
 Incyte Genomics, Inc.
 3160 Porter Dr., Palo Alto, CA 94304, USA
 Tel: 6508454102
 Email: gfu@incyte.com.
 FEATURES Location/Qualifiers
 source 1..796
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_lib="FLP"
 /note="Vector: pDrive Cloning Vector"

ORIGIN

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 Score: 1055.00 Matches: 208
 Percent Similarity: 99.52% Conservativeness: 0
 Best Local Similarity: 99.52% Mismatches: 0
 Query Match: 68.02% Indels: 1
 DB: 6 Gaps: 0

US-10-070-794A-4 (1-305) x CD628192 (1-796)

Qy 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 20
 Db 626 ATGGCTTTCATGACGAGCAGCACCTGCTAGCATGCCATGCCAATAGCTAGCTCAAGCTAGTC 567
 Qy 21 IlePheAspThrMetLeuGluLeuLysLysAlaPheAlaLeuValAlaAenGlyVal 40
 Db 566 ATCTTCACACCATGCTGGAGATCAAGAAGCCCTCTTCTGCTGGGCAACGGGTG 507
 Qy 41 ArgAlaAlaProLeuTrpAspSer-LysLysGlnSerPheValGlyMetLeuThrIleTh 60
 Db 506 CGGCGACCCCTCATGGGACAGCAAGAGCAGAGCTTTGTGGGATGCTGACCATCAC 447
 Qy 60 rAspPheIleLeuValLeuHisArgTyrArgSerProLeuValGlnIleTyrGluI 80
 Db 446 TGACTTCATCTGCTGCTGCTACTACAGTCCCTGCTGCTGCTGCTGCTGCTGATGAT 387
 Qy 80 eGluGlnHisLysIleGluThrTrpArgGluLeuTyrLeuGlnGlyCysPheLysProLe 100
 Db 386 TGAACACACATAGATTGAGACCTGGAGGAGATCTACTGCAAGGCTGCTTCAAGCTCT 327
 Qy 100 uValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuLysAsnAr 120
 Db 326 GGTCTCCATCTCTCTATGATAGCTTTGTAGCTGTCTACACCTCTATCAAGAACCG 267
 Qy 120 gIleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHi 140
 Db 266 GATCCATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 207
 Qy 140 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLe 160
 Db 206 CAACGCTGCTCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 147
 Qy 160 uTyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGl 180
 Db 146 CTACCGGACATCTCAGATTGGGATCGGCACATTCGAGACCTGCTGCTGCTGCTGCTG 87
 Qy 180 uThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPr 200
 Db 86 GACAGCACCATCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 27
 Qy 200 oValValAsnGluCysGlyGlnVal 208
 Db 26 TGTGTCACCAATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2

RESULT 7

CR861174 1990 bp mRNA linear HTC 17-APR-2005
 LOCUS Pongo pygmaeus mRNA; cDNA DKFZp45912016 (from clone DKFZp45912016).
 DEFINITION

ACCESSION CR861174
 VERSION CR861174.1
 KEYWORDS GI:55733123
 SOURCE HTC
 ORGANISM Pongo pygmaeus (orangutan)

ORGANISM

REFERENCE 1 (bases 1 to 1990)
 AUTHORS Koehler, K., Meyer, A., Mewes, H.W., Weil, B., Amid, C., Osanger, A.,
 Fobo G., Han, M. and Wiemann, S.
 CONSRM The German CDNA Consortium
 TITLE Direct Submission
 JOURNAL Submitted (12-NOV-2004) MIPS, Ingolstaedter Landstr.1, D-85764
 Neuherberg, GERMANY

COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 sequenced by BMFZ (Biomedical Research Center at the
 Heinrich-Heine-University, Dueseldorf/Germany) within the CDNA
 sequencing consortium of the German Genome Project. This clone
 (DKFZp45912016) is available at the RZPD Deutsches
 Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
 Please contact RZPD for ordering:
 http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp45912016
 Further information about the clone and the sequencing project is
 available at http://mips.gsf.de/projects/cdna/.

FEATURES

Location/Qualifiers
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 DH10B; sites SfiIa + SfiIb"
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 alternative start"

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 CDS 250..1824
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ORIGIN

Alignment Scores:
 Pred. No.: 6,24e-110 Length: 1990
 Score: 1054.00 Matches: 193
 Percent Similarity: 85.28% Conservativeness: 62
 Best Local Similarity: 84.55% Mismatches: 44
 Query Match: 67.96% Indels: 0
 DB: 4 Gaps: 0

US-10-070-794A-4 (1-305) x CR861174 (1-1990)

Qy 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 20
 Db 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 20

898 ATGCATTATGAGTTCACACAGTGTATGACATCGTCCAAACAGTTCACAAAGCTTGTT 957
Db
Qy 21 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 40
Db 958 GTCTTTGATACATACAAAGTTAAAGAGCCCTCTTCTGTTGGTAGCAACGGGTGTC 1017
Qy 41 ArgAlaAlaProLeuThrPheSerLysLysGlnSerPheValGlyMetLeuThrIleThr 60
Db 1018 CGAGCAGCGCGCTGTGGGAGAGTAAAGAAACAAAGTTTGTAGGAATGCTAAACAATACA 1077
Qy 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80
Db 1078 GATTTCTAATAATACATACATAGTACTATAATACCTATGATGCTACAGATTTATGATTA 1137
Qy 81 GluGlnHisLysIleGluThrTyrArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100
Db 1138 GAGGAACATAAATTTGAAACATGAGGAGGCTTTATTTACAGAAACATTTAAAGCCTTTA 1197
Qy 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120
Db 1198 GTGAATATATCTCCAGATGCAAGCCTCTCGATGCTGTATACCTCTTGATCAAAATAA 1257
Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140
Db 1258 ATCCACAGATGCCGTTATGACCTATCAGTGGGAATGCGCTTTATATACCTTACCCAC 1317
Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160
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Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 180
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Db 1558 GCTGCTGAGAAACATACATAAATCAGATATCATCATGACGACCCAGCCCTTCAGCACCGT 1617
Qy 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIle 260
Db 1618 TCACAGTATTTGAAGGTGTGTGAGTGCATTAAGCTGGAAATACCTGGAGACCATTTGTG 1677
Qy 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280
Db 1678 GACAGATAGTAAGAGCTGAGTCCATCGGCTGGTGGTGGCCAAATGAAGCAGATAGTATT 1737
Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGly 299
Db 1738 GTGGGTATTTTCCCTGTGACATTTCTGCAAGCCCTGATCTCTCACACCCAGCAGGT 1794
RESULT 8
CD628194/c 754 bp mRNA linear EST 12-JAN-2004
LOCUS 56028562H1 FLP Homo sapiens cDNA, mRNA sequence.
DEFINITION CD628194
ACCESSION CD628194
VERSION CD628194.1 GI:40276460
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 754)
AUTHORS Fu, G.K., Wang, J.T., Yang, J., Xu-Young, J. and Stuve, L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput

extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
15203218
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
Location/Qualifiers
1. .754
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"
source
FEATURES
Alignment Scores:
Pred. No.: 7,28e-110 Length: 754
Score: 1048.00 Matches: 207
Percent Similarity: 99.04% Conservative: 0
Best Local Similarity: 99.04% Mismatches: 1
Query Match: 67.57% Indels: 1
DB: 6 Gaps: 0
US-10-070-794a-4 (1-305) x CD628194 (1-754)
Qy 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThr-SerSerLysLeuVa 20
Db 626 ATGCGCTTCTGCGAGGAGCACCTGCTACGATGCCATGGCACTTAGCTTCAAGCTAGT 567
Qy 20 11lePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVa 40
Db 566 CATCTTCGATACCATGCTGGAGATCAAGAGCCCTTCTTGTCTGTGGTGGCCACGGTGT 507
Qy 40 1ArgAlaAlaProLeuThrPheSerLysLysGlnSerPheValGlyMetLeuThrIleTh 60
Db 506 GCGGCGACGCCCTCTATGGGACAGCAAGAGAGAGCTTTGTGGGATGCTGACCATCAC 447
Qy 60 rAspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluI 80
Db 446 TGACTTTCATCTGCTGCTGCTACTACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 387
Qy 80 eGluGlnHisLysIleGluThrTyrArgGluIleTyrLeuGlnGlyCysPheLysProLe 100
Db 386 TGAACACATAAAGATTGAGACCTGGAGAGATCTACTGCAAGGCTGCTTCAAGCCTCT 327
Qy 100 uValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnAr 120
Db 326 GGTCTCCATCTCTCTTAATGATAGCTGTTTGAAGCTGTCTACACCCCTCATCAAGAACCG 267
Qy 120 gIlleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHi 140
Db 266 GATCACCGCTGCGCAGTTCTTGACCCCGGTGTACGCAACCGTACTTCCACATCTCTCACACA 207
Qy 140 sLysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLe 160
Db 206 CAAAGCGCTGCTCAAGTTCCTGCAATCTTTGGTTCCTGCTGCTGCTGCTGCTGCTGCTGCT 147
Qy 160 uTyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGl 180
Db 146 CTACCGCACTATCCAGATTTGGGCATCGGCACATTCGAGACTTGGCTGTGGTGTGGTGG 87
Qy 180 uThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuPr 200
Db 86 GACAGCACCATCTCTGACTGCACTGCACTCTTTGTGGACCGGCGTGTGTCTGCACTGCC 27
Qy 200 oValValAsnGluCysGlyGlnVal 208
Db 26 TGTGTGTCAACGAATGTGTGCTCAGGTC 2
RESULT 9
CX313244

end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen.

This sequence belongs to sequence cluster 6712.f

For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?s=CL0BB0072F11RP1&c=6712.f>.

FEATURES
source
1. .1136
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/notes="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

Alignment Scores:
Pred. No.: 4.2e-105 Length: 1136
Score: 1009.00 Matches: 192
Percent Similarity: 82.99% Conservative: 52
Best Local Similarity: 65.31% Mismatches: 50
Query Match: 65.05% Indels: 0
DB: 5 Gaps: 0

US-10-070-794A-4 (1-305) x BX403964 (1-1136)

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DB	85	TTCAAGAAGTCATCGCTGCTATGACCTGATCCACAGCTCCAAATGGTTGTTATT	144
QY	23	AspThrMetLeuGluIleLysLeuAlaPhePheAlaLeuValAlaAsnGlyValArgAla	42
DB	145	GATACGTCCTCGAGGTGAGAGAAAGCTTTTTCCTTGTGTGACTAAACGGTGTACGAGCT	204
QY	43	AlaProLeuTrpAspSerLysLeuGlnSerPheValGlyMetLeuThrIleThrAspPhe	62
DB	205	GCCCTTTATGGGATAGTAAGAGCAAGTTTGTGGCATGCTGACCATCAGATTC	264
QY	63	IleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGluGln	82
DB	265	ATCAATATCTCGACCGCTACTATAAATCAGCTTGGTACAGATCTATGAGCTAGAGAA	324
QY	83	HisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeuValSer	102
DB	325	CACAAGATAGAACTTGGAGAGAGGTGTATCTCCAGGACTCTTTAAACCGCTTGTCTGC	384
QY	103	IleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIleHis	122
DB	385	ATTTCTCTTAATGCCAGCTGTGTTCCTTCCTTCATTAATTCGGAACAGATATCCAC	444
QY	123	ArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLysArg	142
DB	445	AGGTCGCCAGATTATGGACCCAGATCAGGCAATATCTTTGTACATCTCCACCACAAGCGC	504
QY	143	LeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyrArg	162
DB	505	ATTCTGAAGTTCCTCAAAATGTTTATCACTAGTTCCTCCAGCCAGAGTTCATGTGCCAAG	564
QY	163	ThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGluThrAla	182
DB	565	TTCTGGGAAGAGCTACAGATTCGGACCTATGTCCTCAATATGCTATGTTGCGACTACACC	624
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DB	745	GAAAAGACCTACAAACACCTAGATGTATCTGTGCTAAAGCCCTTGCACATCGATCAT	804
QY	243	CysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAspArg	262
DB	805	TACTTTGAGGGTGTCTCAAGTGCTACCTGCATGAGACTCTGGAGACCATCATCAACAGG	864
QY	263	IleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeuGly	282
DB	865	CTATGGAGACGAGAGGTTACCGACTTGTAGTGTGATGAAATGATGTGGTCAAGGGA	924
QY	283	ValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSer	296
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RESULT 11
BX421925
LOCUS
DEFINITION
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clone CSODH005YN22 5-PRIME, mRNA sequence.
ACCESSION
BX421925 GI:46925182
VERSION
BX421925.2
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
AUTHORS
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE
Full-length cDNA libraries and normalization
JOURNAL
Unpublished (2001)
COMMENT
On May 13, 2003 this sequence version replaced gi:30638442.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

This sequence belongs to sequence cluster 6712.f
For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?s=CSODH005DG11QPI&c=6712.f>.

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/clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE)"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN
Alignment Scores:
Pred. No.: 4.24e-105 Length: 1144
Score: 1009.00 Matches: 192
Percent Similarity: 82.99% Conservative: 52
Best Local Similarity: 65.31% Mismatches: 50
Query Match: 65.05% Indels: 0
DB: 5 Gaps: 0


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Qy 223 GlnGlnThrTyrAenHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThrLeu 242
Db 746 GAAAAGACCTTACAACAACCTAGATGATCTGTGACTAAAGCCTTGCAACATCGATC 805
Qy 243 CysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAspArg 262
Db 806 TACTTTGAGGGTGTCTCAAGTGTCTACCTGCATGAGACTCTGGAGACCATCATCAACAGG 865
Qy 263 IleAlaArgGluGlnValHisArgLeuValValAspGluThrGlnHisLeuLeuGly 282
Db 866 CTAGTGAAGCAGAGGTTCCCGACTTGTAGTGGTGGATGAAATGATGTTGGTCAAGGGA 925
Qy 283 ValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSer 296
Db 926 ATTGTATCATCTGTCTGACATCTCTGAGCCCTGGTGTCTACA 967

RESULT 13
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DEFINITION full-length cDNA clone CSODA012YB06 of Neuroblastoma of Homo sapiens (human).
ACCESSION CR608916
VERSION CR608916.1 GI:50489723
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1577)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVivoGen Corporation 1600 Faraday Avenue
REFERENCE 2 (bases 1 to 1577)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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Alignment Scores: 6.82e-105 Length: 1577
Pred. No.: 1009.00 Matches: 192
Score: 82.99% Conservative: 52
Percent Similarity: 82.99%
Best Local Similarity: 65.31% Mismatches: 50
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Query Match: 65.05% Indels: 0
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US-10-070-794A-4 (1-305) x CR608916 (1-1577)
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Qy 23 AspThrMetLeuGluIleIysIysAlaPhePheAlaLeuValAlaAenGlyValArgAla 42
Db 146 GATACGTCCTCGCAGGTGAAGAAAGCTTTTTCCTTGGTGACTAACCGTGACGAGCT 205
Qy 43 AlaProLeuTyrAspSerIysIysGlnSerPheValGlyMetLeuThrIleThrAspPhe 62
Db 206 GCCCTTTTATGGATAGTAGAAGCAAGATTTCCTGGGCATGCTGACCATCATGATTTC 265
Qy 63 IleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGluGln 82
Db 266 ATCAATATCTCGCACCCTACTATAAATCAGCCTTGGTACAGATCTATGAGCTAGAAGA 325
Qy 83 HisIysIleGluThrTyrArgGluIleTyrLeuGlnGlyCysPheIysProLeuValSer 102
Db 326 CACAAGATAGAAACTTGGAGAGAGGTGTATCTCCAGGACTCTCTTAAACCGCTGTCTGC 385
Qy 103 IleSerProAenAspSerLeuPheGluAlaValTyrThrLeuIleIysAenArgIleHis 122
Db 386 ATTTCCTCTAATGCCAGCTTGTTCCTTCATTAATTCGGAACAGATCCAC 445
Qy 123 ArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisIysArg 142
Db 446 AGCTGCCAGTTATGACCCAGAAATCACTTTGTACATCTCTACCCCAAGCGC 505
Qy 143 LeuLeuIysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyrArg 162
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Db 746 GAAAAGACCTTACAACAACCTAGATGATCTGTGACTAAAGCCTTGCAACATCGATC 805
Qy 243 CysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAspArg 262
Db 806 TACTTTGAGGGTGTCTCAAGTGTCTACCTGCATGAGACTCTGGAGACCATCATCAACAGG 865
Qy 263 IleAlaArgGluGlnValHisArgLeuValValAspGluThrGlnHisLeuLeuGly 282
Db 866 CTAGTGAAGCAGAGGTTCCCGACTTGTAGTGGTGGATGAAATGATGTTGGTCAAGGGA 925
Qy 283 ValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSer 296
Db 926 ATTGTATCATCTGTCTGACATCTCTGAGCCCTGGTGTCTACA 967

RESULT 14
LOCUS CR613967 1584 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CSODI042YD16 of Placentia Cot 25-normalized of Homo sapiens (human).
ACCESSION CR613967
VERSION CR613967.1 GI:50494774
KEYWORDS HTC; CNSLT_cDNA.
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 25, 2006, 21:59:11 ; Search time 157.061 Seconds
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Perfect score: 1551
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Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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9	1009	65.1	1500	3	US-09-949-016-5010

10	1009	65.1	1578	3	US-09-016-434-1113	Sequence 1113, Ap
11	1003	64.7	1576	3	US-09-101-146-63	Sequence 63, Appl
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13	304	16.3	350	3	US-09-513-999C-1659	Sequence 1659, Ap
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15	240	15.5	269	3	US-09-016-434-194	Sequence 194, App
16	198	12.8	645	3	US-09-533-559-4899	Sequence 4899, Ap
17	196.5	12.7	1890	3	US-09-248-796A-432	Sequence 432, App
18	190	12.3	1262	3	US-09-359-161-1	Sequence 1, Appli
19	187	12.1	122772	3	US-09-949-016-14132	Sequence 14132, A
20	153	9.9	523	3	US-09-533-559-673	Sequence 673, App
21	151.5	9.8	1664976	3	US-08-916-421B-1	Sequence 1, Appli
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23	143	9.2	601	3	US-09-949-016-82286	Sequence 82286, A
24	130.5	8.4	622	3	US-08-998-416-987	Sequence 987, App
25	130.5	8.4	3019	3	US-09-359-161-2	Sequence 1, Appli
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28	109	7.0	601	3	US-09-949-016-82262	Sequence 82262, A
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30	107.5	6.9	1500	3	US-09-252-991A-13688	Sequence 13688, A
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32	105.5	6.8	18031	3	US-09-902-540-1180	Sequence 1180, Ap
33	104.5	6.7	1761	3	US-09-033-055A-3	Sequence 3, Appli
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41	98.5	6.4	1469	3	US-09-634-238-42	Sequence 42, Appl
42	97.5	6.3	1533	3	US-09-489-039A-4607	Sequence 4607, Ap
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ALIGNMENTS

RESULT 1
US-09-950-022A-1
; Sequence 1, Application US/09950022A
; Patent No. 6919177
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: No. 6919177el PRKAG3 Alleles and Use fo the Same as Genetic Mark.
; TITLE OF INVENTION: Reproductive
; FILE OF INVENTION: and Meat Quality Traits
; FILE REFERENCE: P04668US3
; CURRENT APPLICATION NUMBER: US/09/950, 022A
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1873
; TYPE: DNA
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) ..(1392)
; OTHER INFORMATION:
US-09-950-022A-1

Alignment Scores:

Pred. No.: 4,53e-175 Length: 1873
Score: 1507.00 Matches: 296
Percent Similarity: 98.36% Conservativeness: 4
Best Local Similarity: 97.05% Mismatches: 5
Query Match: 97.16% Indels: 0
DB: 3 Gaps: 0

US-10-070-794A-4 (1-305) x US-09-950-022A-1 (1-1873)

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RESULT 2

US-09-950-022A-3
; Sequence 3, Application US/09950022A
; Patent No. 6919177
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: No. 6919177el PRKAG3 Alleles and Use fo the Same as Genetic Mark
; TITLE OF INVENTION: Reproductive
; TITLE OF INVENTION: and Meat Quality Traits
; FILE REFERENCE: P04668US3
; CURRENT APPLICATION NUMBER: US/09/950,022A
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1873
; TYPE: DNA
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)-(1392)
; OTHER INFORMATION:
; US-09-950-022A-3

Alignment Scores:

Pred. No.: 4,53e-175 Length: 1873
Score: 1507.00 Matches: 296
Percent Similarity: 98.36% Conservativeness: 4
Best Local Similarity: 97.05% Mismatches: 5
Query Match: 97.16% Indels: 0
DB: 3 Gaps: 0

US-10-070-794A-4 (1-305) x US-09-950-022A-3 (1-1873)

Qy 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 20
Db 478 ATGCACCTTCATCGAGGACACACTGCTACGATGCCATGGGACAGCTCCAAACTGGTC 537
Qy 21 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 40
Db 538 ATCTTCGACACCATGCTGGAGATCAAGAAGCCCTTCTTGGCCCTGGTGGCCAAACGGCGTC 597
Qy 41 ArgAlaAlaProLeuTrpAspSerLysGlnSerPheValGlyMetLeuThrIleThr 60
Db 598 CGAGCGGCACCTTTGTGGGACAGCAAGAAGCAGAGCTTCGTGGGGATGCTGACCATCACA 657
Qy 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80
Db 658 GACTTCATCTTGGTGCTGCACCGCTATTACAGGTCCCGCCCTGGTCCAGATCTACGAGATT 717
Qy 81 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100
Db 718 GAAGACATAAGATTGAGACCTGGAGGAGATCTACCTTCAAGGCTGTCTCAAGCTCTG 777
Qy 101 ValSerIleSerProAsnAspSerLysPheGluAlaValTyrThrLeuIleLysAsnArg 120
Db 778 GTCTCCATCTCTCCCAATGACAGCGCTGTTCGAAGCTGTCTACGCCCTCATCAAGAACCGG 837
Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140
Db 838 ATCCACCGCCTGCGGTCCTGACATCTCTTACAGTCTTACGGTCTGGTCTCAGCCCTGCTGGAATT 897
Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160

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Db      998  AAGCGGCTTCAAGTTCCCTGCACATCTTTGGCACCTGTGCTGCCCGCCCTCTCCTC 957
Qy      161  TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 180
Db      958  TACCGCACCATCCAGATTGGGCATCGGCATCCGAGACTTGGCGGTGCTGGAA 1017
Qy      181  ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuPro 200
Db      1018  ACGCGGCCCATCTCGACCGCATCTTCGTGACCGCGGTGTCTGCGCTGCCT 1077
Qy      201  ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220
Db      1078  GTGTCTAACGAAACTGGACAGGTAGTGGGCTCTACTCTCGCTTTGATGTATCCACTG 1137
Qy      221  AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240
Db      1138  GCTGCCCAACAACATACACCACTGGACATGAATGTGGGAGAGCCCTGAGGCAGCGG 1197
Qy      241  ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIle 260
Db      1198  ACCTGTCTCGAAGCGGTCTCTTCTGACATCTTCTGACATCTTCTGAGCTCTGGTCTCAGCCCTGTGGAAAT 1377
Qy      301  AspAlaLeuGlyAla 305
Db      1378  GATGCCCTCGGGGCC 1392

RESULT 3
US-09-950-022A-5
; Sequence 5, Application US/09950022A
; Patent No. 6919177
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: No. 6919177el PRKAG3 Alleles and Use fo the Same as Genetic Mark
; TITLE OF INVENTION: Reproductive
; TITLE OF INVENTION: and Meat Quality Traits
; FILE REFERENCE: P0468US3
; CURRENT APPLICATION NUMBER: US/09/950,022A
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1873
; TYPE: DNA
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1392)
; OTHER INFORMATION:
US-09-950-022A-5

Alignment Scores:
Pred. No.: 4,53e-175 Length: 1873
Score: 1507.00 Matches: 296
Percent Similarity: 98.36% Conservative: .4
Best Local Similarity: 97.05% Mismatches: 5
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Query Match: 97.16% Indels: 0
DB: 3 Gaps: 0
US-10-070-794A-4 (1-305) x US-09-950-022A-5 (1-1873)
Qy 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 20
Db 478 ATGCACCTTTCATGCGAGGAGCACACCTGTACGATGCCATGGCAGCTCCAAACTGGTC 537
Qy 21 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 40
Db 538 ATCTTCGACACCATGTCTGGAGATCAAGAGGCCCTCTTTGCCCTGGTGGCCACGGCGTC 597
Qy 41 ArgAlaAlaProLeuThrPheSerLysLysGlnSerPheValGlyMetLeuThrIleThr 60
Db 598 CGAGCGGCACCTTTGTGGGACAGCAAGACAGAGCTTCGTGGGATGCTGACCATCACA 657
Qy 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80
Db 658 GACTTTCATCTTGTGTGTCACCGCTATTACAGGTCCCTCCCTGCTGTCAGATCTACGAGATT 717
Qy 81 GluGlnHisLysIleGluThrTyrArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100
Db 718 GAGAACATTAAGATTGAGACCTGGAGGAGATCTACCTTCAGGCTGCTTCAGGCTCTG 777
Qy 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120
Db 778 GTCTCCATCTCTCCCAATGACAGCTGTTCGAAGCTGTCTACGCCCTCATCAAGACCGG 837
Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140
Db 838 ATCCACCGCTGCGGTCCTGGACCTGTCTCGGGGCTGTGCTCCACATCTCTCACACAT 897
Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160
Db 898 AAGCGGCTTCTCAAGTTCCTGTCACATCTTTGGCACCTCTGCTGCTGCCCGGCCCTCTCTCTC 957
Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 180
Db 958 TACCGCACCATCCAAAGATTGGGACATCGGCACATTCGAGACTTGGCCGTGGTCTGGAA 1017
Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 200
Db 1018 ACGCGGCCCATCTCGACCGCATCTTCGTGACCGCGGTGTGTCTGCGCTGCGCT 1077
Qy 201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220
Db 1078 GTGTCAACGAAACTGGACAGGTAGTGGGCTCTACTCTCGCTTTGATGTATCCACTG 1137
Qy 221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240
Db 1138 GCTGCCCAACAACATACACCACTGGACATGAATGTGGGAGAGCCCTGAGGCAGCGG 1197
Qy 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIle 260
Db 1198 ACATGTGTCTGGAAGCGGTCTTCTTCTGACGCCCCACGAGACCTTTGGGGGAAAGTCAAT 1257
Qy 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280
Db 1258 GACCGGATTTGTCGGGAAACAGGTGACCGCTGTGTGCTGTGGATGAGACCCAGCACCTT 1317
Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300
Db 1318 CTGGCGGTGTGTCTCTCTCTGACATCTCTTCTGAGCTCTGTGCTCAGCCCTGTGGAAAT 1377
Qy 301 AspAlaLeuGlyAla 305
Db 1378 GATGCCCTCGGGGCC 1392

RESULT 4
US-09-950-022A-7
; Sequence 7, Application US/09950022A
; Patent No. 6919177
```

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; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: No. 6919177el PRKAG3 Alleles and Use fo the Same as Genetic Mark
; TITLE OF INVENTION: Reproductive
; TITLE OF INVENTION: and Meat Quality Traits
; FILE REFERENCE: P04668US3
; CURRENT APPLICATION NUMBER: US/09/950,022A
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 1873
; TYPE: DNA
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1392)
; OTHER INFORMATION:
US-09-950-022A-7

Alignment Scores:
Pred. No.: 6,01e-175 Length: 1873
Score: 1506.00 Matches: 295
Percent Similarity: 98.36% Conservative: 5
Best Local Similarity: 96.72% Mismatches: 5
Query Match: 97.10% Indels: 0
DB: 3 Gaps: 0

US-10-070-794A-4 (1-305) x US-09-950-022A-7 (1-1873)

Qy 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 20
Db 478 ATGCACCTTCATGTCAGGAGCACACCTGCTACGATGCCATGGGACAGCTCCAAACTGGTC 537
Qy 21 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 40
Db 538 ATCTTCGACACCATGCTGGAGATCAAGAAGGCCCTCTTTGGCCCTGGTGGCCAAACGGCATC 597
Qy 41 ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 60
Db 598 CGAGCGGCACCTTTGTGGGACAGCAGCAGCAGCTTCGTGGGATGCTGACCATCA 657
Qy 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80
Db 658 GACITTCATCTTGGTCTGCACCGCTATTACAGGTCCCGCTGGTCCAGATCTACGAGATT 717
Qy 81 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100
Db 718 GAAGAACAATAAGATTGAGACCTTGGAGGAGAGATCTACCTTCAAGGCTGTTCAAGCCTCTG 777
Qy 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120
Db 778 GTCCTCATCTCTCCCAATGACAGCCTGTTCGAGCTGTCTACGCCCTCATCAAGAACCGG 837
Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140
Db 838 ATCCACCGCGCTCGCGTCTCGACCTGTCTCCGGGGTGTGTCTCCACATCTCCACAT 897
Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160
Db 898 AAGCGCGCTTCTCAAGTTCTCGACATCTTTGGCACCTGTCTGCCCGGCCCTCTCTCTC 957
Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 180
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Db 958 TACCGCACCATCCAGAGATTTGGGCATCGGCACATTCGAGACTTGGCCGCTGGTGGAA 1017
Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 200
Db 1018 ACGGCCCATCTCTGACCGCAGCTTCTCGTGGACCGCGGTGTCTGGCGTGCCT 1077
Qy 201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220
Db 1078 GTGGTCAACGAARACTGGACAGGTAGTGGGCTCTACTCTCGCTTGTATGTGATCCACCTG 1137
Qy 221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240
Db 1138 GCTGCCCAACAAACATACACCACTGGACATCAATATGTGGGAAGCCCTTAGGCGCGG 1197
Qy 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIle 260
Db 1198 ACACCTGTGTCTGAAGCGCTCTTCTGTGCACGCCACAGACCTTGGGGGAAGTCATT 1257
Qy 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280
Db 1258 GACCGGATTGTCCGGGAACAGGTGCACCGCTGTGTCTGTGGATGAGACCCAGACCTT 1317
Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300
Db 1318 CTGGCGTGTGTCTCTCTCTGACATCTCTCAGGCTCTGTGTCTCAGCCCTGTGTGAATT 1377
Qy 301 AspAlaLeuGlyAla 305
Db 1378 GATGCCCTCGGGGCC 1392

RESULT 5
US-09-950-022A-9
; Sequence 9, Application US/09950022A
; Patent No. 6919177
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: No. 6919177el PRKAG3 Alleles and Use fo the Same as Genetic Mark
; TITLE OF INVENTION: Reproductive
; TITLE OF INVENTION: and Meat Quality Traits
; FILE REFERENCE: P04668US3
; CURRENT APPLICATION NUMBER: US/09/950,022A
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 1873
; TYPE: DNA
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1392)
; OTHER INFORMATION:
US-09-950-022A-9

Alignment Scores:
Pred. No.: 1,41e-174 Length: 1873
Score: 1503.00 Matches: 295
Percent Similarity: 98.36% Conservative: 5
Best Local Similarity: 96.72% Mismatches: 5
Query Match: 96.91% Indels: 0
DB: 3 Gaps: 0

US-10-070-794A-4 (1-305) x US-09-950-022A-9 (1-1873)
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Qy 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 20
 Db 478 ATGCATTTTCATGAGGAGCACACCTGCTACCATGCCATGGCAGCAGCTCCAAACTGGTC 537
 Qy 21 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 40
 Db 538 ATCTTCGACACCATGCTGGAGATCAGAGAGCCCTCTTTGCCCTGGTGGCCNACGGGGTC 597
 Qy 41 ArgAlaAlaProLeuTrpAspSerLysGlnSerPheValGlyMetLeuThrIleThr 60
 Db 598 CAAGCGGCACCTTTGTGGGACAGCAAGAGAGAGCTTCGTGGGGATGCTGACCATCACA 657
 Qy 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluLe 80
 Db 658 GACTTCATCTTGGTGGCTGACCGCTATTACAGGTCCCGCTGGTCCAGATCTACGAGATT 717
 Qy 81 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100
 Db 718 GAAGAAATAGATTGAGACCTGGAGGAGATCTACCTTCNAGGCTGCTTCAGCCCTCTG 777
 Qy 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120
 Db 778 GTCTCCATCTCTCCATGACAGCCTGTTCGAGCTGTCTAGCCCTCATCAAGAACCGG 837
 Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140
 Db 838 ATCCACCGCTGCGGGCTCTGGACCTGTCTCCGGGGCTGTGTCTCCACATCTCTCACAT 897
 Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160
 Db 898 AAGCGGCTTCTCAAGTCTCTGCACATCTTTGGACCCCTGTGCCCCGGCCCTCTCTCTC 957
 Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 180
 Db 958 TACCGCACCATCCAAATTTGGGCATCGGCACATTCGAGACTTGGCGGTGTCTGGAA 1017
 Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuPro 200
 Db 1018 ACGCGCGCCATCTCGACCGCATCGACATCTCTGAGCCGGCGTGTGTCTGGCGCTCCT 1077
 Qy 201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220
 Db 1078 GTGGTCAACGAACTGGACAGGTAGTGGGCTCTACTCTGCTTTGATGATCCACTG 1137
 Qy 221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240
 Db 1138 GCTGCCCAACAAACATACACCATCTGGACATGAATGTGGGAGAGCCCTGAGGACCGG 1197
 Qy 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValIle 260
 Db 1198 ACATGTGTCTGGAGGCGTCTTTCTGCGAGCCCGCCAGAGACTTGGGGGAGTCAATT 1257
 Qy 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280
 Db 1258 GACCGGATTGTCGGGAAACAGGTGCAACCGCTGGTGTCTGTGGATGAGACCCAGACCTT 1317
 Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300
 Db 1318 CTGGCGTGGTGTCTCTCTGACATCTTCAGGCTCTGGTCTGAGCCCTGTCTGGNATT 1377
 Qy 301 AspAlaLeuGlyAla 305
 Db 1378 GATGCCCTCGGGCC 1392

RESULT 6
 US-08-878-989-14
 ; Sequence 14, Application US/08878989
 ; Patent No. 5885803
 ; GENERAL INFORMATION:
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Corley, Neil C.
 ; APPLICANT: Guegler, Karl G.

APPLICANT: Lal, Preeti
 APPLICANT: Goli, Surya K.
 APPLICANT: Shah, Purvi
 TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
 TITLE OF INVENTION: KINASES
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/878,989
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J J
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0321 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166
 TELEX:
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1435 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: PENITUT01
 CLONE: 1452972
 US-08-878-989-14

Alignment Scores:
 Pred. No.: 1,03e-120 Length: 1435
 Score: 1064.00 Matches: 195
 Percent Similarity: 85.95% Conservative: 62
 Best Local Similarity: 65.22% Mismatches: 42
 Query Match: 68.60% Indels: 0
 DB: 2 Gaps: 0

US-10-070-794A-4 (1-305) x US-08-878-989-14 (1-1435)

Qy 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 20
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 Qy 21 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 40
 Db 248 GTCTTTGATACATACATTACAAGTTAAAGGCTCTCTTTGCTTTGGTAGCCACGGGTG 307
 Qy 41 ArgAlaAlaProLeuTrpAspSerLysGlnSerPheValGlyMetLeuThrIleThr 60
 Db 308 CGAGCAGCCCTCTGTGGGAGAGTAAAGGATTTGTAGGATGCTTAACAATTACA 367
 Qy 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluLe 80
 Db 368 GATTTTCAATAATATACATACATGATCTATAAATCACCTATGTCATGATGATTA 427
 Qy 81 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100
 Db 428 GAGGAACATAAAATTCAGACATGGGAGGCTTTATTTTACAGAAACATTTTAAGCCTTTA 487

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Qy 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120
Db 488 GTGAATATATCTCCAGATCAAGCCTCTCGATCTGTATCTCTTGTATCAAAATAAA 547
Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140
Db 548 ATCCACAGATGTCGCGTATTGACCTTATGAGTGGGAATGCACCTTATATATCTTACCCAC 607
Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160
Db 608 AAAGAAATCTCAAGTCTCTCCAGCTTTTATGCTGATATGCAAGACCTGCTTCATG 667
Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 180
Db 668 AAGCAGAACCTGGATGAGCTTGGAAATAGGAACGTACCACACATTCGCTTCATACATCCA 727
Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuPro 200
Db 728 GACACTCCCATCATCAAGCCTTGAACATATTTGTGGAAGACCAATATCAGCTCTGCCT 787
Qy 201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220
Db 788 GTTGTGGATGAGTCAGGAAGAGTTGTAGATATTTATCCAAATTTGATGTAATTAATCTT 847
Qy 221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240
Db 848 GCTGCTGAGAAACATACATAAATAGCTAGATATCAGGTGACCGTACCCAGCGCTTCAGCACCGT 907
Qy 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIle 260
Db 908 TCACAGTATTTGAGGTGTTGTGAAGTGCATTAAGCTGGAAATACCTGGAGACCATCGTG 967
Qy 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280
Db 968 CACAGATAGTAAGAGCTGAGGTCCATCGGTGGTGGTGAATGAAGCAGATAGTATT 1027
Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGly 299
Db 1028 GTGGTATTATTTCCCTGTCGACATTTCTGCAAGCCTGATCTCTCACACACGAGGT 1084
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RESULT 7

US-09-272-796-14
; Sequence 14, Application US/09272796
; Patent No. 6207148

GENERAL INFORMATION:

; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl G.
; APPLICANT: Lal, Preeti
; APPLICANT: Goli, Surya K.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
; TITLE OF INVENTION: KINASES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/272,796
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/878,989

; FILING DATE: 08/878,989

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J J

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0321 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-0555

; TELEFAX: 415-845-4166

; TELEX:

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1435 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: PENITUT01

; CLONE: 1452972

; US-09-272-796-14

Alignment Scores:

Pred. No.: 1.03e-120 Length: 1435
Score: 1064.00 Matches: 195
Percent Similarity: 85.95% Conservative: 62
Best Local Similarity: 65.22% Mismatches: 42
Query Match: 68.60% Indels: 0
DB: 3 Gaps: 0

US-10-070-794A-4 (1-305) x US-09-272-796-14 (1-1435)

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Qy 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 20
Db 188 ATGCGATTCATGAGGTCCACACAGTGTATGACATCGTTCACACAGTTCACAGCTTGT 247
Qy 21 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 40
Db 248 GTCTTTGATACACTACATTTACAAGTTAAAAGCGCTTCCTTGGTTGGTAGCAACGGTGC 307
Qy 41 ArgAlaAlaProLeuTyrAspSerLysGlnSerPheValGlyMetLeuThrIleThr 60
Db 308 CGAGCAGCGGCACCTGTGGGAGAGTAAAAAAGTTTTGTAGGAATGCTTAACCAATTACA 367
Qy 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80
Db 368 GATTTCAATAATATACATAGATACATTAATAATCACCCTATGCTATGTCACAGATTATGAATTA 427
Qy 81 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100
Db 428 GAGGAACATATAAATGAAACATGAGGGAGCTTTATTTACAAAGAAACATTTAAGCCTTTA 487
Qy 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120
Db 488 GTGAATATATCTCCAGATGCAAGCCTCTTCGATCTGTATACTCTTGTATCAAAATAAA 547
Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140
Db 548 ATCCACAGATTGCCCCGTATTGACCTCATAGTGGGAATGCACCTTATATATCTTACCCAC 607
Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160
Db 608 AAAGAAATCTCAAGTCTCTCCAGCTTTTATGCTGATATGCTCAAGACCTTGCCTTCATG 667
Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 180
Db 668 AAGCAGAACCTGGATGAGCTTGGAAATAGGAACGTACCACCAATTCGCTTCATACATCCA 727
Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuPro 200
Db 728 GACACTCCCATCATCAAGCCTTGAACATATTTGTGGAAGACCAATATCAGCTCTGCCT 787
Qy 201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220
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Db 788 GTTGTGATGAGTCAGGAAAGTTGTAGATATTATTCCAAATTTGATGATTAATTAATCTT 847
Qy 221 AlalaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240
Db 848 GCTGCTGAGAAAACATCAATAACCTAGATATACCGTGCACCGCCCTTCAGCACCGT 907
Qy 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValle 260
Db 908 TCACAGTATTGTAAGGTGTTGTGAAGTGCATAAGCTGGAATTAAGTGCAGACCATCGTG 967
Qy 261 AspArgileAlaAqGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280
Db 968 GACAGATAGTAAGAGCTGAGCTCATCCGCTGCTGTGTGTGTAATGAAGCAGATAGTATT 1027
Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGly 299
Db 1028 GTGGGTATTATTCCCTGTGGGACATTCTGCAAGCCCTGATCCTCACACCAGCAGGT 1084
RESULT 8
US-09-949-016-2390
; Sequence 2390, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2390
; LENGTH: 1506
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2390
Alignment Scores:
Pred. No.: 1,11e-120 Length: 1506
Score: 1064.00 Matches: 195
Percent Similarity: 85.95% Conservative: 62
Best Local Similarity: 85.22% Mismatches: 42
Query Match: 68.60% Indels: 0
DB: 3 Gaps: 0
US-10-070-794A-4 (1-305) x US-09-949-016-2390 (1-1506)
Qy 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 20
Db 318 ATGGCAATTCAGAGTCACACAGTGTATGACATCGTTCCACAGTTCACAGCTTGT 377
Qy 21 IlePheAspThrMetGluIleLysLysAlaPheAlaLeuAlaAsnGlyVal 40
Db 378 GTCTTTGATACATACATCAAGTAAAGGCCCTTCTTTGTTGGTAGCCACCGGTGTC 437
Qy 41 ArgAlaAlaProLeuTyrAspSerLysGlnSerPheValGlyMetLeuThrIleThr 60
Db 438 CGAGCAGCCCATCTGTGGAGAGTAAACAAAGTTTGTAGGAATGCTAACCAATTACA 497
Qy 61 AspPheLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80
Db 498 GATTTCATAAATATACATACATAGTACTATAAATCACCTATGTTACAGATTATGAATTA 557
Qy 81 GluGlnHisLysIleGluThrTyrArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100
Db 558 GAGGAACATAAAATTTGAACATGAGGAGGAGCTTTATTTTACAGAAACATTTTAACGCTTTA 617

Qy 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120
Db 618 GTGAATATATCTCCAGATCAAGCCTCTTCGATGCTGTATACCTCTTGATCAAAATAAA 677
Qy 121 IleHisArgLeuProValLeuAspProValSerGlyValLeuHisLysLeuThrHis 140
Db 678 ATCCACAGATTGCGGTATTATGACCTATCAGTGGGAAATGCACCTTATATATACCTCCAC 737
Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160
Db 738 AAAAGAATCTCAAGTCTCCAGCTTTTATGCTGATATGCCAAAGCCTGCTTCATG 797
Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 180
Db 798 AAGCAGAACCTGGATGAGCTTGAATAGGAACCTACCAACATTTGCTTCATACATCCA 857
Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 200
Db 858 GACACTCCCATCATCAAGCCTTGAACATATTTGTGGAAGACGATATCAGCTCTGCT 917
Qy 201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220
Db 918 GTTGTGATGAGTCAGGAAAGTTGTAGATATTATTCCAAATTTGATGTAATTAATCTT 977
Qy 221 AlalaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240
Db 978 GCTGCTGAGAAAACATCAATAACCTAGATATCAGGTGACCCAGGCCCTTCAGCACCGT 1037
Qy 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValle 260
Db 1038 TCACAGTATTGTAAGGTGTTGTGAAGTGCATAAGCTGGAATTAAGTGCAGACCATCGTG 1097
Qy 261 AspArgileAlaAqGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280
Db 1098 GACAGATAGTAAGAGCTGAGTCCATCGCTGCTGTGTGTAATGAAGCAGATAGTATT 1157
Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGly 299
Db 1158 GTGGGTATTATTCCCTGTGGGACATTCTGCAAGCCCTGATCCTCACACCAGCAGGT 1214
RESULT 9
US-09-949-016-5010
; Sequence 5010, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5010
; LENGTH: 1500
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5010
Alignment Scores:
Pred. No.: 6.52e-114 Length: 1500
Score: 1009.00 Matches: 192
Percent Similarity: 82.99% Conservative: 52
Best Local Similarity: 65.31% Mismatches: 50
Query Match: 65.05% Indels: 0
DB: 3 Gaps: 0

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US-10-070-794A-4 (1-305) x US-09-949-016-5010 (1-1500)

Qy 3 PheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValIlePhe 22
Db 110 TTCATGAAGTCTCATCGTGTATGACCTGATCCCAAGCTCCAAATGGTTGTATT 169
Qy 23 AspThrMetLeuGluIleLysLeuAlaPheAlaLeuValAlaAsnGlyValArgAla 42
Db 170 GATACGTCCTCGAGGTGAGAAAGCTTTTTCCTTTGGTGACTAAACGGTGTACGAGCT 229
Qy 43 AlaProLeuTrpAspSerLysGlnSerPheValGlyMetLeuThrIleThrAspPhe 62
Db 230 GCCCTTTATGGGATAGTAAGACAAAGTTTGTGGCATGCTGACCATCACTGATTC 289
Qy 63 IleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGluGln 82
Db 290 ATCAATATCTCGACCGCTACTATAAATCAGCTTGTGTACAGATCTATGAGCTAGAAGAA 349
Qy 83 HisLeuValLeuThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeuValSer 102
Db 350 CACAAGATAGAAACTTGGAGAGAGGTGATCTCCAGGACTCTTTAAACCGCTTGTCTGC 409
Qy 103 IleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIleHis 122
Db 410 ATTTCTCTATGCCAGCTTGTGTGATGCTCTCTTCATTAATTCGGAACAAGATCCAC 469
Qy 123 ArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLysArg 142
Db 470 AGGCTGCCAGTATTATGCCAGAAATCAGCAATACTTTGTATCATCTCTCACCAAGCGC 529
Qy 143 LeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyrArg 162
Db 530 ATTTGGAAGTTCCTCAAAATGTTTATCATCTGAGTTCCTCCAGCCAGAGTTTCATGTCCAAG 589
Qy 163 ThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGluThrAla 182
Db 590 TCTCTGGAGAGCTACAGATTGGCACCTATGCCAATATGCTATGTTGGCATACCACC 649
Qy 183 ProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProValVal 202
Db 650 CCGCTCTATGTGGCTCTCGGGATTTTGTACAGCATCGAGTCTCAGCCCTGCCAGTGTGT 709
Qy 203 AsnGluCysGlyGlnValValClyLeuTyrSerArgPheAspValIleHisLeuAlaAla 222
Db 710 GATGAGAAGGGCGGTGTGGTGACATCTACTCCAAAGTTTGATGTTATCAATCTGGCAGCA 769
Qy 223 GlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThrLeu 242
Db 770 GAAAGAGCTTACAACAACCTAGATGATCTGTGACTAAAGCTTGAACATCGATCAGAT 829
Qy 243 CysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAspArg 262
Db 830 TACTTTGAGGTGTCTCAAGTCTACCTGATGATGAGACTCTGGAGACCATCATCAACAGG 889
Qy 263 IleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeuLeuGly 282
Db 890 CTAGTGGAGCAGAGGTTTCAACGACTTGTAGTGGTGGATGAAATGATGTGTCTCAAGGGA 949
Qy 283 ValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSer 296
Db 950 ATTGTATCATGTCTGACATCTCTGAGGCCCTTGGTGTCTCACA 991

RESULT 10
US-09-016-434-1113
; Sequence 1113, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1578 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1335855
; US-09-016-434-1113

Alignment Scores:
Pred. No.: 7,07e-114 Length: 1578
Score: 1009.00 Matches: 192
Percent Similarity: 82.99% Conservative: 52
Best Local Similarity: 65.31% Mismatches: 50
Query Match: 65.05% Indels: 0
DB: 3 Gaps: 0

US-10-070-794A-4 (1-305) x US-09-016-434-1113 (1-1578)

Qy 3 PheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValIlePhe 22
Db 188 TTCATGAAGTCTCATCGTGTATGACCTGATCCCAAGCTCCAAATGGTTGTATT 247
Qy 23 AspThrMetLeuGluIleLysLysLeuAlaPheAlaLeuValAlaAsnGlyValArgAla 42
Db 248 GATACGTCCTCGAGGTGAAGAAAGCTTTTTCCTTTGGTGACTAAACGGTGTACGAGCT 307
Qy 43 AlaProLeuTrpAspSerLysGlnSerPheValGlyMetLeuThrIleThrAspPhe 62
Db 308 GCCCTTTATGGGATAGTAAGAAAGTTTTCCTTTGGGCATGCTGACCATCACTGATTC 367
Qy 63 IleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGluGln 82
Db 368 ATCAATATCTCGACCGCTACTATAAATCAGCTTGTGTACAGATCTATGAGCTAGAAGAA 427
Qy 83 HisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeuValSer 102
Db 428 CACAAGATAGAAACTTGGAGAGAGGTGTATCTCCAGGACTCTCTTTAAACCGCTTGTCTGC 487
Qy 103 IleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIleHis 122
Db 488 ATTTCTCTAATGCCAGCTTGTGTGATGCTCTCTTCATTAATTCGGAACAAGATCCAC 547
Qy 123 ArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLysArg 142
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Db 548 AGGCTGCAGATTATGACCCAGAAATCAGGCAATATCTTTGTACATCTCCACCCCAAGCGC 607
Qy 143 LeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyrArg 162
Db 608 ATTCTGAAGTCTCTCAAAATGTTTATCACTGAGTTCCTCCCAAGCCAGAGTTTCATGTCACG 667
Qy 163 ThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGluThrAla 182
Db 668 TCTCTGGAAGAGCTACAGATTGCGACCTATGCAATATGTTGATGTTGCGACCTACCAAGC 727
Qy 183 ProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProValVal 202
Db 728 CCCGCTATGCTGCTGCGGATTTTGTACAGATCGAGTCTCAGCCCTGCGCAGTGGTG 787
Qy 203 AsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeuAlaAla 222
Db 788 GATGAGAAGGGCGTGTGGTGGACATCTACTCCCAAGTTTGTATGTTATCAATCTGGCAGCA 847
Qy 223 GlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThrLeu 242
Db 848 GAAAGACCTACACCAACCTAGATGATCTGTGACTAAAGCCTTGCAACATCGATCATCAT 907
Qy 243 CysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAspArg 262
Db 908 TACTTTGAGGGTGTCTCAAGTGTCTACCTGCATGAGACTCTGGAGACCATCATCAACAGG 967
Qy 263 IleAlaArgGlnValHisArgLeuValValLeuValAspGluThrGlnHisLeuLeuGly 282
Db 968 CTAGTGAAGCAGAGTTTCCCGACTTGTAGTGTGTGATGAAATGATGTGTGTCAGGGA 1027
Qy 283 ValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSer 296
Db 1028 ATTGTATCACTGTCTGACATCTCTGACGCGCTGCGGCGCTGCTGCTCACA 1069

RESULT 11

US-09-101-146-63
; Sequence 63, Application US/09101146
; Patent No. 6124125
; GENERAL INFORMATION:
; APPLICANT: Dartmouth College, St. Vincent's Institute of
; APPLICANT: Medical Research, Kemp et al.
; TITLE OF INVENTION: No. 6124125el AMP Activated Protein Kinase
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESS: Jane Massey Licata, Esq.
; STREET: 66 E. Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PC
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.0 FOR WINDOWS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/101.146
; FILING DATE: October 7, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PN7450
; FILING DATE: 8 JAN 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: DC-0050
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (856) 810-1515
; TELEFAX: (856) 810-1454
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1576
; TYPE: Nucleic acid

; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: NO
US-09-101-146-63
Alignment Scores:
Pred. No.: 3,87e-113 Length: 1576
Score: 1003.00 Matches: 191
Percent Similarity: 82.65% Conservative: 52
Best Local Similarity: 64.97% Mismatches: 51
Query Match: 64.67% Indels: 0
DB: 3 Gaps: 0
US-10-070-794A-4 (1-305) x US-09-101-146-63 (1-1576)
Qy 3 PheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValIlePhe 22
Db 187 TTCTGAGTCTCATGCTGCTATGACCTGATCCCAAGTCCCAATTTGGTTGTATT 246
Qy 23 AspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyValArgAla 42
Db 247 GATACGTCCCTGCGAGGTGAAGAAAGCTTTTGTGTTGTTGCTGACTAACGGTGTACGAGCT 306
Qy 43 AlaProLeuThrAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAspPhe 62
Db 307 GCCCCTTTATGGATAGTAAGAAGCAAAAGTTTGTGGGCATGCTGACCATCCTGATTTTC 366
Qy 63 IleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIleGluGln 82
Db 367 ATCAATATCTCGCACCGCTACTATAATACGCTTGTGATGATGATGATGATGATGATGATG 426
Qy 83 HisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeuValSer 102
Db 427 CACAAGATAGAACTTGGAGAGAGGTGTATCTCCAGGACTCTTTAAACCGCTTGTCTGC 486
Qy 103 IleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArgIleHis 122
Db 487 ATTTCTCTAAATGCCAGCTTGTGTGATGCTGCTCTCTTCAATTAATTCGCAACAGATCCAC 546
Qy 123 ArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHisLysArg 142
Db 547 AGCTGCCAGTTATGACCCAGAAATCAGGCAATACTTTGTACATCTCTCCACCCCAAGCGC 606
Qy 143 LeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyrArg 162
Db 607 ATTCTGAAGTCTCTCAAAATGTTTATCACTGAGTTCCTCCCAAGCCAGAGTTTCATGTCACG 666
Qy 163 ThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGluThrAla 182
Db 667 TCTCTGGAAGAGCTACAGATTGCGACCTATGCCAATATTTGCTATGTTGCTGCTGCTGCTG 726
Qy 183 ProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuProValVal 202
Db 727 CCCGCTATGCTGCTCTGCGGATTTTGTACAGATCGAGTCTCAGCCCTGCGCAGTGGTG 786
Qy 203 AsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeuAlaAla 222
Db 787 GATGAGAAGGGCGTGTGGTGGACATCTACTCCCAAGTTTGTATGTTATCAATCTGGCAGCA 846
Qy 223 GlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArgThrLeu 242
Db 847 GAAAGACCTACACCAACCTAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 906
Qy 243 CysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIleAspArg 262
Db 907 TACTTTGAGGGTGTCTCAAGTGTCTACCTGCTGAGACTCTGGAGACCATCATCAACAGG 966
Qy 263 IleAlaArgGlnValHisArgLeuValValLeuValAspGluThrGlnHisLeuLeuGly 282
Db 967 CTAGTGAAGCAGAGTTTCCCGACTTGTAGTGTGTGATGATGATGATGATGATGATGATGATG 1026
Qy 283 ValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSer 296
Db 1028 ATTGTATCACTGTCTGACATCTCTGACGCGCTGCGGCGCTGCTGCTCACA 1069

Db 1027 ATTGTATCACTGTCTGACATCCTGCAGGCCCTGGTGCTCACA 1068

RESULT 12

US-09-949-016-16752
 ; Sequence 16752, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 16752
 ; LENGTH: 20347
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-949-016-16752

Alignment Scores:
 Pred. No.: 4.89e-46 Length: 20347
 Score: 472.50 Matches: 197
 Percent Similarity: 25.49% Conservative: 50
 Best Local Similarity: 20.33% Mismatches: 47
 Query Match: 30.46% Indels: 680
 DB: 3 Gaps: 11

US-10-070-794A-4 (1-305) x US-09-949-016-16752 (1-20347)

Qy 3 PheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValIlePhe 22
 Db 14940 TTTCAAGTCTCATCGTGTGATGACCTGATCCCAAGCTCCAAATGGTGATTT 14999
 Qy 23 AspThr 24
 Db 15000 GATACGTCCTGCAGGTGGGTGAATCTCTTTTCCCTTCCCTTTGGAGCCTGTGGTT 15059
 Qy 24 24
 Db 15060 TAATACCTCTCATCTCATCTCAAGGGTAATATCTTATCTTCTGTGAAGTAGT 15119
 Qy 24 24
 Db 15120 CTCATGTTTATCCCAACATGCCAAACACTGTCTTTTTTACAGTCTGCCCTGTGGA 15179
 Qy 25 Met-LeuGluIleLysLysAlaPhePheAlaLeuVa 36
 Db 15180 TTTGCTTTATGATTATTAATGCTGTGGTACAGGTGAAGAGCTTTTTTGTGTTGGT 15239
 Qy 36 lalaAsnGlyValArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheVal- 54
 Db 15240 GACTAACGGTGTACGAGCTGCCCTTTATGGATAGTAAGAAGCAAGTTTGTGGGTAA 15299
 Qy 54 54
 Db 15300 GCMAAAGTTTCTGGAACAATATTATTGGCATCTGTGCTGGGCGAGGAGACAGCTTC 15359
 Qy 55 GlyMetLeuThrIleThrAspPheIleL 64
 Db 15360 AGGAGTGTCTGAGGCTCTGCTTCTCTAGGCATGCTGACCATCACTGATTCATCA 15419
 Qy 64 euValLeuHisArgTyrTyrArgSerProLeu- 74
 Db 15420 ATATCTGCACCGCTACTATAAATCAGC-CTTGGTAAGGAACCTTAAACCAATGACCAA 15478

Qy 74 74
 Db 15479 ATCATTTCCTGCCCTAAATCCTCATTTCTTCAATTTCTTTTCTCCNAGCAAGCCAGAG 15538
 Qy 75 ValGlnI 77
 Db 15539 GGCTTAAGGAAGCAGAGAGATCAGGTCTCAAAATTCGTGTCTTCTGCTTTCAGGTACAGA 15598
 Qy 77 leTyrGluIleGluGlnHisLysIleGluThrTrpArg- 89
 Db 15599 TCTATGAGCTAGAAGAACAACAGATAGAAAATTGGAG-AGGTATGTAGAGAAATTTGGGTT 15657
 Qy 89 89
 Db 15658 ATAAAGGATAAAGGATGGCGGTTTCTGGGAACACTTTTCCATGGTGGTATTTTGTG 15717
 Qy 90 GluIleTyrLeuGlnGlyCysPheLysProValSerI 103
 Db 15718 ACCATCCCTTTTCCCTTCAGAGGTGTATCTCCAGGACTCTTTAAACCCGTTGTCTGCA 15777
 Qy 103 leSerProAsn- 106
 Db 15778 TTTCTCTAATGCCAGGTGAGTTCCAGTTACCCATCTGTCCAAAAAGCGAAGAGATTTT 15837
 Qy 106 106
 Db 15838 GTCATCAGCCTAGCTAATGCCCTAGACACCAGGAAGGGGAAGAGAGAGAAAGACA 15897
 Qy 106 106
 Db 15898 CAC 15957
 Qy 106 106
 Db 15958 CTCATTCTCACT 16017
 Qy 106 106
 Db 16018 CTTCCCTAACATCAGTTTCCCTGTGTGAGCAATACACTGTATGGACTGTTTAAATCAC 16077
 Qy 107 AspSerLeuPheGluIleVal 113
 Db 16078 CCCAGCCCCAGCAGTGTGGAATTTATTATCTCCACCTCTCACAGCTTGTGTGATGCTG 16137
 Qy 113 alTyrThrLeuIleLysAsnArgIleHisArgLeuProValLeuAspProValSerGlyA 133
 Db 16138 TCTCTTCAATTCGGAACAAGATCCACAGGCTGCCAGTTCAGCTTATTGACCCAGATCAGGCA 16197
 Qy 133 snValLeuHisIleLeuThrHisLysArgLeuLeuLysPheLeuHisIlePhe- 150
 Db 16198 ATACTTTGTACATCTCACCCCAAGCGCATTCCTGAAGTTCCTCAAAATTTGTTGTAAGTG 16257
 Qy 150 150
 Db 16258 CTCCTCAGCCCGAGTCTCTTTTCTCTTTTCTCTTTTCTCTTTTCTCTTTTCTCTTTTCT 16317
 Qy 150 150
 Db 16318 GAGAGACGAGGTCTCACTGTGTGCTCAGGCTAGTGTCAAACTCCTGAGCTCAAGTGATC 16377
 Qy 150 150
 Db 16378 CTCCGGCTCAGCCTCCCAAGTGTAGGATTACAGGTGTGAGCCACTGCATCCAGCCCC 16437
 Qy 150 150
 Db 16438 ACTTCTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 16497
 Qy 150 150
 Db 16498 CGTGACAGGCGCTATCATGCTCAGTCCAGCTCCAAACCTCTTGGTCTCAGGTGACCCC 16557
 Qy 150 150

Db 16558 CGACCTCAACCCCGAGAGAGCTGGGACTACACGTGTGTATCCACACACCTGGCTAATTT 16617
Qy 150 ----- 150
Db 16618 TTTGGTATTTTATAGAGATAGGTTTTCATGTTGTCCTGAGCTGCTGAGCTCCT 16677
Qy 150 ----- 150
Db 16678 GGGCTCAAGCAATATGTCCTCCCTCAGCTCCCAAGTGTGGGATTATAGGCATAAGCCG 16737
Qy 150 ----- 150
Db 16738 GCGCACCCAGCCCTTATTTCTAATATATCTGGTGTGGAGGGGGTATCCAAAGGTGGCTTTG 16797
Qy 151 -----GlySerLeuLeu-----ProArgPro 158
Db 16798 GGTGCTTGAAGTTAAGCTGATGTTCTTCTCAGTCACTGAGTTCCCAAG-CCAG 16856
Qy 158 erPheLeuTyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValV 178
Db 16857 AGTTTCATGTCAGCTCTCTGGAAGAGCTACAGATTGGCACCCTATGCCAATATTGCTATGG 16916
Qy 178 alLeuGluThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerA 198
Db 16917 TTGCACCTACACCCCGTCTATGTGGCTCTGGGGATTTTTGTACAGCATCGAGTCTCAG 16976
Qy 198 laLeuProValValAsnGluCys----- 205
Db 16977 CCCTGCCAGTGTGGATGAGAA-GGGTGAGAGATTGGGCAGAGGAGGAGGGAAGAT 17035
Qy 205 ----- 205
Db 17036 CCAGGCAAGTCAGGGTGGCTCTGGGAAGATCTGCTTTTCCCTCAGCTTAGCCAGAGGGT 17095
Qy 205 ----- 205
Db 17096 GATTCTATGATAGGGGGAGCTTTAGATCCAGATCCTCTTACTGAGCTGCCTGTGTCC 17155
Qy 206 ----GlyGlnValValGlyLeuTyrSerPheAspValIle----- 218
Db 17156 CCCTAGGGCGTGTGGTGCACATCTACTCCAAGTTTGATTTGATTCGTGAGTGATGTGGAG 17215
Qy 218 ----- 218
Db 17216 GGTCTGGAGGTAGGGAAGTGGTGGGGGGGGGCACTGTTAAATATGCGAGAGGAGAAG 17275
Qy 218 ----- 218
Db 17276 GAGTCTCTCTGTGATCTAAGGGTCTTAGAAGCTTCCAGGCTTCCAAATCTATTGAAA 17335
Qy 218 ----- 218
Db 17336 AGGAATTGATGATGGTGTGGCTGTGGCTGACAAATTGCCCTGAATCCCTCTGTGA 17395
Qy 218 ----- 218
Db 17396 GGTGGATGGTTTCAGGGTTTGGAGGTGGCTCTCTTGTCTTCCCTGCAAGCTCCTTCTC 17455
Qy 219 -----HisLeuAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyC 235
Db 17456 TGTCTCCCAAGATCTGGCAGCAGAAAGACCTACACACCTAGATGTATCTGTGACTA 17515
Qy 235 luAlaLeuArgGlnArgThrLeuCysLeuGlyValLeuSerCysGlnProHisGluS 255
Db 17516 AAGCTTGGCAACATCATGATACATTTCTTGGGTGTCTCAAGTGTCTACCTGCATGAGA 17575
Qy 255 erLeuGlyGluValIleAspArgIleAla-----ArgGlu----- 266
Db 17576 CTCTGGAGACCATCATCAACAGGCTAGT-GGAAGCAGAGGTAGGGAGCCAGCAACCCCTA 17634
Qy 266 ----- 266

Db 17635 AAGGAGCTGAGGGGAGCAGCGCTTGTGAGAGTGGGGTTTGGCAAGAGAGATAGGGGCGAGAGGG 17694
Qy 267 -----GlnValH 269
Db 17695 GCTTCCCTCAGGCGCAGCACTAAACATTTCCCTTTCCTCCCTTGTGCTCTGTGCCAGGTTT 17754
Qy 269 isArgLeuValLeuValAspGluThrGlnHisLeuLeuGlyValValSerLeuSerAspI 289
Db 17755 ACCGACTTGTAGTGGTGGATGAATAATGATGTGGTCAAGGGAATTGTATCATCTGCTGACA 17814
Qy 289 leLeuGlnAlaLeuValLeuSer 296
Db 17815 TCTTGCAGGCCCTGGTGTCTCA 17837
RESULT 13
US-09-513-999C-1659
; Sequence 1659, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCES: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 1659
; LENGTH: 350
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 48..350
US-09-513-999C-1659
Alignment Scores:
Pred. No.: 3,94e-28 Length: 350
Score: 304.00 Matches: 56
Percent Similarity: 90.00% Conservative: 7
Best Local Similarity: 80.00% Mismatches: 7
Query Match: 19.60% Indels: 0
DB: 3 Gaps: 0
US-10-070-794A-4 (1-305) x US-09-513-999C-1659 (1-350)
Qy 3 PheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValIlePhe 22
Db 141 TTCATGAAGTCTCATCGTGTCTATGACCTGATCCCAAGCTCCAAATTTGGTTGATTT 200
Qy 23 AspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyValArgAla 42
Db 201 GATACGTCCTCGCAGGTGAAGAAGCTTTTGTCTTGGTACTAACCGGTGACGAGCT 260
Qy 43 AlaProLeuThrAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAspPhe 62
Db 261 GCCCTTTTATGGGATAGTAAGAACAAAGTTTGTGGGCATGCTGACCATCAGTATTC 320
Qy 63 IleLeuValLeuHisArgTyrTyrArgSer 72
Db 321 ATCAATATCTCGCCCGCTACTATAATCA 350
RESULT 14
US-09-248-796A-4769
; Sequence 4769, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA, ALBICAN

; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 4769
; LENGTH: 762
; TYPE: DNA
; ORGANISM: Candida albicans
; US-09-248-796A-4769

Alignment Scores:
Pred. No.: 3,02e-21 Length: 762
Score: 252.50 Matches: 62
Percent Similarity: 50.91% Conservative: 50
Best Local Similarity: 28.18% Mismatches: 73
Query Match: 16.28% Indels: 35
DB: 3 Gaps: 6

US-10-070-794A-4 (1-305) x US-09-248-796A-4769 (1-762)

Qy 3 PheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuValIlePhe 22
Db 115 TTTTACAAACAAACATCTTACGATGCTCTACCTGTGATATATAGATTAAATTTTG 174
Qy 23 AspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAenGlyValArgAla 42
Db 175 GATACTTCATTTAGTGAAGAAAGTCATTAATATTTTATTACAAATAATATAGTTTCA 234
Qy 43 AlaProLeuTyrAspSerLysLysGlnSerPheValGlyMetLeuThrIleThrAspPhe 62
Db 235 GCACCGTTATGATACCAACATCCAGATTCGCTGATGTTTAAATCATCATCGGATTT 294
Qy 63 IleLeuValLeuHisArgTyrTyrArgSerPro-----HisLysIleGluThrTrp 73
Db 295 ATCAATGTGATACATACATCTTCAATTCACAAATTCAGAAAGTTTGAAGTATGATCAACTA 354
Qy 74 ---LeuValGlnIleTyrGluIleGluGln-----HisLysIleGluThrTrp 88
Db 355 ACATTGGGTGATTAAGAGAATTAAGAAAGCCATAGCTGATGATCAATCGAACA--- 411
Qy 89 ArgGluIleTyrLeuGlnGlyCysPheLysProLeuValSerIleSerProAsnAspSer 108
Db 412 -----GCATCAATACACCCATTCAGATCA 435
Qy 109 LeuPheGluAlaValTyrThrLeuIleLysAsnArgIleHisArgLeuProValLeuAsp 128
Db 436 TTATATGAAGCATGTGTCAAGATGTTGGAATCAAAAGCTAGAAAGTATCCCATTAATGAT 495
Qy 129 ProValSerGlyAsn-----ValLeuHisIleLeuThrHisLysArgLeuLeu 144
Db 496 GAAGATGAAACAACTAAACGTAATGTCGTAGTGTGTTAACTCAATACAGAAATTTG 555
Qy 145 LysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeuTyrArgThrIle 164
Db 556 AAATTTGGCTTTG-----AATGTAAAGAAACGAAATGTTATTGAACCCCTC 606
Qy 165 GlnAspLeu---GlyIleGlyThrPheArgAspLeuAlaValLeuGluThrAlaPro 183
Db 607 AAGATTTTGGTGGGTGGGTGATGTGAAAGAAAGTTGCTTACATGTACTATGGACACACT 666
Qy 184 IleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuProValValAsn 203
Db 667 GTCATAGAGATCAATTTAATTAATGAGAAATTCGTCTCTTCAATACCAATATGTCAC 726

RESULT 15
US-09-016-434-194
; Sequence 194, Application US/09016434
; Patent No. 6500938

; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 194:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PENITUT01
; CLONE: 1452972
; US-09-016-434-194

Alignment Scores:
Pred. No.: 1.96e-20 Length: 269
Score: 240.00 Matches: 47
Percent Similarity: 77.27% Conservative: 21
Best Local Similarity: 53.41% Mismatches: 20
Query Match: 15.47% Indels: 0
DB: 3 Gaps: 0

US-10-070-794A-4 (1-305) x US-09-016-434-194 (1-269)
Qy 176 AlaValValLeuGluThrAlaProIleLeuThrAlaLeuAspIlePheValAspArg 195
Db 1 GCCTTCATACATCAGACACTCCCATCATCAAGCCITGACATATTTTGGAAAGACGA 60
Qy 196 ValSerAlaLeuProValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPhe 215
Db 61 ATATCAGCTCTGCTGTTGTCATGAGTCAGCAAGAAAGTTGTAGATATTTATTCCTCAATTT 120
Qy 216 AspValIleHisLeuAlaAlaGlnGlnThrTyrHisLeuAspMetSerValGlyGlu 235
Db 121 GATGTAATTAATCTTGTCTGTCGAGAAACATACATAACCTAGATATCCTCGTGACCCAG 180
Qy 236 AlaLeuArgGlnArgThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSer 255
Db 181 GCCCTTCAGCACCCTTCACAGTATTTTGAAGTGTGTGGAAGTGCATTAAGTGCAGAAATA 240
Qy 256 LeuGlyGluValIleAspArgIle 263
Db 241 CTGGAGACCATCGTGGACAGAATA 264

Search completed: January 26, 2006, 03:32:42
Job time : 178.061 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 26, 2006, 01:18:45 ; Search time 656.008 Seconds
(without alignments)
3844.711 Million cell updates/sec

Title: US-10-070-794A-4

Perfect score: 1551

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Ygapop 10.0	Ygapext 0.5	
Egapop 6.0	Egapext 7.0	
Delop 6.0	Delext 7.0	

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-Q=/cgn2_1/USPTO.spool.p/US10070794/runat 24012006.164417.8900/app_query.fasta_1.1102
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-MATRIX=blosom62 -TRANS=human40.cdi -LIST=45 -MODE=LOCAL -OUTFMT=ptc -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USERS=US10070794.CCGN 1.1 2064 @runat 24012006.164417.8900 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=10 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELEX=6 -DELEXT=7

Database :

Published Applications NA Main:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1551	100.0	1470	9	US-10-503-175-1
2	1551	100.0	1647	3	US-09-826-581-5
3	1551	100.0	1647	7	US-10-705-137-5
4	1551	100.0	2781	7	US-10-473-670-30
5	1525	98.3	2290	9	US-10-756-149-1235
6	1507	97.2	1873	3	US-09-950-022-1
7	1507	97.2	1873	3	US-09-950-022-3

8	1507	97.2	1873	3	US-09-950-022-5	Sequence 5, Appli
9	1507	97.2	1873	10	US-11-075-134-1	Sequence 1, Appli
10	1507	97.2	1873	10	US-11-075-134-3	Sequence 3, Appli
11	1507	97.2	1873	10	US-11-075-134-5	Sequence 5, Appli
12	1506	97.1	1873	3	US-09-950-022-7	Sequence 7, Appli
13	1506	97.1	1873	10	US-11-075-134-7	Sequence 7, Appli
14	1503	96.9	1873	3	US-09-950-022-9	Sequence 9, Appli
15	1503	96.9	1873	10	US-11-075-134-9	Sequence 9, Appli
16	1479	95.4	1518	9	US-10-503-175-3	Sequence 3, Appli
17	1064	68.6	1167	9	US-10-466-162-11	Sequence 11, Appli
18	1064	68.6	1435	3	US-09-769-970-14	Sequence 14, Appli
19	1064	68.6	2223	3	US-10-466-162-13	Sequence 13, Appli
20	1009	65.1	1578	6	US-10-305-720-1113	Sequence 1113, Ap
21	1009	65.1	1578	9	US-10-505-680-407	Sequence 407, App
22	1009	65.1	1578	9	US-10-466-162-15	Sequence 15, Appli
23	1009	65.1	1691	3	US-09-925-297-2	Sequence 2, Appli
24	862.5	55.6	1467	9	US-10-450-763-20069	Sequence 20069, A
25	851.5	54.9	3261	10	US-11-097-143-25526	Sequence 25526, A
26	758	48.9	547	7	US-10-276-774-261	Sequence 261, App
27	747.5	48.2	11527	5	US-10-108-605-70	Sequence 70, Appli
28	747.5	48.2	39651	10	US-11-097-143-25525	Sequence 25525, A
29	687	44.3	2303	9	US-10-450-763-20071	Sequence 20071, A
30	640.5	41.3	1722	3	US-09-826-581-3	Sequence 3, Appli
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32	621	40.0	9100	9	US-10-503-175-5	Sequence 5, Appli
33	621	40.0	26000	9	US-10-503-039-1	Sequence 1, Appli
34	501	32.3	602	5	US-10-106-698-2295	Sequence 2295, Ap
35	408	26.3	765	6	US-10-264-237-248	Sequence 248, App
36	357	23.0	1533	7	US-10-425-114-8857	Sequence 8857, Ap
37	357	23.0	2339	8	US-10-425-115-2938	Sequence 2938, Ap
38	352.5	22.7	1507	7	US-10-425-114-29527	Sequence 29527, A
39	352.5	22.7	3077	7	US-10-424-599-44858	Sequence 44858, A
40	352	22.7	1014	3	US-09-826-581-4	Sequence 4, Appli
41	352	22.7	1014	7	US-10-705-137-4	Sequence 33827, A
42	350.5	22.6	1387	7	US-10-425-114-33827	Sequence 33827, A
43	348	22.4	2315	7	US-10-424-599-79689	Sequence 79689, A
44	347.5	22.4	1844	7	US-10-425-114-1948	Sequence 1948, Ap
45	347.5	22.4	2416	8	US-10-425-115-90096	Sequence 90096, A

ALIGNMENTS

RESULT 1
US-10-503-175-1
; Sequence 1, Application US/10503175
; Publication No. US20050172348A1
; GENERAL INFORMATION:
; APPLICANT: Andersson, Leif
; APPLICANT: Marklund, Stefan
; TITLE OF INVENTION: Transgenic animals expressing prkag3
; FILE REFERENCE: 11145-020U51
; CURRENT APPLICATION NUMBER: US/10/503,175
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: PCT/IB03/00912
; PRIOR FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 60/353,430
; PRIOR FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1470
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1470)
; OTHER INFORMATION:
US-10-503-175-1

Alignment Scores:
Pred. No.: 5.59e-192 Length: 1470
Score: 1551.00 Matches: 305
Percent Similarity: 100.00% Conservative: 0

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Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-070-794A-4 (1-305) x US-10-503-175-1 (1-1470)

Qy 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 20
Db 553 ATGGCTTCATGCGAGGAGCACACCTGCTAGCATGCCATGCGCACTAGCTCCAAGCTAGTC 612
Qy 21 IlePheAspThrMetLeuGluIleLysLysValAlaPheAlaLeuValAlaAsnGlyVal 40
Db 613 ATCTTCGACACCATGCTGGAGATCAAGAGCCCTCTTTGCTCTGGTGGCCAAACGGTGTG 672
Qy 41 ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 60
Db 673 CGGCGACGCCCTCTATGGGACAGCAAGAGCAGAGCTTTGTGGGATGCTGACCATCACT 732
Qy 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80
Db 733 GACTTCATCTCTGCTGCTGCTACTACAGGTCTTGAAGCTGTCTACACCCCTCATCAAGACCGG 792
Qy 81 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100
Db 793 GAACACATAGATTGAGACCTGGAGGAGATCTACTGCGAGGCTGCTTCAAGCCTCTG 852
Qy 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120
Db 853 GTCTCCATCTCTCTAATGATGAGCTGTGTTGAAGCTGTCTACACCCCTCATCAAGACCGG 912
Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140
Db 913 ATCCATCGCCTGCGCTGCTTCTTGACCGGTGTCAGGCAACGTACTCCACATCTCCACAC 972
Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160
Db 973 AAACGCTTGCTCAAGTTCCTGCACATCTTTGGTTCCTGCTGCCCGGCCCTCTCTCTC 1032
Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 180
Db 1033 TACCGCATATCAAGATTTCGGCATCGGCACATTCGAGACTTGGCTGTGGTGTGGAG 1092
Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuPro 200
Db 1093 ACAGCACCATCTCTGACTGCACTGACATCTTTGTGGACCGGCGTGTGCTGCACTGCT 1152
Qy 201 ValValAsnGluCysGlyValValGlyValLeuTyrSerArgPheAspValIleHisLeu 220
Db 1153 GTGGTCAACGAATGTGGTCAGGTGTTGGGCTCTATTCGCCCTTTGATGTGATTCACCTG 1212
Qy 221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240
Db 1213 GCTGCCAGCAAACTTACACCATCGACATGAGTGTGGGAGAAGCCCTGAGGCAGAGG 1272
Qy 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGlySerLeuGlyGluValIle 260
Db 1273 ACATATGTCTGGAGGAGTCTCTTTCCTGCCAGCCCCACGAGCTTGGGGGAAGTGTATC 1332
Qy 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280
Db 1333 GACAGGATTGCTCGGAGCAGGATACAGGCTGGTGTGTAGTGGAGCAGACCCAGCATCTC 1392
Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300
Db 1393 TTGGCGGTGGTCTCCCTCTCCGACATCTTCCAGGCACCTGCTCAGGCCTGCTGCGCATC 1452
Qy 301 AspAlaLeuGlyAla 305
Db 1453 GATGCCCTCGGGGCC 1467
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RESULT 2

US-09-826-581-5

; Sequence 5, Application US/09826581

```
Patent No. US20020142310A1
GENERAL INFORMATION:
APPLICANT: Andersson, Leif
APPLICANT: Luthman, L. Holger
APPLICANT: Marklund, Stefan
TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNIT
FILE REFERENCE: 11145-007001
CURRENT APPLICATION NUMBER: US/09/826,581
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: US 60/195,665
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 1647
TYPE: DNA
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: CDS
LOCATION: (20)...(1486)
US-09-826-581-5
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Alignment Scores:
Pred. No.: 6,77e-192 Length: 1647
Score: 1551.00 Matches: 305
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
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US-10-070-794A-4 (1-305) x US-09-826-581-5 (1-1647)

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Qy 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 20
Db 572 ATGGCTTCATGCGAGGAGCACACCTGCTAGCATGCCATGCGCACTAGCTCCAAGCTAGTC 631
Qy 21 IlePheAspThrMetLeuGluIleLysLysValAlaPheAlaLeuValAlaAsnGlyVal 40
Db 632 ATCTTCGACACCATGCTGGAGATCAAGAGCCCTCTTTGCTCTGGTGGCCAAACGGTGTG 691
Qy 41 ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 60
Db 692 CGGCGACGCCCTCTATGGGACAGCAAGACGAGCTTTGTGGGATGCTGACCATCACT 751
Qy 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80
Db 752 GACTTCATCTCTGCTGCTGCTGCTACTACAGGTCTCCCTCTGGTCCAGATCTATGAGATT 811
Qy 81 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100
Db 812 GAACACATAGATTGAGACCTGGAGGAGATCTACTGCGAAGCTGCTTCAAGCCTCTG 871
Qy 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120
Db 872 GTCTCCATCTCTCTAATGATAGCTGTGTTGAAGCTGTCTACACCCCTCATCAAGACCGG 931
Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140
Db 932 ATCCATCGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 991
Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160
Db 992 AAACGCTTGCTCAAGTTCCTGACATCTTTGGTTCCTGCTGCTGCTGCTGCTGCTGCTGCT 1051
Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 180
Db 1052 TACCGCATATCAAGATTTCGGCATCGGCACATTCGAGACTTGGCTGTGGTGTGGAG 1111
Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuPro 200
Db 1112 ACAGCACCATCTCTGACTGCACTGACATCTTTTGGAGCCGCGTGTGCTGCACTGCTCT 1171
Qy 201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220
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Db 1172 GTGTCAACGAATGTGTGAGTCTTATTCCTGCTTGTATGATTCACCTG 1231
 Qy 221 AlaAlaGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240
 Db 1232 GCTGCCAGCAACCTACACCACTGACATGATGCTGGAGAGCCCTGAGGAGAGG 1291
 Qy 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValIle 260
 Db 1292 ACACTATGTCTGGAGGAGTCTTTTCTGCGAGCCCAACAGAGCTTGGGGGAGTGCATC 1351
 Qy 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280
 Db 1352 GACAGGATGCTCGGAGCAGGTACACAGGCTGTGTGTAGTGAGCAGAGCCCAAGCACTC 1411
 Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300
 Db 1412 TTGGCGGTGTCTCCCTCTCCGACATCTTCAGGCACTGTGTCTCAGCCCTGTCTGGCATC 1471
 Qy 301 AspAlaLeuGlyAla 305
 Db 1472 GATGCCCTCGGGCC 1486

RESULT 3

US-10-705-137-5
 ; Sequence 5, Application US/10705137
 ; Publication No. US20040121385A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, Leif
 ; APPLICANT: Luthman, L. Holger
 ; APPLICANT: Marklund, Stefan
 ; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNIT
 ; FILE REFERENCE: 11145-007002
 ; CURRENT APPLICATION NUMBER: US/10/705.137
 ; CURRENT FILING DATE: 2003-11-10
 ; PRIOR APPLICATION NUMBER: US 09/826,581
 ; PRIOR FILING DATE: 2001-04-05
 ; PRIOR APPLICATION NUMBER: US 60/195,665
 ; PRIOR FILING DATE: 2000-04-07
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: FAST-SEQ for Windows Version 4.0
 ; SEQ ID NO 5
 ; LENGTH: 1647
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (20)...(1486)
 US-10-705-137-5

Alignment Scores:
 Pred. No.: 6.77e-192 Length: 1647
 Score: 1551.00 Matches: 305
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 7 Gaps: 0

US-10-070-794A-4 (1-305) x US-10-705-137-5 (1-1647)

Qy 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 20
 Db 572 ATGGCTTTCATGCGAGGACACACCTGTACGATGCCAATGCACTAGTCCAAAGTAGTC 631
 Qy 21 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 40
 Db 632 ATCTTGACACCACTGCTGGAGATCAAGAGGCTTCTTCTCTGTGGTGGCCCAAGCTGTG 691
 Qy 41 ArgAlaAlaProLeuTyrAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 60
 Db 692 CGGGCAGCCCTCTATGGGACAGCAGACAGCTTTGTGGGATGCTGACATCACT 751
 Qy 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80

Db 752 GACTTCATCTCTGTGTGTCATCGCTACTACAGTCCCTCCCTGTCAGATCTATGAGATT 811
 Qy 81 GluGlnHisLysIleGluThrTyrAlaGluIleTyrLeuGlnGlyCysPheLysProLeu 100
 Db 812 GAACAACATAGATTGAGACCTGGAGGAGATCTACTGCAAGGCTGCTTCAGACCTCTG 871
 Qy 101 ValSerIleSerProLeuAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120
 Db 872 GTCTCCATCTCTCTAATGATAGCTGTTTGAAGCTGTCTACACCTCTCATCAAGAACCGG 931
 Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140
 Db 932 ATCCATCGCTGCTGCTGTGTTGACCCGGTGTCAAGCAACGTACTCCACATCTCTCACAC 991
 Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160
 Db 992 AAACGCTGCTCAAGTTCCTGTCACATCTTTGTTGCTGCTGCTGCTGCTGCTGCTGCT 1051
 Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGlu 180
 Db 1052 TACCGCACTATCCAGATTGGGCATCGGCACATTCGAGACTTGGCTGTGGTGTCTGGAG 1111
 Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 200
 Db 1112 ACAGCACCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1171
 Qy 201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220
 Db 1172 GTGCTCAACGAATGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1231
 Qy 221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240
 Db 1232 GCTGCCAGCAACCTACACCACTGGACATGATGAGTGTGGAGAGCCCTGAGGACAGG 1291
 Qy 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValIle 260
 Db 1292 ACACTATGTCTGGAGGAGTCTTTCTGTCAGCCCAACAGAGCTTGGGGGAGTGCATC 1351
 Qy 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280
 Db 1352 GACAGATTGCTCGGAGCAGGTACACAGCTGTGTGTAGTGAGCAGACCCAGCATCTC 1411
 Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300
 Db 1412 TTGGCGGTGTCTCCCTCTCCGACATCTTCAGGCACTGTGTCTCAGCCCTGTCTGGCATC 1471
 Qy 301 AspAlaLeuGlyAla 305
 Db 1472 GATGCCCTCGGGCC 1486

RESULT 4

US-10-473-670-30
 ; Sequence 30, Application US/10473670
 ; Publication No. US20040110180A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RECIPON, Shirley A.; BURRILL, John D.;
 ; APPLICANT: MARCUS, Gregory A.; ZINGLER, Kurt A.;
 ; APPLICANT: TANG, Y. Tom; THORNTON, Michael;
 ; APPLICANT: BOROMSKY, Mark L.; BAUGHN, Marian R.;
 ; APPLICANT: BURFORD, Neil; LEE, Soo Yeun;
 ; APPLICANT: GANDHI, Ameena R.; SWARNAKAR, Anita;
 ; APPLICANT: YAO, Monique G.; RAMKUMAR, Jayalaxmi;
 ; APPLICANT: CHAWLA, Narinder K.; LU, Dyung Aina M.;
 ; APPLICANT: ARVIZU, Chandra S.; ISON, Craig H.;
 ; APPLICANT: DING, Li; LU, Yan;
 ; APPLICANT: GURURAJAN, Rajagopal; WALSH, Roderick T.;
 ; APPLICANT: GANDHI, Ameena R.; SWARNAKAR, Anita;
 ; APPLICANT: FORSYTHE, Ian J.; YUE, Henry;
 ; APPLICANT: AU-YOUNG, Janice K.; ELLIOTT, Vicki S.;
 ; APPLICANT: LEE, Sally
 ; TITLE OF INVENTION: KINASES AND PHOSPHATASES
 ; FILE REFERENCE: PI-0398 USN

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; CURRENT APPLICATION NUMBER: US/10/473,670
; CURRENT FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: PCT/US02/10818
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 60/282,119
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/283,588
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/283,759
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/285,589
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: US 60/287,037
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/287,036
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/288,608
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/288,712
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/289,909
; PRIOR FILING DATE: 2001-05-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PERL Program
; SEQ ID NO 30
; LENGTH: 2781
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 7474666CB1
US-10-473-670-30

Alignment Scores:
Pred. No.: 1,65e-191 Length: 2781
Score: 1553.00 Matches: 305
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-070-794A-4 (1-305) x US-10-473-670-30 (1-2781)

Qy 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerIysLeuVal 20
Db 573 ATGGCTTTCATCGAGGACACACCTGCTACGATGCCATGGCAACTAGCTCCAAGCTAGTC 632
Qy 21 IlePheAspThrMetLeuGluIleIysIysAlaPhePheAlaLeuValAlaAsnGlyVal 40
Db 633 ATCTTCGACACCATGCTGGAGATCAAGAAGGCTTCTTTGTCTGTGGTGGCCACCGGTGTG 692
Qy 41 ArgAlaAlaProLeuTyrAspSerIysIysGlnSerPheValGlyMetLeuThrIleThr 60
Db 693 CGGGCAGGCCCTCTATGGACGACGACGAAGACGAGCTTTGTGGGATGCTGCACCATCACT 752
Qy 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80
Db 753 GACTTCATCCTGGTGTGCTGCTACTACAGTCCCGCTGGTCCAGATCTATGAGATT 812
Qy 81 GluGlnHisIysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheIysProLeu 100
Db 813 GAACAACATAAGATTGAGACCTGGAGGAGGATCTACCTGCAAGGCTGCTTCAAGCCTCTG 872
Qy 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleIysAsnArg 120
Db 873 GTCTCCATCTCTCTATGATGAGCTGTGTGAAGCTGTCTACACCTCATCAAGAACCGG 932
Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140
Db 933 ATCCATCGCTGCTGCTGCTTCTTACCCGGTGTGAGCAACGTAAGTCTCCATCTCCACAC 992
Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160
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Db 993 AAACGCTGCTCAAGTTCCTGACATCTTGGTTCCTGCTGCCCGCCCTCTCTCTCCTC 1052
Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGlu 180
Db 1053 TACCGCACTATCCAAGATTGGGCACTCGGCACATTCGAGACTTGGCTGTGGTGGAG 1112
Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 200
Db 1113 ACAGCAACCCATCTGACTGCACTGGACATCTTTGTGACCGGCTGTGTCTGCACTGCT 1172
Qy 201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220
Db 1173 GTGTCACCAAGATGTGTCAGTCTGGGCTCTATTCCCGCTTTGATGTGATTCACCTG 1232
Qy 221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240
Db 1233 GCTGCCAGCAAACTACAACACCTGGACATGATGATGTGGAGAAGCCCTGAGGACAGG 1292
Qy 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValIle 260
Db 1293 ACATATGCTGTGGAGGAGTCTTCTCTGCAGCCCAAGAGCTTTGGGGAAGTATC 1352
Qy 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280
Db 1353 GACAGGATTGCTCGGAGCAGGTACACAGGCTGGTCTAGTGGACGAGACCAGCATCTC 1412
Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300
Db 1413 TTGGGCGTGGTCTCTCCCTCTCCGACATCTTTCAGGCACTGGTGTGCTCAGCCCTGTGGCATC 1472
Qy 301 AspAlaLeuGlyAla 305
Db 1473 GATGCCCTCGGGGCC 1487

RESULT 5
US-10-756-149-1235
; Sequence 1235, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756,149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1235
; LENGTH: 2290
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-756-149-1235

Alignment Scores:
Pred. No.: 3,05e-188 Length: 2290
Score: 1525.00 Matches: 299
Percent Similarity: 99.34% Conservative: 3
Best Local Similarity: 98.36% Mismatches: 2
Query Match: 98.32% Indels: 0
DB: 9 Gaps: 0

US-10-070-794A-4 (1-305) x US-10-756-149-1235 (1-2290)

Qy 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerIysLeuVal 20
Db 574 ATGGCTTTCATCGAGGACACACCTGCTACGATGCCATGGCAACTAGCTCCAAGCTAGTC 633
Qy 21 IlePheAspThrMetLeuGluIleIysIysAlaPhePheAlaLeuValAlaAsnGlyVal 40
Db 634 ATCTTCGACACCATGCTGGAGATCAAGAAGGCTTCTTTGTCTGTGGTGGCCACCGGTGTG 693
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QY 41 ArgAlaAlaProLeuTrpAspSerIysGlnSerPheValGlyMetLeuThrIleThr 60
Db 694 CGGCAGCCCCCTCATGGGACAGAAAGCAGAGCTTTGTGGGATGCTGACCATCACT 753
QY 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80
Db 754 GACTTCATCTCTGGTGTGTCATCGCTACTACAGGTCCCGCTGGTCCAGATCTATGAGATT 813
QY 81 GluGlnHisIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100
Db 814 GAACAACATAAGATTGAGACCTGGAGGAGATCTACCTGCAAGGCTGCTTCAAGCCTCTG 873
QY 101 ValSerIleSerProAsnAspSerIlePheGluAlaValTyrThrLeuIleLysAsnArg 120
Db 874 GTCTCCATCTCTCCTAATAGATAGCTGTTTGAAGCTGTCTACACCTCATCAAGACCGG 933
QY 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisLeuThrHis 140
Db 934 ATCCATGCGCTGCTGCTTCTGACCCGGTGTACGCAACGCTACTCCATCCTCACACAC 993
QY 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160
Db 994 AAACGCTGCTCAAGTCTCTGACATCTTTGGTTCCCTGCTGCCCGGCCCTCTCTCTC 1053
QY 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGlu 180
Db 1054 TACGCACTATCAAGATTGGGCATCGGCACATCTTCGACCGGCTGTGTGCTGGAG 1113
QY 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuPro 200
Db 1114 ACAGACCCATCTCTGACTGCACTGGACATCTTTGTGACCGGCTGTGTGCACTGCCT 1173
QY 201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220
Db 1174 GTGCTCAACGAATGTGTGCTGAGTGTGGGCTCTATTTCCCGCTTTGATGTATCACTG 1233
QY 221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240
Db 1234 GCTGCCAGCAAACTCAACACCTGACATGATGTGTGGAGAGGCGCTTGGAGAGG 1293
QY 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIle 260
Db 1294 ACATATGCTTGGAGGAGTCTCTTCTGTCAGCCCCACAGAGCTTTGGGGAGTGTATC 1353
QY 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280
Db 1354 GACAGGATGCTCGGAGCAGGTACACAGCTGTGTGTGTGACGAGACCCAGCATCTC 1413
QY 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300
Db 1414 TTGGCGTGTCTCTCCCTCTCCGACATCTTTCAGGCACTGTGTGTGCTCAGCCCTGTG 1473
QY 301 AspAlaLeuGly 304
Db 1474 GATCCCTCGGGG 1485

RESULT 6

US-09-950-022-1
; Sequence 1, Application US/09950022
; Publication No. US20030017470A1
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: Novel PKA33 Alleles and Use fo the Same as Genetic Markers for
; FILE OF INVENTION: Reproductive and Meat Quality Traits
; FILE REFERENCE: P04668US3
; CURRENT APPLICATION NUMBER: US/09/950,022
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239

; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1873

; TYPE: DNA
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1392)
US-09-950-022-1

Alignment Scores:

Pred. No.:	4,98e-186	Length:	1873
Score:	1507.00	Matches:	296
Percent Similarity:	98.36%	Conservative:	4
Best Local Similarity:	97.05%	Mismatches:	5
Query Match:	97.16%	Indels:	0
DB:	3	Gaps:	0

US-10-070-794A-4 (1-305) x US-09-950-022-1 (1-1873)

QY 1 MetArgPheMetGlnGlnHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 20
Db 478 ATGCACCTTCATGCAGGAGCACACCTGCTACGATGCCATGGCAGCAGCTCCAAACTGGTC 537
QY 21 IlePheAspThrMetLeuGluIleLysLysAlaPheAlaLeuValAlaAsnGlyVal 40
Db 538 ATCTTTCGACACCATGCTGGAGATCAAGAAGGCCCTTCTTTCCTGGTGGCAACGGCGTC 597
QY 41 ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 60
Db 598 CGAGCGGCGCTTTGTGGGACAGCAAGACAGAGCTTCGTGGGATGCTGACCATCACA 657
QY 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80
Db 658 GACTTCATCTTGTGTGCTGCACCGCTATTACAGGTGCCCTGCTCCAGATCTACGAGATT 717
QY 81 GluGlnHisIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100
Db 718 GAAGAACATAAAGATTGAGACCTGGAGGAGATCTACCTTCAAGGCTGCTTCAAGCCTCTG 777
QY 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120
Db 778 GTCTCCATCTCTCCCAATGACACCTGTTCCAGAGCTGTCTACGCCCTCATCAAGACCGG 837
QY 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140
Db 838 ATCCACCGCTGCGGCTGCTGACCGCTGCTCCGGGCTGTGCTCCACATCTCCACAT 897
QY 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160
Db 898 AAGCGGCTTCTCAAGTTCCTGACATCTTTGGCACCTTGTGGCACCGCTGCTGCCCTCTC 957
QY 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGlu 180
Db 958 TACCGCACCATCCAGATTTGGGACATCCGACATTCGAGACTTGGCGGTGGTCTGGAA 1017
QY 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuPro 200
Db 1018 ACGGCGCCCATCTGACCGCAGCTGGACATCTTGTGGACCGGCTGTGCTGGCTGCTG 1077
QY 201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220
Db 1078 GTGGTCAACGAACACTGCAGAGGTAGTGGGCTCTACTCTCGCTTTCATGTGATCCACCTG 1137
QY 221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240
Db 1138 GCTGCCCAACAAACATACACACCTGGACATGAATGTGGAGAGCCCTTGGAGCGCG 1197
QY 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIle 260

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Db 1198 AACTGTGTCTGGAGGCGTCCTTCTCTGCAGCCCGACAGACCTTGGGGAGTCATT 1257
Qy 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280
Db 1258 GACCGGATTGTCGGGAACAGGTGACCGCTGCTGCTGCTGATGAGACCCAGACCTT 1317
Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300
Db 1318 CTGGCGTGTGTCTCTGACATCTTTCAGGCTCTGGTGTCTGACCCCTGCTGGAATT 1377
Qy 301 AspAlaLeuGlyAla 305
Db 1378 GATGCCCTCGGGGCC 1392

RESULT 7
US-09-950-022-3
; Sequence 3, Application US/09950022
; Publication No. US20030017470A1
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: Novel PRKAG3 Alleles and Use to the Same as Genetic Markers for
; TITLE OF INVENTION: Reproductive and Meat Quality Traits
; FILE REFERENCE: P04668US3
; CURRENT APPLICATION NUMBER: US/09/950,022
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1873
; TYPE: DNA
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1392)
US-09-950-022-3

Alignment Scores:
Pred. No.: 4, 98e-186 Length: 1873
Score: 1507.00 Matches: 296
Percent Similarity: 98.36% Conservative: 4
Best Local Similarity: 97.05% Mismatches: 5
Query Match: 97.16% Indels: 0
DB: 3 Gaps: 0

US-10-070-794A-4 (1-305) x US-09-950-022-3 (1-1873)
Qy 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerIysLeuVal 20
Db 478 ATGCACCTTCATGCAGGACACACCTGCTACGATGCGATGCGGACGACCTCCAAACTGGTCT 537
Qy 21 IlePheAspThrMetLeuGluIleIysAlaPhePheAlaLeuValAlaAsnGlyVal 40
Db 538 ATCTTCGACACCATCTGAGATCAAGAGGCTTCTTTGGCCCTGGTGGCCAAACGGCTC 597
Qy 41 ArgAlaAlaProLeuTyrAspSerIysGlnSerPheValGlyMetLeuThrIleThr 60
Db 598 CGAGCGGACACCTTTGTGGACAGCAGACGACGCTTCGTTGGGATGCTGACCATCACA 657
Qy 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80
Db 658 GACTTCATCTTGGTGTGACCGCTATTACAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 717
Qy 81 GluGlnHisIysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheIysProLeu 100
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Db 718 GAAGAACATAAGATTGAGACCTCGAGCGAGATCTACCTTCAAGGCTGCTTCAAGGCTCTG 777
Qy 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleIysAsnArg 120
Db 778 GTCTCCATCTCTCCCAATGACAGCCTGTTGGAAGCTGTGTACGCCCTCATCAAGAACCGG 837
Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140
Db 838 ATCCACCGCTGCGGTCTCTGGACCTGTCTCCGGGGCTGTGTCTCCACATCTCTCACAT 897
Qy 141 LysArgLeuLeuIysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160
Db 898 AAGCGCTTCTCAAGTTCTTGCCATCTTTGGCACCTGTCTGCCCGCGCTCTCTCTCTC 957
Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGlu 180
Db 958 TAGCGCACCATCCAAGATTGCGCATCGGCACATTCGAGACTTGGCGCTGGTCTGGAA 1017
Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 200
Db 1018 ACGCGCCCATCTCTGACCGCACCTGGACATCTTGTGGACCGCGGTGTGTCTGCGTGCCT 1077
Qy 201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220
Db 1078 GTGGTCAACGAACACTGGACAGGTAGTGGGCTCTCTACTCTCGCTTGTATGTATCCACTG 1137
Qy 221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240
Db 1138 GCTGCCCAACAACATACAAACCACTGGACATGAATGTGGAGAAGCCCTTGAGGACGCGG 1197
Qy 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIle 260
Db 1198 AACTGTGTCTGGAAGCGTCTTCTCTGCGAGCCCGACGACCTTGGGGGAAGTCAAT 1257
Qy 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280
Db 1258 GACCGGATTGTCGGGAACAGGTGACCGCTGCTGCTGCTGATGAGACCCAGCACCTT 1317
Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300
Db 1318 CTGGCGTGTGTCTCTCTGACATCTTTCAGGCTCTGGTGTCTGAGCCCTGCTGGAATT 1377
Qy 301 AspAlaLeuGlyAla 305
Db 1378 GATGCCCTCGGGGCC 1392

RESULT 8
US-09-950-022-5
; Sequence 5, Application US/09950022
; Publication No. US20030017470A1
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: Novel PRKAG3 Alleles and Use to the Same as Genetic Markers for
; TITLE OF INVENTION: Reproductive and Meat Quality Traits
; FILE REFERENCE: P04668US3
; CURRENT APPLICATION NUMBER: US/09/950,022
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 1873
; TYPE: DNA
; ORGANISM: Sus scrofa
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FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1392)
US-09-950-022-5

Alignment Scores:

Pred. No.: 4,98e-186 Length: 1873
Score: 1507.00 Matches: 296
Percent Similarity: 98.36% Conservatives: 4
Best Local Similarity: 97.05% Mismatches: 5
Query Match: 97.16% Indels: 0
DB: 3 Gaps: 0

US-10-070-794A-4 (1-305) x US-09-950-022-5 (1-1873)

Qy 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 20
Db 478 ATGCACCTTCATGTCAGGAGCACACCTGTACGATGCCATGGGACGAGCTCCAACTGGTC 537
Qy 21 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 40
Db 538 ATCTTCGACACCATGCTGGAGATCAAGAAGGCTTCTTTGCCCTGGTGGCCAAAGCGGTC 597
Qy 41 ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 60
Db 598 CGAGCGGACCTTTGTGGGACAGCAAGAGAGCTTCGTGGGGATGCTGACCATCACA 657
Qy 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80
Db 658 GACTTCATCTGGTGTGACCGCTATTACAGTCCCGCTGGTCCAGATCTACGAGATT 717
Qy 81 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100
Db 718 GAAGACATAGATTGAGACCTGGAGGAGATCTACCTTCAAGGCTGCTTCAAGGCTCTG 777
Qy 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120
Db 778 GTCTCCATCTCTCCATGACAGGCTGTTCGAGCTGTCTACGCCCTCATCAAGACCGG 837
Qy 121 IleHisArgLeuProValLeuAspProValSerLysValLeuHisIleLeuThrHis 140
Db 838 ATCCACCGCTGCGGCTGTGGACCTGTCTCCGGGCTGTGCTCCACATCTCCACAT 897
Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160
Db 898 AAGCGGCTTCTCAAGTTCCTGCACATCTTTGGCACCTGTCTGCCCGGCTCTCTCTC 957
Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGlu 180
Db 958 TACCGCACCATCCAAAGATTTGGGCATCGGCACATTCGAGACTTGGCGGTGGTGGAA 1017
Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 200
Db 1018 ACGGGCGCCATCTGACCGCATCTGGACATCTTGTGACCGGCTGTGTCTGGCGCTCCT 1077
Qy 201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220
Db 1078 GTGGTCAACAAACCTGACAGGATGTGGGCTCTACTCTCGCTTTGATGTGATCCACCTG 1137
Qy 221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240
Db 1138 GCTGCCCAACAAACATACACACCTTGACATGAATGTGGGAGAGCCCTGAGGAGCGG 1197
Qy 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIle 260
Db 1198 ACATGTGTCTGGAGGCGTCTTCTTCGACGCCCCACAGACCTTGGGGGAGTCAATT 1257
Qy 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280
Db 1258 GACCGGATTGTCCGGGAACAGGTGCACCGCTGTGTGCTGTGATGAGACCCAGCACCTT 1317
Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300

Db 1318 CTGGGCGTGTGTCCCTCTCTGACATCCTTACGGCTCTGTGTGCTACGCCCTGTGGAATT 1377
Qy 301 AspAlaLeuGlyAla 305
Db 1378 GATGCCCTCGGGGCC 1392
RESULT 9
US-11-075-134-1
; Sequence 1, Application US/11075134
; Publication No. US20050208551A1
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: Novel PRKAG3 Alleles and Use fo the Same as Genetic Markers for
; TITLE OF INVENTION: Reproductive
; TITLE OF INVENTION: and Meat Quality Traits
; FILE REFERENCE: P04668US3
; CURRENT APPLICATION NUMBER: US/11/075,134
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: US/09/950,022
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 1873
; TYPE: DNA
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1392)
; OTHER INFORMATION:
US-11-075-134-1
Alignment Scores:
Pred. No.: 4,98e-186 Length: 1873
Score: 1507.00 Matches: 296
Percent Similarity: 98.36% Conservatives: 4
Best Local Similarity: 97.05% Mismatches: 5
Query Match: 97.16% Indels: 0
DB: 10 Gaps: 0
US-10-070-794A-4 (1-305) x US-11-075-134-1 (1-1873)
Qy 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerLysLeuVal 20
Db 478 ATGCACCTTCATGTCAGGAGCACACCTGTACGATGCCATGGGACGAGCTCCAACTGGTC 537
Qy 21 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 40
Db 538 ATCTTCGACACCATGCTGGAGATCAAGAAGGCTTCTTTGCCCTGGTGGCCAAAGCGGTC 597
Qy 41 ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 60
Db 598 CGAGCGGACCTTTGTGGGACAGCAAGAGAGCTTCGTGGGGATGCTGACCATCACA 657
Qy 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80
Db 658 GACTTCATCTGGTGTGACCGCTATTACAGTCCCGCTGGTCCAGATCTACGAGATT 717
Qy 81 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100
Db 718 GAAGACATAGATTGAGACCTGGAGGAGATCTACCTTCAAGGCTGCTTCAAGGCTCTG 777
Qy 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120

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778 GTCTCCATCTCTCCCATGACAGCCTGTTCGAAGCTGTCTACGGCCCTCATCAAGAACCGG 837
Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140
Db 838 ATCCACCGCCTGCGGCTCTGGACCTGTCTCCGGGGCTGTCTCCACATCTCTCCACAT 897
Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160
Db 898 AAGCGGCTTCTCAAGTCTCTGCACATCTTTGGCACCTGTCTGGCCCGGCGCTCTCTCTC 957
Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 180
Db 958 TACCGCACCATCCAAAGATTGGGGCATGGCACATTCGACATCTGGCGGTGTCTGGAA 1017
Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuPro 200
Db 1018 ACGCGCCCATCTCTGACCGCACTGGACATCTTCGTGGACCGCGCTGTCTGTGCGCTGCCT 1077
Qy 201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220
Db 1078 GTGGTCAACGAACTGGACAGGTAGTGGCGCTCTACTCTCGCTTTGATGTGATCCACCTG 1137
Qy 221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240
Db 1138 GCTGCCCAACAAACATACACCACTGGACATGATGTGGGAGAGCCCTGAGGCAGCGG 1197
Qy 241 ThrLeuCysLeuGluGlyGlnValValSerCysGlnProHisGlnSerLeuGlyGluValIle 260
Db 1198 ACCTGTGTCTGGAAGGCGTCTTTCTTCGACGCCCCACGAGACCTTGGGGAGTCAAT 1257
Qy 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280
Db 1258 GACCGGATTGTCCGGGAACAGGTGACCGCTGTCTGGTGTCTGGATGAGACCCAGCACCTT 1317
Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300
Db 1318 CTGGCGGTGTGTCTCTCTGACATCTTTCAGGCTCTGTGTCTCAGCCCTGTCTGGAATT 1377

RESULT 10
US-11-075-134-3
; Sequence 3, Application US/11075134
; Publication No. US20050208551A1
; GENERAL INFORMATION:
; APPLICANT: Rothechild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; TITLE OF INVENTION: Novel PRKAG3 Alleles and Use fo the Same as Genetic Markers for
; TITLE OF INVENTION: Reproductive
; TITLE OF INVENTION: and Meat Quality Traits
; FILE REFERENCE: P04668US3
; CURRENT APPLICATION NUMBER: US/11/075,134
; PRIOR FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: US/09/950,022
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1873
; TYPE: DNA
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: CDS
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; LOCATION: (1)..(1392)
; OTHER INFORMATION:
US-11-075-134-3
Alignment Scores:
Pred. No.: 4,98e-186 Length: 1873
Score: 1507.00 Matches: 296
Percent Similarity: 98.36% Conservative: 4
Best Local Similarity: 97.05% Mismatches: 5
Query Match: 97.16% Indels: 0
DB: 10 Gaps: 0
US-10-070-794A-4 (1-305) x US-11-075-134-3 (1-1873)
Qy 1 MetArgPheMetGlnGluHisThrCysTyrAspAlaMetAlaThrSerSerIleValLeuVal 20
Db 478 ATGCACCTTATGACGAGGACACCTGCTACGATGCCATGGCACCAGCTCTCAAACTGGTC 537
Qy 21 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 40
Db 538 ATCTTCGACACCATGCTGGAGATCAGAAAGCCCTTCTTTGCCCTGGTGGCCAAAGCGGTC 597
Qy 41 ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 60
Db 598 CGAGCGGCACCTTTGTGGGACAGCAAGACAGAGCTTCGTGGGGATGCTGACCATCACA 657
Qy 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80
Db 658 GACTTCATCTTGTGGTGTGACCGCTATTACAGGTCCCTCTGCTCCAGATCTACGAGATT 717
Qy 81 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100
Db 718 GAAGAACATTAAGATTGAGACTGGAGGGAGATCTACCTTCAAGGCTGCTTCAAGCCCTCTG 777
Qy 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120
Db 778 GTCTCCATCTCTCCCAATGACAGCTGTTCGAAGCTGTCTACGCCCTCATCAAGAACCGG 837
Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140
Db 838 ATCCACCGCCTGCGGCTCTGGACCTGTCTCCGGGGCTGTGCTCCACATCTCTCACAT 897
Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160
Db 898 AAGCGGCTTCTCAAGTCTCTGCACATCTTTGGCACCTGTCTGCCCGGCGCTCTCTCTC 957
Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 180
Db 958 TACCGCACCATCCAAAGATTGGGGCATGGCACATTCGAGACATTTGGCGGTGTCTGGAA 1017
Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuPro 200
Db 1018 ACGCGCCCATCTCTGACCGCACTGGACATCTTCGTGGACCGCGCTGTGTCTGCGCTGCT 1077
Qy 201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220
Db 1078 GTGGTCAACGAACTGGACAGGTAGTGGCGCTCTACTCTCGCTTTGATGTGATCCACCTG 1137
Qy 221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240
Db 1138 GCTGCCCAACAAACATACACCACTGGACATGATGTGGGAGAGCCCTGAGGGACGCGG 1197
Qy 241 ThrLeuCysLeuGluGlyGlnValValSerCysGlnProHisGlnSerLeuGlyGluValIle 260
Db 1198 ACCTGTGTCTGGAAGGCGTCTTTCTTCGACGCCCCACGAGACCTTGGGGAGTCAAT 1257
Qy 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280
Db 1258 GACCGGATTGTCCGGGAACAGGTGACCGCTGTCTGGTGTCTGGATGAGACCCAGCACCTT 1317
Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300
Db 1318 CTGGCGGTGTGTCTCTCTGACATCTTCTGAGCTCTGGTGTCTGAGCCCTGTCTGGAATT 1377
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Qy 301 AspalaleuGlyAla 305
Db 1378 GATGCCCTCGGGCC 1392

RESULT 11
US-11-075-134-5
; Sequence 5, Application US/11075134
; Publication No. US20050208551A1
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: Novel PRKAG3 Alleles and Use fo the Same as Genetic Markers for
; TITLE OF INVENTION: Reproductive
; FILE REFERENCE: P04668US3
; CURRENT APPLICATION NUMBER: US/11/075,134
; CURRENT FILING DATE: 2005-03-08
; PRIOR FILING DATE: 2001-09-10
; PRIOR FILING DATE: 2001-09-10
; PRIOR FILING DATE: 2000-09-08
; PRIOR FILING DATE: 2001-01-08
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1873
; TYPE: DNA
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1392)
; OTHER INFORMATION:
US-11-075-134-5

Alignment Scores:
Pred. No.: 4.98e-186 Length: 1873
Score: 1507.00 Matches: 296
Percent Similarity: 98.36% Conservative: 4
Best Local Similarity: 97.05% Mismatches: 5
Query Match: 97.16% Indels: 0
DB: 10 Gaps: 0

US-10-070-794A-4 (1-305) x US-11-075-134-5 (1-1873)

Qy 1 MetArgPheMetGlnGluHisThrCysGlyTyrAspAlaMetAlaThrSerLysLeuVal 20
Db 478 ATGCACCTTCATGAGGAGCACACTGCTAGTGCATGCGGACGAGCTCAAACTGGTC 537

Qy 21 IlePheAspThrMetLeuGluIleLysLeuAlaPhePheAlaLeuValAlaAsnGlyVal 40
Db 538 ATCTTCGACACCATGCTGGAGATCAAGAGGCTTCTTCCCTGGTGGCCAAAGCGGTC 597

Qy 41 ArgAlaPheProLeuThrAspSerLysGlnSerPheValGlyMetLeuThrIleThr 60
Db 598 CGAGCGGCACCTTTGTGGGACAGCAAGAGCAGCTTCGTGGGGATGCTGACCATCACA 657

Qy 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80
Db 658 GACTTCATCTGTGGCTGACCGCTATTACAGGTCCCTGGTCCAGATCTACGAGATT 717

Qy 81 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100
Db 718 GAAGAACAATAAGATTGAGACCTGGAGGAGATCTACCTTCAAGGCTGCTTCAAGCCTCTG 777

Qy 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120
Db 778 GTCTCCATCTCTCCCAATGACAGCTGTTCGAGCTGTCTACGCCCTCTCATCAAGAACCGG 837
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Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140
Db 838 ATCCACCGCTGCGGTCCTGGACCCCTGTCTCCGGGGCTGTGCTCCACATCTCTCACACAT 897

Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160
Db 898 AAGCGGCTTCTCAAGTTCTTCGCACATCTTTGGCACCTGTGTCGCCCGGCTCTCTCTCCTC 957

Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 180
Db 958 TACGGCACCATCCAGATTGCGGCATCGGCACATTCGAGACTTGGCCGTGGTCTGGAA 1017

Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuPro 200
Db 1018 ACGCGGCCCATCTGACCGCACATCTTGTGGACCGCGTGTGTCTGCGCTGCT 1077

Qy 201 ValValAsnGlnCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220
Db 1078 GTGGTCAACGAAACTGGACAGGTAGTGGGCTCTTACTCTCGCTTTGTATGTATCCACCTG 1137

Qy 221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240
Db 1138 GCTGCCCAACAACATACACACCTGACATGATGTGGAGAACCCCTGAGGACGCGG 1197

Qy 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIle 260
Db 1198 ACATGTGTCTGGAGGCGTCTTCTCTGCGACCCACGAGACTTGGGGGAAGTCATT 1257

Qy 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280
Db 1258 GACCGGATTGTCGGGAAACAGGTGCACCGCTGTGCTCGTGGATGAGACCCAGCACCTT 1317

Qy 281 LeuGlyValValSerLeuSerAspIleLeuGluAlaLeuValLeuSerProAlaGlyIle 300
Db 1318 CTGGCGGTGTGTGCTCTCTGACATCTTTCAGGCTCTGGTGTCTGAGCTCTGCTGGAATT 1377

Qy 301 AspalaleuGlyAla 305
Db 1378 GATGCCCTCGGGCC 1392

RESULT 12
US-09-950-022-7
; Sequence 7, Application US/09950022
; Publication No. US20030017470A1
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: Novel PRKAG3 Alleles and Use fo the Same as Genetic Markers for
; TITLE OF INVENTION: Reproductive and Meat Quality Traits
; FILE REFERENCE: P04668US3
; CURRENT APPLICATION NUMBER: US/09/950,022
; CURRENT FILING DATE: 2001-09-10
; PRIOR FILING DATE: 2001-09-10
; PRIOR FILING DATE: 2000-09-08
; PRIOR FILING DATE: 2000-09-08
; PRIOR FILING DATE: 2001-01-08
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 1873
; TYPE: DNA
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1392)
US-09-950-022-7

Alignment Scores:
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Pred. No.: 6.74e-186 Length: 1873
Score: 1506.00 Matches: 295
Percent Similarity: 98.36% Conservatives: 5
Best Local Similarity: 96.72% Mismatches: 5
Query Match: 97.10% Indels: 0
DB: 3 Gaps: 0

US-10-070-794A-4 (1-305) x US-09-950-022-7 (1-1873)

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Db 478 ATGCACCTTCATGCGAGGACACACCTGCTAGCATGCCATGGCAGCAGCTCCAAACTGGTC 537
Qy 21 IlePheAspThrMetLeuGluLeuLysAlaPhePheAlaLeuValAlaAsnGlyVal 40
Db 538 ATCTTCACACCATGCTGGAGATCAAGAAGCCCTCTTTGCCCTGGTGGCCAAAGCGGATC 597
Qy 41 ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 60
Db 598 CGAGCGGACCTTTGTGGACAGCAGCAGAGCTTCGTGGGGATGCTGACCATCACA 657
Qy 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80
Db 658 GACTTCATCTCTGCTGCTGACCGCTATTACAGGTCCCTGCTGGTCCAGATCTACGAGATT 717
Qy 81 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100
Db 718 GAAGACATATAGATTGAGACCTGGAGGAGATCTACCTTCAAGGCTGCTTCAAGCCCTCTG 777
Qy 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120
Db 778 GTCTCCATCTCTCCAAATGACAGCTGTTTGAAGCTGTCTAGCGCCTCATCAAGAACGG 837
Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140
Db 838 ATCCAGCGCCTGCGGCTCTGACCTTCCGGGGCTGTGCTCCAGATCTCCACATCTCCACAT 897
Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160
Db 898 AAGCGGCTTCTCAAGTTCTCTGACATCTTTGGACCTTGTGCGCCCGGCTCTCTCTCTCTC 957
Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 180
Db 958 TACGACCATCCAGATTGGGCATCGGCATCTCCGAGACTTGGCGGTGGTGGTGGTGGAA 1017
Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 200
Db 1018 ACGCGCCCATCTCTGACCGCATCTGACATCTTCGTGGAGCGCGCTGTCTGCGCTGCT 1077
Qy 201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220
Db 1078 GTGGTCAACGAACACTGGACAGGTAGTGGGCTCTACTCTCGCTTTGATGATCCACCTG 1137
Qy 221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240
Db 1138 GCTGCCCAACAAACATACACCATCTGGACATGATGTGGAGAGCCCTGAGGACGCGG 1197
Qy 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGluSerLeuGlyGluValIle 260
Db 1198 ACATGTGCTTGGAGGCTCTCTTCTCTCGAGCCGCCACGAGACCTTGGGGAGAGTCATT 1257
Qy 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280
Db 1258 GACCGGATTTGTCGGGAAACAGGTGACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1317
Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300
Db 1318 CTGGGCGGTGGTGTCTCTGACATCTCTTACAGCTCTGCTGCTGCTGCTGCTGCTGCTGCT 1377
Qy 301 AspAlaLeuGlyAla 305
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RESULT 13

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US-11-075-134-7
; Sequence 7, Application US/11075134
; Publication No. US20050208551A1
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: Novel PRKAG3 Alleles and Use fo the Same as Genetic Markers for
; TITLE OF INVENTION: Reproductive
; TITLE OF INVENTION: and Meat Quality Traits
; FILE REFERENCE: P04668US3
; CURRENT APPLICATION NUMBER: US/11/075,134
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: US/09/950,022
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 1873
; TYPE: DNA
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1392)
; OTHER INFORMATION:
; US-11-075-134-7
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Alignment Scores: 6.74e-186 Length: 1873
Pred. No.: 1506.00 Matches: 295
Score: 98.36% Conservatives: 5
Percent Similarity: 96.72% Mismatches: 5
Best Local Similarity: 97.10% Indels: 0
Query Match: 10 Gaps: 0
DB:

US-10-070-794A-4 (1-305) x US-11-075-134-7 (1-1873)

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Db 478 ATGCACCTTCATGCGAGGACACACCTGCTAGCATGCCATGGCAGCAGCTCCAAACTGGTC 537
Qy 21 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 40
Db 538 ATCTTCACACCATGCTGGAGATCAAGAAGCCCTCTTTGCCCTGGTGGCCAAAGCGGATC 597
Qy 41 ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 60
Db 598 CGAGCGGACCTTTGTGGACAGCAGCAGAGCTTCGTGGGGATGCTGACCATCACA 657
Qy 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80
Db 658 GACTTCATCTTGGTGTGCTGACCGCTATTACAGGTCCCTGCTGGTCCAGATCTTACGAGATT 717
Qy 81 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100
Db 718 GAAGACATATAGATTGAGACCTGGAGGAGATCTACCTTCAAGGCTGCTTCAAGGCTCTG 777
Qy 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120
Db 778 GTCTCCATCTCTCCCAATGACAGCTGTTTGAAGCTGTCTACGCCCTCATCAAGAAGCGG 837
Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140
Db 838 ATCCAGCGCCTGCGGCTCTGAGCCCTGTCTCCGGGGTGTGCTCCACATCTCTCACAT 897
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Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160
Db 898 AAGCGGTCTCTCAAGTCTCTGCACATCTTTGGCACCTCTGTCGCCCGCCCTCTCTCTC 957
Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 180
Db 958 TACCGCACCATCCAAAGATTGGGCATTCGGCACATTCGAGACTTGGCCGTGTCTGGAA 1017
Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgArgValSerAlaLeuPro 200
Db 1018 ACGCGCCCATCTCTGACCGCATCTGCACATCTTCTGTCGACCGCGTGTCTGCGCTGCT 1077
Qy 201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220
Db 1078 GTGGTCAACGAACCTGACACAGGTAGTGGGCTCTACTCTCGCTTTGATGTATCCACTG 1137
Qy 221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240
Db 1138 GCTGCCACACACATACACCATCTGCACATGATGATGTGGAGAGCCCTTGAGCAGCGG 1197
Qy 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValIle 260
Db 1198 ACCTGTGTCTGGAAGCGCTCTTCTCTGCCAGCCCCACGAGACCTTTGGGGAGTCAAT 1257
Qy 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280
Db 1258 GACCGGATGTGCGGGAACAGGTGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1317
Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300
Db 1318 CTGGGCGTGTGTCTCTCTGACATCTTCTGAGCTCTGCTGCTGCTGCTGCTGCTGCTG 1377
Qy 301 AspAlaLeuGlyAla 305
Db 1378 GATGCCCTCGGGGCC 1392

RESULT 14
US-09-950-022-9
; Sequence 9, Application US/09950022
; Publication No. US20030017470A1
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: Novel PRKAG3 Alleles and Use fo the Same as Genetic Markers for
; TITLE OF INVENTION: Reproductive and Meat Quality Traits
; FILE REFERENCE: P04668US3
; CURRENT APPLICATION NUMBER: US/09/950,022
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 1873
; TYPE: DNA
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1392)
US-09-950-022-9

Alignment Scores:
Pred. No.: 1.67e-185 Length: 1873
Score: 1503.00 Matches: 295
Percent Similarity: 98.36% Conservative: 5
Best Local Similarity: 96.72% Mismatches: 5
Query Match: 96.91% Indels: 0

DB: 3 Gaps: 0
US-10-070-794A-4 (1-305) x US-09-950-022-9 (1-1873)
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Db 478 ATGCACCTTCATGACGAGCACACCTGCTACGATGCCATGGGACACGCTCAAACTGGTC 537
Qy 21 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 40
Db 538 ATCTTCGACACCATCTGTCGAGATCAAGAAGCCCTTCTTTCCTGCTGGTGGCCACGCGGTC 597
Qy 41 ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 60
Db 598 CAAGCGGCACCTTTGTGGGACAGCAAGACAGAGCTTCGTGGGGATGCTGACCATCACA 657
Qy 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80
Db 658 GACTTCATCTTGTGTCTGTCACCCGCTATTACAGGTGCCCTCTGCTGCTGCTGCTGCTG 717
Qy 81 GluGlnHisLysIleGluThrTyrArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100
Db 718 GAAGACATTAAGATTGAGACCTGAGGGAGATCTACCTTCAAGGCTGCTTCAAGCCTCTG 777
Qy 101 ValSerIleSerProLeuAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120
Db 778 GTCTCCATCTCTCCCAATGACAGCCTGTTCCAAAGCTGTTACGCGCTCATCAAGACCGG 837
Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140
Db 838 ATCCACCGCTGTCGGGTCTGAGACCTGCTCCGGGGCTGTGTCTCCACATCTCTCACA 897
Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160
Db 898 AAGCGGTCTCTCAAGTCTCTGCACATCTTTGGCACCTCTGTCGCCCGCCCTCTCTCTC 957
Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValValLeuGlu 180
Db 958 TACCGCACCATCCAAAGATTGGGCATCGGCACATTCGAGACTTGGCGGTGTCTGGAA 1017
Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 200
Db 1018 ACGCGCCCATCTCTGACCGCATCTGTCGACATCTTCTGTCGACCGCGTGTCTGCGCTGCT 1077
Qy 201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220
Db 1078 GTGGTCAACGAACCTGACACAGGTAGTGGGCTCTACTCTCGCTTTGATGTATCCACTG 1137
Qy 221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240
Db 1138 GCTGCCACACACATACACCATCTGTCGACATGATGATGTGGAGAGCCCTTGAGCAGCGG 1197
Qy 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValIle 260
Db 1198 ACCTGTGTCTGGAAGCGCTCTTCTCTGCCAGCCCCACGAGACCTTTGGGGAGTCAAT 1257
Qy 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280
Db 1258 GACCGGATGTGCGGGAACAGGTGTCACCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1317
Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300
Db 1318 CTGGGCGTGTGTCTCTCTGACATCTTCTGAGCTCTGCTGCTGCTGCTGCTGCTGCTG 1377
Qy 301 AspAlaLeuGlyAla 305
Db 1378 GATGCCCTCGGGGCC 1392

RESULT 15
US-11-075-134-9
; Sequence 9, Application US/11075134
; Publication No. US20050208551A1
; GENERAL INFORMATION:

APPLICANT: Rothschild, Max
APPLICANT: Ciobanu, Dan
APPLICANT: Malek, Massoud
APPLICANT: Plastow, Graham
TITLE OF INVENTION: Novel PRKAG3 Alleles and Use fo the Same as Genetic Markers for
TITLE OF INVENTION: Reproductive
TITLE OF INVENTION: and Meat Quality Traits
FILE REFERENCE: P046680S3
CURRENT APPLICATION NUMBER: US/11/075,134
CURRENT FILING DATE: 2005-03-08
PRIOR APPLICATION NUMBER: US/09/950,022
PRIOR FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/231045
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/260,239
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/299,111
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patent in version 3.1
SEQ ID NO 9
LENGTH: 1873
TYPE: DNA
ORGANISM: Sus scrofa
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1392)
OTHER INFORMATION:
US-11-075-134-9

Alignment Scores:
Pred. No.: 1.67e-185 Length: 1873
Score: 1503.00 Matches: 295
Percent Similarity: 98.36% Conservative: 5
Best Local Similarity: 96.72% Mismatches: 5
Query Match: 96.91% Indels: 0
DB: 10 Gaps: 0

US-10-070-794A-4 (1-305) x US-11-075-134-9 (1-1873)

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Qy 21 IlePheAspThrMetLeuGluIleLysLysAlaPhePheAlaLeuValAlaAsnGlyVal 40
Db 538 ATCTTCGACACCATGCTGGAGATCAAGAAAGCGCTTCTTTGGCCCTGGTGGCCAAAGCGCGTC 597
Qy 41 ArgAlaAlaProLeuTrpAspSerLysLysGlnSerPheValGlyMetLeuThrIleThr 60
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Qy 61 AspPheIleLeuValLeuHisArgTyrTyrArgSerProLeuValGlnIleTyrGluIle 80
Db 658 GACTTCATCTTGGTGTGCTGACCGCTATTACAGGTCCCGCTGGTCCAGATCTACGAGATT 717
Qy 81 GluGlnHisLysIleGluThrTrpArgGluIleTyrLeuGlnGlyCysPheLysProLeu 100
Db 718 GAAGAACATAGATTGAGACCTGGAGGAGATCTACCTTCAAGGCTGCTTCAAGCGCTCTG 777
Qy 101 ValSerIleSerProAsnAspSerLeuPheGluAlaValTyrThrLeuIleLysAsnArg 120
Db 778 GTCTCCATCTCTCCCAATGACAGCTGTTCGAAGCTGTCTAGCCCTCATCAAGAACCGG 837
Qy 121 IleHisArgLeuProValLeuAspProValSerGlyAsnValLeuHisIleLeuThrHis 140
Db 838 ATCCACCGCTCCCGGTCTGGACCTGTCTCCGGGGCTGTGCTCCACATCTCTCACAT 897
Qy 141 LysArgLeuLeuLysPheLeuHisIlePheGlySerLeuLeuProArgProSerPheLeu 160
Db 898 AAGCGGCTTCTCAAGTTCCTGCACATCTTTGGCACCTGTGCGCCGCGCTCTCTTCCTC 957
Qy 161 TyrArgThrIleGlnAspLeuGlyIleGlyThrPheArgAspLeuAlaValLeuGlu 180

Db 958 TACCGACCATCCAGATTTCGGCATCGGCACATTCGAGACTTGGCCGTGGTGGAA 1017
Qy 181 ThrAlaProIleLeuThrAlaLeuAspIlePheValAspArgValSerAlaLeuPro 200
Db 1018 ACGCGGCCCATCTCGACCGCATCGGACATCTTCGTGGACCGCGTGTCTCGCGCTGCCT 1077
Qy 201 ValValAsnGluCysGlyGlnValValGlyLeuTyrSerArgPheAspValIleHisLeu 220
Db 1078 GTGGTCAACGAAACTGGACAGGTAGTGGGCTCTACTCTCGCTTTGATGTATCCACTG 1137
Qy 221 AlaAlaGlnGlnThrTyrAsnHisLeuAspMetSerValGlyGluAlaLeuArgGlnArg 240
Db 1138 GCTGCCCAACAACATACACACCTGGACATGATGTGGGAGAAGCCCTGAGGCAGCGG 1197
Qy 241 ThrLeuCysLeuGluGlyValLeuSerCysGlnProHisGlnSerLeuGlyGluValIle 260
Db 1198 ACACTGTGTCTGGAAAGCGTCTTTCCTGCGACGCCACGAGACCTTGGGGGGAAGTCATT 1257
Qy 261 AspArgIleAlaArgGluGlnValHisArgLeuValLeuValAspGluThrGlnHisLeu 280
Db 1258 GACCGGATTGTCCGGGAACAGGTGCACCGCTGTGTCTGTGGATGAGACCCACACCTT 1317
Qy 281 LeuGlyValValSerLeuSerAspIleLeuGlnAlaLeuValLeuSerProAlaGlyIle 300
Db 1318 CTGGGCGTGTGTCTCCCTCTCTGACATCTTCAGGCTCTGGTGTCTCAGCCCTGTCTGAATT 1377
Qy 301 AspAlaLeuGlyAla 305
Db 1378 GATGCCCTCGGGGCC 1392

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Job time : 671.008 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 24, 2006, 22:15:19 ; Search time 13.485 Seconds
(without alignments)
229.213 Million cell updates/sec

Title: US-10-070-794A-4
Perfect score: 1551
Sequence: 1 MRFQHTCYDMATSSKLV.....LSDIQLQVLSPAGIDALGA 305

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 70609 seqs, 10134256 residues

Total number of hits satisfying chosen parameters: 70609

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	111	7.2	494	7	US-11-156-084-34
4	107.5	6.9	498	6	US-10-467-657-5006
5	102	6.6	461	7	US-11-156-084-35
6	100.5	6.5	495	7	US-11-156-084-36
7	99	6.4	330	7	US-11-156-084-230
8	89.5	5.8	488	6	US-10-793-626-2308
9	87	5.6	1251	7	US-11-043-889-22
10	86.5	5.6	506	7	US-11-055-822-946
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12	85.5	5.5	554	6	US-10-467-657-8240
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15	77.5	5.0	449	6	US-10-485-517-272
16	77.5	5.0	467	7	US-11-156-084-115
17	77	5.0	274	6	US-10-467-657-2140
18	77	5.0	323	7	US-11-156-084-336
19	77	5.0	816	7	US-11-090-439-48
20	76.5	4.9	313	7	US-11-156-084-269
21	76.5	4.9	412	7	US-11-093-808-10
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41	75	4.8	984	7	US-11-055-822-594	Sequence 594, App
42	75	4.8	1225	7	US-11-053-100-50	Sequence 50, Appli
43	74.5	4.8	354	6	US-10-467-657-2224	Sequence 2224, Ap
44	74	4.8	306	7	US-11-156-084-342	Sequence 342, App
45	74	4.8	368	6	US-10-793-626-742	Sequence 742, App

ALIGNMENTS

RESULT 1
US-11-156-084-26
; Sequence 26, Application US/11156084
; Publication No. US20060010515A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology LLC
; TITLE OF INVENTION: Controlled expression of cytokinin biosynthetic genes leads to
; FILE REFERENCE: (38-21)
; CURRENT APPLICATION NUMBER: US/11/156,084
; CURRENT FILING DATE: 2005-06-17
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-11-156-084-26

Query Match 7.2%; Score 111; DB 7; Length 466;
Best Local Similarity 23.2%; Pred. No. 0.0031;
Matches 69; Conservative 45; Mismatches 90; Indels 90; Gaps 16;

QY	69	YRSPVLQYIEIQHKIETWREIYLOGCFKPLVISPNDSLFEAV-----YTLIKN	119
DB	120	YTIQAVSVKFLDDAAEDT-----ECCADVASVVDQDMVSVFGRDDLHSHGYELKE	173
QY	120	RIHRLPVLDPVSNVHLTHKLLKFLHFGSLLRPSFLY--RTIQDLG-IGTFR-DL	175
DB	174	-----LDPVAANRHPNNHNRKINQYLSLHASRGVLPKLYQCKTAENWGCINASRPDY	226
QY	176	AVV-----LETAPILTALDIFVDRRVSAIPVNVCEGVVGLY-----S	213
DB	227	CLICMDAETA-----VLDRVVEQVRDAMDAGLDEVYDIYKPGADYTRGLRQSIGVREFE	282
QY	214	RFQVHILAAQQTNYHL-----DMSVGEALRQRTLCLEGVLSGOPHES-----LGEVIDRI	263
DB	283	DFLKIHIL-SETCAGHLTSLSDNDKVMKENLRK-----ILNFPKDDKLRLMLEEADRV	334
QY	264	-----ARQVHRLVIV-----DETQHLGLGVLSLSILQALVLSPA	298
DB	335	KLNTRLLRRQRKRRVSRLETVFGWNIHYIDATEYILS--KSEESWNAQVVKPA	385

RESULT 2
US-11-156-084-33
; Sequence 33, Application US/11156084
; Publication No. US20060010515A1


```

; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology LLC
; TITLE OF INVENTION: Controlled expression of cytokinin biosynthetic genes leads to
; TITLE OF INVENTION: agronomically interesting phenotypes
; FILE REFERENCES: (38-21)
; CURRENT APPLICATION NUMBER: US/11/156,084
; CURRENT FILING DATE: 2005-06-17
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-11-156-084-33

```

Query Match	7.2%;	Score 111;	DB 7;	Length 466;
Best Local Similarity	23.2%;	Pred. No. 0.0031;		
Matches	68;	Conservative	45;	Mismatches 90;
				Indels 90;
				Gaps 16;
Qy	69	YRSPVLQVIEIEQHKIETWREIYLOGCFKPLVSI	SPNDSLFEAV-----	YTLIKN 119
Db	120	YIIQAVVSKFLDDDAEDT-----	EECCADVASVDDQDMVVESVGRKDLLSHGYELLKE	173
Qy	120	RIHRLPVLDPVSGNVLIHLTKRLKLLKHLFGSL	LPPEFLY--RTTQDLG-IGTFP-DL	175
Db	174	-----LDPAANRIHPNNHRKINQVLSHASKV	LPSPKDIYOGKTAENMGCINASRPY	226
Qy	176	AVV---LETAPILTALBIFVDRRVSALPVVNECQ	VVGLY-----	S 213
Db	227	CLICMDAETA-----VLDRYVEQRVDMVDAG	LLDEVDIYKPGADYTRGLRQSGVREFE	282
Qy	214	RFVDIHLAAQTYNHL-----DMSVGEALRQ	RTCLLEGVLSQPHES---LGEVIDRI	263
Db	283	DFLKHL-SETCAGHLTSLNDDKVMKENLRK-----	ILNFFPKDKLRIMLEEARDRV	334
Qy	264	-----AREQVHRLVLV-----DETQHL	LGWVLSLDTLQALVSPA	298
Db	335	KLNTRLLRRKRVSLSETVFGNIIHVIDATEYILS	--KSEESWNAOVKPA	385

RESULT 3
 US-11-156-084-34
 ; Sequence 34, Application US/11156084
 ; Publication No. US20060010515A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Monsanto Technology LLC
 ; TITLE OF INVENTION: Controlled expression of cytokinin biosynthetic genes leads to
 ; TITLE OF INVENTION: agronomically interesting phenotypes
 ; FILE REFERENCE: (38-21)
 ; CURRENT APPLICATION NUMBER: US/11/156,084
 ; CURRENT FILING DATE: 2005-06-17
 ; NUMBER OF SEQ ID NOS: 364
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 34
 ; LENGTH: 494
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 ; US-11-156-084-34

Query Match	7.2%	Score 111;	DB 7;	Length 494;
Best Local Similarity	23.2%;	Pred. No. 0.0034;		
Matches 68;	Conservative 45;	Mismatches 90;	Indels 90;	Gaps 16;
Qy	69	YYSRPLVQVRIEQHKIETWREIYLOGCFKPLVSI SPNDSLFEAV-----YTI LKN 119		
Db	120	YYIQAVSVKFLDDAAEDT-----EECADVASVVDQDMVVESVFGRRDLSHGVELLKE 173		
Qy	120	RIHRLPVLDPVSGNVLLHILTKRLKLFHIFGSLLPSPFLY--RTQDILG-IGTFR-DL 175		
Db	174	-----LDPVAARIIPNNHKKVINYLSHASRGVLPFSKLYOGKTAENWGCINASRPDY 226		
Qy	176	AVV---LETAPILTALDIFVDRRRYSALPVVNECCQVWGLY-----S- 213		

Db	227	CLICMDAETA-----VLDRYVEQRVDAMVDAGLLDEVDYIYKPGADYTRGLRQSIGVREFE	282
Qy	214	RFDVIIHLAAQTYNHL-----DMSVGRLAQRTCLGVLSCQPHES-----LGEVIDRI	263
Db	283	DFLKIHL-SETCAGHLTSLSDDKVMKNLEK-----ILNFPKDDKULRIMLEEADRV	334
Qy	264	-----AREQVRLVLV-----DETQHLGLVGVSLSDIIQALVLSPA	298
Db	335	KLNTERRLLRRQKRVSLSETVFGNNIHYIDATEYILS--KGESWNAQVVKPA	385

```

RESULT 4
US-10-467-657-5006
; Sequence 5006, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCES:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 5006
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5006

```

Query Match	6.9%;	Score 107.5;	DB 6;	Length 498;
Best Local Similarity	26.3%;	Pred. No. 0.0074;		
Matches 36;	Conservative 31;	Mismatches 57;	Indels 13;	Gaps 4;
Qy	170	GTFFDLAVLETA	DILTDALDIFVD--RRVSALPVVNECGVGVGLYSRFDVTHLAAQOYT	N 227
Db	102	GVWKDPVTVA	PTTLIREVLEMRQRKRMGLPPV--ENGKVVGI	VTNRDL- 154
Qy	228	HLDMVGSEALR	QRTLCLGVLSCOPHSEGLVIDRIAREQVHRVLVLYD	ETQHLGVLVSL 287
Db	155	RVDLPVSAIM	TPR---ERLVTPEGTSIDEARELMHTYKVERVLVNLK	EXDELKGLITIK 210
Qy	288	DILQALVLS	PAGIDALG 304	
Db	211	DILKTTTFP	NANKDSEG 227	

```

RESULT 5
US-11-156-084-35
; Sequence 35, Application US/11156084
; Publication No. US20060010515A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology LLC
; TITLE OF INVENTION: Controlled expression
; FILE REFERENCE: (38-21)
; CURRENT APPLICATION NUMBER: US/11/156, 084
; CURRENT FILING DATE: 2005-06-17
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-11-156-084-35

```

APPLICANT: Monsanto Technology LLC
TITLE OF INVENTION: Controlled expression of cytokinin biosynthetic genes leads to agronomically interesting phenotypes

Matches	68;	Conservative	45;	Mismatches	90;	Indels	100;	Gaps	16;
Qy	69	YYSRLPQYIYBIEQKHTREIYLQGCFLPVLSIPNSDSLFEAV-----YTLIKN	119						
Db	105	YIQAIVSKFLDDAAEDT-----EBCADVASVVDQDMVVESVFGRDDLSHGVELLKE	158						
Qy	120	RIHRLPVLDPVSGNVLHILTHKRLKLFHIFGSLLPSPSFLYR-----TIQDL	167						
Db	159	-----LDPVAANRIHPNNHNRKINQVLSLHASRGVLPKLYQGKTAEDVSFFLTSRQNW	211						
Qy	168	G-ICTFR-DLAVV---LETAPILLTALIDIFVDRRVSALPVNVCCQGVLY-----	212						
Db	212	GCINASRFDYCLICMDAETA-----VLDRYVEQRVDAMVDAGILLDEVYDIYKPGADYTRGL	267						
Qy	213	-----SRFDVTHLAAQOTYNHL-----DMSVGEALRQRTLCEGLVSLSCQPHES--	255						
Db	268	RQSIGVREFEDFLKIHL-SETCAGHLISLSDNDKVMKENLRK-----ILNFPKDKLR	319						
Qy	256	--LGEVIDRI-----AREQVHRLVLV-----DTEOHLGLGVLSLDTLQALVL	295						
Db	320	IMLEEADRVKLNTRLLRRQKRVRSLTEVFGWNHIVIDATEYILS--KSEESMNAQVV	377						
Qy	296	SPA	298						
Db	378	KPA	380						

```

RESULT 6
US-11-156-084-36
; Sequence 36, Application US/11156084
; Publication No. US20060010515A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology LLC
; TITLE OF INVENTION: Controlled expression of cytokinin biosynthetic genes leads to
; TITLE OF INVENTION: agronomically interesting phenotypes
; FILE REFERENCE: (38-21)
; CURRENT APPLICATION NUMBER: US/11/156,084
; CURRENT FILING DATE: 2005-06-17
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-11-156-084-36

```

Query Match	6.5%;	Score 100.5;	DB 7;	Length 495;
Best Local Similarity	21.8%;	Pred. No. 0.035;		
Matches	69;	Conservative	47;	Mismatches 93;
			Indels 107;	Gaps 16;
Qy	63	ILVLHYRSPLOQIYIEQHKEHTWEIYLOQCFKLVSISPNDLSFEAV-----	113	
Db	113	VLVGTHYIYQVWSKFLDDAAEDT-----ECCADVASVQDDMVVSVQDDMVVES	166	
Qy	114	-----YTLTKNIHRLPVLDPVSGNVLHLTHKRLKFLHIFGSLLRPSFLY--	161	
Db	167	VFGRDDLSHCYELLKE-----LDPVAANHHPNNHKKINQVLSLHASRGVLPFKLYQG	219	
Qy	162	RTTQDLG-IGTFR-DIAVW--LETAPILFALDIFVDRRVSALPVWNECQVGLY----	212	
Db	220	KTAENMGGINASRFDYCLICWAETA-----VLDRYVEQRVDAMDVAGLLDEVYDIYKPGA	275	
Qy	213	-----SREFDVTHLAAQTYNHL-----DMSVGENLRQRTLCLEGVLSCQ	251	
Db	276	DYTRGLRQSTGVREFEDFLKIHL-SETCAGHLTSLSNDDKVMKENLRK-----	327	
Qy	252	PHES-----LGEVDRI-----AREQVHRLVLV-----DETQHLIG	282	
Db	328	KDDKLRIWLEAADRVKLTNLRLLRQKRRVSRLLKRRVSRLETVFGWNIHYDATEYILS	387	
Qy	283	VWLSLDILQALVLSPA	298	
Db	388	--KSEESWNAOVKPA	401	

RESULT 7
 US-11-156-084-230
 ; Sequence 230, Application US/11156084
 ; Publication No. US20060010515A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Monsanto Technology LLC
 ; TITLE OF INVENTION: Controlled expression of cytokinin biosynthetic genes leads to
 ; FILE OF INVENTION: agronomically interesting phenotypes
 ; FILE REFERENCE: (38-21)
 ; CURRENT APPLICATION NUMBER: US/11/156,084
 ; CURRENT FILING DATE: 2005-06-17
 ; NUMBER OF SEQ ID NOS: 364
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 230
 ; LENGTH: 330
 ; TYPE: prt
 ; ORGANISM: Arabidopsis thaliana
 US-11-156-084-230

Query Match	6.4%; Score 99; DB 7; Length 330;
Best Local Similarity	23.9%; Pred. No. 0.028;
Matches	63; Conservative 40; Mismatches 77; Indels 84; Gaps 15;
Qy	98 KPLVSI ^{SP} NDLS ^{PEAV} -----YTLIKR ^{IR} HL ^{PV} DPVSGN ^{VH} IL TH KRLK ^{LP} L 148
Db	7 RSVVQMLQDMV ^{ES} VFGRDLSHG ^{YELL} KE-----LDPVAAN ^{IR} HPNNH ^{RK} ING ^{YLS} 59
Qy	149 IFGSL ^{LP} PRPS ^{FLY} --RTIQDLG--IGTFR--DLAVV---LETAPIL ^{TALD} IFD ^{RV} RSAL ^{PV} 201
Db	60 LHASRGVL ^{PS} KL ^{YQ} GKTAEN ^{WG} CINAS ^{RF} YCI ^{MD} AE ^{TA} -----VLDRV ^{YE} Q ^{RV} ADAM ^{VD} 115
Qy	202 VNECGOV ^{GLY} -----SRFDV ^{HL} AAQ ^{TYN} HL-----DMS ^{VGEA} 236
Db	116 AGLLDEV ^{YD} YIK ^{PGAD} YTRGL ^{ROS} IGV ^{REF} FL ^{KIHL} --SETCAG ^{HT} TS ^{SNDD} KV ^{MKN} 174
Qy	237 LRQ ^{TL} CLEGL ^{VSC} OP ^{HS} -----LGEVID ^{RI} -----AREQ ^{VH} RL ^{VLV} ----- 274
Db	175 LRK-----ILN ^{FPK} DD ^{KL} RI ^{MLEE} AD ^{RV} KL ^{NTR} ELL ^{RQ} K ^{RV} SR ^{LET} V ^{FCW} NI ^{THY} 227
Qy	275 DETO ^{HL} LG ^{VVS} LD ^{ILQAL} VL ^{SPA} 298
Db	228 DAT ^{EY} IL ^S --KS ^{ES} WNA ^{OV} V ^{KEA} 249

```

RESULT 8
US-10-793-626-2308
; Sequence 2308, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2308
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2308

```

Query Match	5.8%;	Score 89.5;	DB 6;	Length 488;
Best Local Similarity	22.3%;	Pred. No. 0.4;		
Matches 71;	Conservative 59;	Mismatches 122;	Indels 67;	Gaps 15;


```
US-11-055-822-948
; Sequence 948, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; FILE REFERENCE: BGI-121CPN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 948
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-948

Query Match          5.5%; Score 85.5; DB 7; Length 158;
Best Local Similarity 24.1%; Pred. No. 0.2;
Matches 34; Conservative 29; Mismatches 57; Indels 21; Gaps 5;

QY 153 LLPRPSLYTIDGLGTRDLAVLETPILTALDIFVDRVSALPVVNECGVGL- 211
Db 29 LLPDASDVVPSEVDTSTQLTRNRL-----NTPILSA-----AMDTVTARMAGMA 75
QY 212 -YSRFDVIH--LAAQQTYNHLDMSVGBALRQRTLCLEGVLSQPHESLGEVIDRIAREQV 268
Db 76 RHGGIGVLRHNLISIQEQAENVEL-----VKSESQWTDPTCTPDMISIQEVDLCAFR 131
QY 269 HRLVLVDETOHLGWSLSDI 289
Db 132 SGLPVVDDEAGKLVGICTNRDM 152

RESULT 12
US-10-467-657-8240
; Sequence 8240, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11

US-11-055-822-948
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8240
; LENGTH: 554
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8240

Query Match          5.5%; Score 85.5; DB 6; Length 554;
Best Local Similarity 25.5%; Pred. No. 1.2;
Matches 47; Conservative 26; Mismatches 62; Indels 49; Gaps 11;

QY 2 RFMQHTCYDAMATSSKLVIKKAFFALVANGVRAAPLWDSKKQSFVGMILTID 61
Db 251 RYAIRFCYRRRLCNKKISVFQIIFE-TLAFFSIVETPI-----DFLRGT---VRIAD 300
QY 62 -----FILVLH---RYRSPVLQIYEIEQ-----HKIETWREIYLOGCCKP 99
Db 301 HKTVRLHPGHPHILIKHITARVRCNPVALFAEVPNLLLVIRDIPVPRQIYLHLITP 360
QY 100 ---LVSISPNDSLFEAVYTLIKNRIHRLP-----VLDPVSGNVLHILTHKRLKFL 147
Db 361 EAMLINIFPD---FPAP-RRIKRTVRLNPNPISCRFIIFPVSRSAVHIY-RKRTIVPI 415
QY 148 HIFG 151
Db 416 QIFG 419

RESULT 13
US-10-873-528-64
; Sequence 64, Application US/10873528
; Publication No. US20050276814A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics Limited
; APPLICANT: Gilbert, Christophe FG
; APPLICANT: Hansbro, Philip M
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21129W0
; CURRENT APPLICATION NUMBER: US/10/873,528
; CURRENT FILING DATE: 2004-06-23
; PRIOR APPLICATION NUMBER: US/09/769,787
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: GB 9816337.1
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: US 60/125164
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 64
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-873-528-64

Query Match          5.2%; Score 80.5; DB 6; Length 319;
Best Local Similarity 21.4%; Pred. No. 1.7;
Matches 34; Conservative 28; Mismatches 50; Indels 47; Gaps 5;

QY 101 VSISPNDSLFE-----AVYTLIKNRIHRLPVLDPVSGNVLHILTHKRLKFLHIFGSLP 155
Db 20 IBITPSANTEIAPPDGIQOVLSNLLKL-VDPNV--NALLTANYIRILSWAVIFGIAMR 76
QY 156 RPS-----FLYRIQDLGIGTFRDLAVLE----- 180
Db 77 EAKNSQELLKTIADVTSKIVEIINLAPFGILGIVFKTISDKGVGSLANYIGILLVLT 136
QY 181 ----TAPILTALDIFVDRVSALPVVNECGVGLYSRF 215
Db 137 TMLFVAPVNVPLIAFFFMRRNPYPVPLVWNCURVSGVTAF 175
```

RESULT 14

US-11-082-389-78
 ; Sequence 78, Application US/11082389
 ; Publication No. US20050244935A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pompejus, Markus
 ; APPLICANT: Kroger, Burkhard
 ; APPLICANT: Schroder, Hartwig
 ; APPLICANT: Zelder, Oskar
 ; APPLICANT: Haberhauser, Gregor
 ; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
 ; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
 ; TITLE OF INVENTION: TRANSPORT
 ; FILE REFERENCE: BGI-131CPCN
 ; CURRENT APPLICATION NUMBER: US/11/082,389
 ; CURRENT FILING DATE: 2005-03-16
 ; PRIOR APPLICATION NUMBER: US 09/603024
 ; PRIOR FILING DATE: 2000-06-23
 ; PRIOR APPLICATION NUMBER: US 60/141031
 ; PRIOR FILING DATE: 1999-06-25
 ; PRIOR APPLICATION NUMBER: US 60/143262
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: US 60/151281
 ; PRIOR FILING DATE: 1999-08-27
 ; PRIOR APPLICATION NUMBER: DE 19930487.4
 ; PRIOR FILING DATE: 1999-07-01
 ; PRIOR APPLICATION NUMBER: DE 19930489.0
 ; PRIOR FILING DATE: 1999-07-01
 ; PRIOR APPLICATION NUMBER: DE 19931549.3
 ; PRIOR FILING DATE: 1999-07-08
 ; PRIOR APPLICATION NUMBER: DE 19931550.7
 ; PRIOR FILING DATE: 1999-07-08
 ; PRIOR APPLICATION NUMBER: DE 19932134.5
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: DE 19941379.7
 ; PRIOR FILING DATE: 1999-08-31
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 446
 ; SEQ ID NO 78
 ; LENGTH: 564
 ; TYPE: PRT
 ; ORGANISM: Corynebacterium glutamicum

US-11-082-389-78
 Query Match 5.1%; Score 79; DB 7; Length 564;
 Best Local Similarity 23.9%; Pred. No. 5.1;
 Matches 48; Conservative 31; Mismatches 54; Indels 68; Gaps 11;
 Qy 142 RLKFLHIF-----GSLLP-----PSFLYRTIQLG--IGTFEDL 175
 Db 306 RLRSFVHLRLRSMGYFTMSGRIMTRMTDIDNLSFLQSLAQTVVSVGLIGVVTML 365
 Qy 176 A-----VVLETAPILTALDIFVDRRSALPVVNECGQVGLYSRFDVHLAAQOTYN 227
 Db 366 AITDAQALVALSVVPIIIVTL-IFRAIS-----SR---LYTASREQAS 406
 Qy 228 HLDMSVGPALRQRTLCLGVLSQPHESLGEVIDRIA--REOVHRLVLVDQTO---HLLG 282
 Db 407 QVNAVPHES-----IAGLRTAQHMRMEDQVFDNYAGEAEFRRLRVKVSQTATAIYPPG 459
 Qy 283 VVLSLDILOALVLSFAGIDAL 303
 Db 460 LGALSEIAQALVL---GFGAL 477

RESULT 15

US-10-485-517-272
 ; Sequence 272, Application US/10485517
 ; Publication No. US20050256299A1
 ; GENERAL INFORMATION:
 ; APPLICANT: University of Sheffield
 ; APPLICANT: Biosynexus Incorporated

APPLICANT: Foster, Simon
 APPLICANT: Mond, James
 TITLE OF INVENTION: Antigenic Polypeptides
 FILE REFERENCE: F100629WO
 CURRENT APPLICATION NUMBER: US/10/485,517
 CURRENT FILING DATE: 2004-02-02
 PRIOR APPLICATION NUMBER: GB 0118825.9
 PRIOR FILING DATE: 2001-08-02
 PRIOR APPLICATION NUMBER: GB 0200349.9
 PRIOR FILING DATE: 2002-01-09
 NUMBER OF SEQ ID NOS: 424
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 272
 LENGTH: 449
 TYPE: PRT
 ORGANISM: Staphylococcus aureus
 US-10-485-517-272
 Query Match 5.0%; Score 77.5; DB 6; Length 449;
 Best Local Similarity 18.8%; Pred. No. 5.2;
 Matches 46; Conservative 46; Mismatches 82; Indels 71; Gaps 9;
 Qy 79 EIRQHKIETWREIYLQCFK-----PLVSI SPNDSLFEAVVTLKNRIHRL 124
 Db 198 EINQTEL-----AYMQNIFSDERHAKDIMVPRQTOMITLNEPFPNVDLLETIKHQFTY 252
 Qy 125 PVLDPVSGNVHLTHKRLKELHIFGSLPR9SFLYRTIQLDGLGTF-RDLAVVLETP 183
 Db 253 PITD--DGDKDHKGFINVKEFLTEYAS-----CKTIK---IANYIHLPWISVTR 299
 Qy 184 ILTALDIFVDRRSALPVVNECGQVGLYSRFDVHLAAQOTYNHLDMSVGEALRQRTL 243
 Db 300 ISDALIRMQREHVMSLIIDEYGGTAGILTMDIL----- 334
 Qy 244 LEGVLSQPHESLGEVIDRIAQOVHRLVLD-ETQHLGVVSLSDILOALVL---SPAG 299
 Db 335 -----BEIVGEIRDEFDDDEVNDIVKIDNKTFQVNGRVLDDLTTEFGIEFDDSED 385
 Qy 300 IDALG 304
 Db 386 IDTIG 390
 Search completed: January 24, 2006, 22:31:43
 Job time : 14.485 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 24, 2006, 22:04:33 ; Search time 25.3836 Seconds
(without alignments)
993.400 Million cell updates/sec

Title: US-10-070-794A-4
Perfect score: 1551
Sequence: 1 MRFMQHCTCDMATSSKLV.....LSDLQALVLSGADALGA 305

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Issued Patents AA:*
- 1: /cgn2_6/ptodata/1/iaa/5_COMB.pap.*
 - 2: /cgn2_6/ptodata/1/iaa/6_COMB.pap.*
 - 3: /cgn2_6/ptodata/1/iaa/H_COMB.pap.*
 - 4: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pap.*
 - 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pap.*
 - 6: /cgn2_6/ptodata/1/iaa/backfile1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1507	97.2	464	2	US-09-950-022A-2
2	1507	97.2	464	2	US-09-950-022A-4
3	1507	97.2	464	2	US-09-950-022A-6
4	1506	97.1	464	2	US-09-950-022A-8
5	1503	96.9	464	2	US-09-950-022A-10
6	1064	68.6	328	1	US-08-878-989-7
7	1064	68.6	328	2	US-09-272-796-7
8	1064	68.6	413	2	US-09-949-016-8261
9	1009	65.1	331	1	US-08-878-989-21
10	1009	65.1	331	2	US-09-101-146-64
11	1009	65.1	331	2	US-09-272-796-21
12	1009	65.1	331	2	US-09-538-092-1211
13	1009	65.1	336	2	US-09-949-016-10881
14	1007	64.9	330	2	US-09-359-161-6
15	457	29.5	322	2	US-09-359-161-7
16	457	29.5	322	2	US-09-538-092-297
17	304	19.6	101	2	US-09-513-999C-5736
18	252.5	16.3	254	2	US-09-248-796A-18872
19	214	13.8	379	2	US-09-359-161-5
20	196.5	12.7	629	2	US-09-248-796A-14535
21	190	12.3	373	2	US-09-359-161-3
22	104.5	6.7	375	2	US-09-328-352-6078
23	99.5	6.4	490	2	US-09-252-991A-30355
24	98.5	6.4	375	2	US-09-634-238-260
25	97.5	6.3	510	2	US-09-489-039A-11778
26	97	6.3	622	2	US-09-605-703B-2098
27	96.5	6.2	481	2	US-09-252-991A-31708

ALIGNMENTS

RESULT 1

US-09-950-022A-2
; Sequence 2, Application US/09950022A

; Patent No. 6919177

; GENERAL INFORMATION:

; APPLICANT: Rothschild, Max

; APPLICANT: Ciobanu, Dan

; APPLICANT: Malek, Massoud

; APPLICANT: Plastow, Graham

; TITLE OF INVENTION: No. 6919177el PRKAG3 Alleles and Use fo the Same as Genetic Mark

; TITLE OF INVENTION: Reproductive

; TITLE OF INVENTION: and Meat Quality Traits

; FILE REFERENCE: P04668US3

; CURRENT APPLICATION NUMBER: US/09/950, 022A

; PRIOR FILING DATE: 2001-09-10

; PRIOR APPLICATION NUMBER: 60/231045

; PRIOR FILING DATE: 2000-09-08

; PRIOR APPLICATION NUMBER: 60/260,239

; PRIOR FILING DATE: 2001-01-08

; PRIOR APPLICATION NUMBER: 60/299,111

; PRIOR FILING DATE: 2001-06-18

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2

; LENGTH: 464

; TYPE: PRT

; ORGANISM: Sus scrofa

US-09-950-022A-2

Query Match 97.2%; Score 1507; DB 2; Length 464;

Best Local Similarity 97.0%; Pred. No. 1.1e-166;

Matches 296; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY	1	MRFMQHCTCDMATSSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMLTIT	60
DB	160	MRFMQHCTCDMATSSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMLTIT	219
QY	61	DFILVLYRSPVQIYEIQHKIETWREIYLGQCFKPLVISPNDLSFEAVYTLKNR	120
DB	220	DFILVLYRSPVQIYEIEHKIETWREIYLGQCFKPLVISPNDLSFEAVYTLKNR	279
QY	121	IHRLPVLDPVSGNVLHILTHKLLKELHFGSLPRPSFLYRTIQDLGIGTFDRLAVLE	180
DB	280	IHRLPVLDPVSGAVLHILTHKLLKELHFGTLPRPSFLYRTIQDLGIGTFDRLAVLE	339
QY	181	TAPILTALDIFVDRRYSALPVNCCQVGLYSRFDVIHLAAQOQTYNHLDMVGEALRQR	240
DB	340	TAPILTALDIFVDRRYSALPVNCCQVGLYSRFDVIHLAAQOQTYNHLDMVGEALRQR	399
QY	241	TLCLEGLVSCQPHEISGEVIDRIAREQVHRLVLVDETHQLLGVVLSLSDILQALVLPAGI	300

Db 400 TLLCEGLVSCQPHETLGEVIDRIVREQVHRLVLDVDETHLLGVVSLDILQALVLSGAGI 459
Qy 301 DALGA 305
Db 460 DALGA 464

RESULT 2
US-09-950-022A-4
; Sequence 4, Application US/09950022A
; Patent No. 6919177
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: No. 6919177el PRKAG3 Alleles and Use fo the Same as Genetic Mark
; TITLE OF INVENTION: Reproductive
; TITLE OF INVENTION: and Meat Quality Traits
; FILE REFERENCE: P04668US3
; CURRENT APPLICATION NUMBER: US/09/950,022A
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-950-022A-4

Query Match 97.2%; Score 1507; DB 2; Length 464;
Best Local Similarity 97.0%; Pred. No. 1.le-166;
Matches 296; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
Qy 1 MRFMOEHTCYDAMATSSKLVIPTMTLEIKKAPFALVANGVRAAPLWDSKKQSFVGMILTIT 60
Db 160 MHFMOEHTCYDAMATSSKLVIPTMTLEIKKAPFALVANGVRAAPLWDSKKQSFVGMILTIT 219
Qy 61 DFILVLRHYRSPVQIYEIEBQHKIETWREIYLOGCFKPLVSI SPNDSLFEAVVTLIKNR 120
Db 220 DFILVLRHYRSPVQIYEIEBQHKIETWREIYLOGCFKPLVSI SPNDSLFEAVVTLIKNR 279
Qy 121 IHRPLVLDPVSGNVLHILTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 180
Db 280 IHRPLVLDPVSGNVLHILTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 339
Qy 181 TAPILTALDIFVDRVRSALPVVNECGVGLYSRFDVIHLAAQOTYNNHLDMSVGEALRQR 240
Db 340 TAPILTALDIFVDRVRSALPVVNETGVVGLYSRFDVIHLAAQOTYNNHLDMSVGEALRQR 399
Qy 241 TLLCEGLVSCQPHESLGEVIDRIAREQVHRLVLDVDETHLLGVVSLDILQALVLSGAGI 300
Db 400 TLLCEGLVSCQPHETLGEVIDRIAREQVHRLVLDVDETHLLGVVSLDILQALVLSGAGI 459
Qy 301 DALGA 305
Db 460 DALGA 464

RESULT 3
US-09-950-022A-6
; Sequence 6, Application US/09950022A
; Patent No. 6919177
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan

; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: No. 6919177el PRKAG3 Alleles and Use fo the Same as Genetic Mark
; TITLE OF INVENTION: Reproductive
; TITLE OF INVENTION: and Meat Quality Traits
; FILE REFERENCE: P04668US3
; CURRENT APPLICATION NUMBER: US/09/950,022A
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-950-022A-6

Query Match 97.2%; Score 1507; DB 2; Length 464;
Best Local Similarity 97.0%; Pred. No. 1.le-166;
Matches 296; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
Qy 1 MRFMOEHTCYDAMATSSKLVIPTMTLEIKKAPFALVANGVRAAPLWDSKKQSFVGMILTIT 60
Db 160 MHFMOEHTCYDAMATSSKLVIPTMTLEIKKAPFALVANGVRAAPLWDSKKQSFVGMILTIT 219
Qy 61 DFILVLRHYRSPVQIYEIEBQHKIETWREIYLOGCFKPLVSI SPNDSLFEAVVTLIKNR 120
Db 220 DFILVLRHYRSPVQIYEIEBQHKIETWREIYLOGCFKPLVSI SPNDSLFEAVVTLIKNR 279
Qy 121 IHRPLVLDPVSGNVLHILTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 180
Db 280 IHRPLVLDPVSGNVLHILTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 339
Qy 181 TAPILTALDIFVDRVRSALPVVNECGVGLYSRFDVIHLAAQOTYNNHLDMSVGEALRQR 240
Db 340 TAPILTALDIFVDRVRSALPVVNETGVVGLYSRFDVIHLAAQOTYNNHLDMSVGEALRQR 399
Qy 241 TLLCEGLVSCQPHESLGEVIDRIAREQVHRLVLDVDETHLLGVVSLDILQALVLSGAGI 300
Db 400 TLLCEGLVSCQPHETLGEVIDRIAREQVHRLVLDVDETHLLGVVSLDILQALVLSGAGI 459
Qy 301 DALGA 305
Db 460 DALGA 464

RESULT 4
US-09-950-022A-8
; Sequence 8, Application US/09950022A
; Patent No. 6919177
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max
; APPLICANT: Ciobanu, Dan
; APPLICANT: Malek, Massoud
; APPLICANT: Plastow, Graham
; TITLE OF INVENTION: No. 6919177el PRKAG3 Alleles and Use fo the Same as Genetic Mark
; TITLE OF INVENTION: Reproductive
; TITLE OF INVENTION: and Meat Quality Traits
; FILE REFERENCE: P04668US3
; CURRENT APPLICATION NUMBER: US/09/950,022A
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231045
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/260,239
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/299,111
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 8

; LENGTH: 464

; TYPE: PR1

; ORGANISM: Sus scrofa

US-09-950-022A-8

Query Match 97.1%; Score 1506; DB 2; Length 464;

Best Local Similarity 96.7%; Pred. No. 1.5e-166;

Matches 295; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MRMOETCTVDAMATSKLVIFDTMLTKKAFKALVANGVRAAPLWDSKKQSFVGMLTIT 60

Db 160 MHFMQETCTVDAMATSKLVIFDTMLTKKAFKALVANGVRAAPLWDSKKQSFVGMLTIT 219

Qy 61 DFILVLRHYRSPVLQIYEIEHQKIEIETWREIYLGCGCFKPLVSPNDLSFPAVYTLIKNR 120

Db 220 DFILVLRHYRSPVLQIYEIEEHKIEIETWREIYLGCGCFKPLVSPNDLSFPAVYTLIKNR 279

Qy 121 IHRPLVLDPVSGNVHLTHKRLKFLHIFGSLPRPSFLYRTIQDGLGIGTFRDLAVVLE 180

Db 280 IHRPLVLDPVSGNVHLTHKRLKFLHIFGSLPRPSFLYRTIQDGLGIGTFRDLAVVLE 339

Qy 181 TAPILTALDIFVDRRVSALPVNVECGVGLYSRFDVIHLAAQOTYNHLDMSVGEALRQR 240

Db 340 TAPILTALDIFVDRRVSALPVNVECGVGLYSRFDVIHLAAQOTYNHLDMSVGEALRQR 399

Qy 241 TLCLEGVLSQPHESLGEVDIRARQVHRLVLDVETQHLGVVSLSDIILQALVLSPAGI 300

Db 400 TLCLEGVLSQPHETLGEVIDRIVREQVHRLVLDVETQHLGVVSLSDIILQALVLSPAGI 459

Qy 301 DALGA 305

Db 460 DALGA 464

RESULT 5

US-09-950-022A-10

; Sequence 10, Application US/09950022A

; Patent No. 6919177

; GENERAL INFORMATION:

; APPLICANT: Rothschild, Max

; APPLICANT: Ciobanu, Dan

; APPLICANT: Malek, Massoud

; APPLICANT: Plastow, Graham

; TITLE OF INVENTION: No. 6919177el PRKAG3 Alleles and Use fo the Same as Genetic Mark

; TITLE OF INVENTION: Reproductive

; FILE REFERENCE: P04668US3

; CURRENT FILING DATE: 2001-09-10

; PRIOR FILING DATE: 2001-09-10

; PRIOR FILING DATE: 2000-09-08

; PRIOR FILING DATE: 2000-09-08

; PRIOR FILING DATE: 2001-01-08

; PRIOR FILING DATE: 2001-06-18

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 10

; LENGTH: 464

; TYPE: PR1

; ORGANISM: Sus scrofa

US-09-950-022A-10

Query Match

Best Local Similarity 96.9%; Score 1503; DB 2; Length 464;

Matches 295; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MRMOETCTVDAMATSKLVIFDTMLTKKAFKALVANGVRAAPLWDSKKQSFVGMLTIT 60

Db 160 MHFMQETCTVDAMATSKLVIFDTMLTKKAFKALVANGVRAAPLWDSKKQSFVGMLTIT 219

Qy 61 DFILVLRHYRSPVLQIYEIEHQKIEIETWREIYLGCGCFKPLVSPNDLSFPAVYTLIKNR 120

Db 220 DFILVLRHYRSPVLQIYEIEEHKIEIETWREIYLGCGCFKPLVSPNDLSFPAVYTLIKNR 279

Qy 121 IHRPLVLDPVSGNVHLTHKRLKFLHIFGSLPRPSFLYRTIQDGLGIGTFRDLAVVLE 180

Db 280 IHRPLVLDPVSGNVHLTHKRLKFLHIFGSLPRPSFLYRTIQDGLGIGTFRDLAVVLE 339

Qy 181 TAPILTALDIFVDRRVSALPVNVECGVGLYSRFDVIHLAAQOTYNHLDMSVGEALRQR 240

Db 340 TAPILTALDIFVDRRVSALPVNVECGVGLYSRFDVIHLAAQOTYNHLDMSVGEALRQR 399

Qy 241 TLCLEGVLSQPHESLGEVDIRARQVHRLVLDVETQHLGVVSLSDIILQALVLSPAGI 300

Db 400 TLCLEGVLSQPHETLGEVIDRIVREQVHRLVLDVETQHLGVVSLSDIILQALVLSPAGI 459

Qy 301 DALGA 305

Db 460 DALGA 464

RESULT 6

US-08-878-989-7

; Sequence 7, Application US/08878989

; Patent No. 5885803

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Hillman, Jennifer L.

; APPLICANT: Corley, Neil C.

; APPLICANT: Guegler, Karl G.

; APPLICANT: Lal, Preeti

; APPLICANT: Goli, Surya K.

; APPLICANT: Shah, Purvi

; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN

; TITLE OF INVENTION: KINASES

; NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/878,989

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J J

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0321 US

; TELEPHONE: 415-855-0555

; TELEFAX: 415-845-4166

; TELEX:

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 328 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: PENITUT01

; CLONE: 1452972

US-08-878-989-7

Db 286 DTPIIKALNIPVERRISALPVDSESGKVDIYKFDVINLAAEKTYYNNLDITVTQALQHR 345
 Qy 241 TLCLEGVLSQCPHESLGEVIDRIAREQVHRLVLDVDETHLGLGVVSLSDILOALVLS 299
 Db 346 SQYEGVGVKNCKLILETIVDRIVRAEVRHLVVNEADSVIGIISLSDILOALVLS 404

RESULT 9

US-08-878-989-21
 ; Sequence 21, Application US/08878989
 ; Patent No. 5885803
 ; GENERAL INFORMATION:
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Corley, Neil C.
 ; APPLICANT: Guegler, Karl G.
 ; APPLICANT: Lal, Preeti
 ; APPLICANT: Goli, Surya K.
 ; APPLICANT: Shah, Purvi
 ; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
 ; TITLE OF INVENTION: KINASES
 ; NUMBER OF SEQUENCES: 21
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/878,989
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J J
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0321 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-0555
 ; TELEFAX: 415-845-4166
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 21:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 331 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: GenBank
 ; CLONE: 1335856
 ; US-08-878-989-21

Query Match 65.1%; Score 1009; DB 1; Length 331;
 Best Local Similarity 65.3%; Pred. No. 8e-109;
 Matches 192; Conservative 52; Mismatches 50; Indels 0; Gaps 0;
 Qy 3 FMOEHTCYDAMATSSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKQSFVGMILTIDF 62
 Db 32 FMKSHRCYDLIPTSSKLVVDFDTSLQVKKAFALVTNGVRAAPLWDSKQSFVGMILTIDF 91
 Qy 63 ILVLRHYRSPVQIYEIOHKIETWREIYLCQCFKPLVSI SPNDSLFEAVYTLIKNRH 122
 Db 92 INILHRYKSAVQIYELEBKETWREIYLCQSFPLVCISPNASLFDVAVSSLIKNKH 151

Qy 123 RLPVLDPVSGNVHLTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLETA 182
 Db 152 RLPVIDPESGNTLYILTHKRLKFLHIFTEFPKPFMSKSLBELQIGTYANIAMVRTTT 211
 Qy 183 PILTALDIFVDRVRSALPVVNECGVGVGLYSRSDVHLAAQQTYNHLDMSVGEALRQRTL 242
 Db 212 PVTVALGIFVQHRVSALPVVDEKRVVDIYKFDVINLAAEKTYYNNLDVSVTKALQHRSH 271
 Qy 243 CLEGVLSQCPHESLGEVIDRIAREQVHRLVLDVDETHLGLGVVSLSDILOALVLS 296
 Db 272 YFEGVLKCYLHETLEIINRLVEAEVRHLVVNDVVKGVLSLSDILOALVLT 325

RESULT 10

US-09-101-146-64
 ; Sequence 64, Application US/09101146
 ; Patent No. 6124125
 ; GENERAL INFORMATION:
 ; APPLICANT: Dartmouth College, St. Vincents Institute of
 ; APPLICANT: Medical Research, Kemp et al.
 ; TITLE OF INVENTION: No. 6124125el AMP Activated Protein Kinase
 ; NUMBER OF SEQUENCES: 64
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Jane Massey Licata, Esq.
 ; STREET: 66 E. Main Street
 ; CITY: Marlton
 ; STATE: NJ
 ; COUNTRY: USA
 ; ZIP: 08053
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.5 INCH, 1.44 Mb STORAGE
 ; COMPUTER: IBM PC
 ; OPERATING SYSTEM: WINDOWS 95
 ; SOFTWARE: WORDPERFECT 6.0 FOR WINDOWS
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/101,146
 ; FILING DATE: October 7, 1998
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PN7450
 ; FILING DATE: 8 JAN 1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jane Massey Licata
 ; REGISTRATION NUMBER: 32,257
 ; REFERENCE/DOCKET NUMBER: DC-0050
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (856) 810-1515
 ; TELEFAX: (856) 810-1454
 ; INFORMATION FOR SEQ ID NO: 64:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 331
 ; TYPE: Amino Acid
 ; TOPOLOGY: Linear
 ; US-09-101-146-64

Query Match 65.1%; Score 1009; DB 2; Length 331;
 Best Local Similarity 65.3%; Pred. No. 8e-109;
 Matches 192; Conservative 52; Mismatches 50; Indels 0; Gaps 0;
 Qy 3 FMOEHTCYDAMATSSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKQSFVGMILTIDF 62
 Db 32 FMKSHRCYDLIPTSSKLVVDFDTSLQVKKAFALVTNGVRAAPLWDSKQSFVGMILTIDF 91
 Qy 63 ILVLRHYRSPVQIYEIOHKIETWREIYLCQCFKPLVSI SPNDSLFEAVYTLIKNRH 122
 Db 92 INILHRYKSAVQIYELEBKETWREIYLCQSFPLVCISPNASLFDVAVSSLIKNKH 151

Qy 123 RLPVLDPVSGNVHLTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLETA 182
 Db 152 RLPVIDPESGNTLYILTHKRLKFLHIFTEFPKPFMSKSLBELQIGTYANIAMVRTTT 211
 Qy 183 PILTALDIFVDRVRSALPVVNECGVGVGLYSRSDVHLAAQQTYNHLDMSVGEALRQRTL 242
 Db 212 PVTVALGIFVQHRVSALPVVDEKRVVDIYKFDVINLAAEKTYYNNLDVSVTKALQHRSH 271

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Db 212 PVYVALGIFVQHRVSALPVVDEKGRVVDIYKSDVINLAAEKTNNLNDVSVTKALQHRSH 271
Qy 243 CLEGVLSQCPHESLGEVIDRIAREQVHRLVLDVETQHLGLGVSLSDILOALVLS 296
Db 272 YFEGVLKCYLHETLETIINRLVEAEVHRLVVDVENDVVGKIGVSLSDILOALVLT 325

RESULT 11
US-09-272-796-21
; Sequence 21, Application US/09272796
; Patent No. 6207148
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl G.
; APPLICANT: Lal, Preeti
; APPLICANT: Goli, Surva K.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
; TITLE OF INVENTION: KINASES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/272,796
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/878,989
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0321 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 331 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1335856
US-09-272-796-21

Query Match 65.1%; Score 1009; DB 2; Length 331;
Best Local Similarity 65.3%; Pred. No. 8e-109;
Matches 192; Conservative 52; Mismatches 50; Indels 0; Gaps 0;

Qy 3 FMOEHTCYDAMATSSKLVIQFDTMLIKKAFVALVANGVRAAPLWDSKKQSFVGMLTITDF 62
Db 32 FMKSHRCYDLIPTSSKLVVFDTSLOVKKAFALVTVNGVRAAPLWDSKKQSFVGMLTITDF 91
Qy 63 ILVLHRYRSPVLQVIYEIQHKIETWREIYLQGCFKPLVSPNDSLSEAVYTLIKNRIH 122
Db 92 INILHRYYSALVQIYELEEHKIETWREIYLDQSFKPLVCISPNASLFDVAVSLIRNKIH 151
Qy 123 RLPVLDPVSGNVHLHILTHKRLKFLHFGSLPPSPFLYRTIQDLGIGTFDRLAVVLETA 182
Db 152 RLPVIDPESGNTLYLTHKRLKFLHFGSLPPSPFLYRTIQDLGIGTFDRLAVVLETA 211
Qy 183 PILTALDIFVDRRVVSALPVVNECGVGLYSRFDVIHLAAQOYTNHLDMSVGEALRQRTL 242
Db 212 PVYVALGIFVQHRVSALPVVDEKGRVVDIYKSDVINLAAEKTNNLNDVSVTKALQHRSH 271
Qy 243 CLEGVLSQCPHESLGEVIDRIAREQVHRLVLDVETQHLGLGVSLSDILOALVLS 296
Db 272 YFEGVLKCYLHETLETIINRLVEAEVHRLVVDVENDVVGKIGVSLSDILOALVLT 325

RESULT 12
US-09-538-092-1211
; Sequence 1211, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurapatSeqFormatter Version 0.9
; SEQ ID NO 1211
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number P54619
US-09-538-092-1211

Query Match 65.1%; Score 1009; DB 2; Length 331;
Best Local Similarity 65.3%; Pred. No. 8e-109;
Matches 192; Conservative 52; Mismatches 50; Indels 0; Gaps 0;

Qy 3 FMOEHTCYDAMATSSKLVIQFDTMLIKKAFVALVANGVRAAPLWDSKKQSFVGMLTITDF 62
Db 32 FMKSHRCYDLIPTSSKLVVFDTSLOVKKAFALVTVNGVRAAPLWDSKKQSFVGMLTITDF 91
Qy 63 ILVLHRYRSPVLQVIYEIQHKIETWREIYLQGCFKPLVSPNDSLSEAVYTLIKNRIH 122
Db 92 INILHRYYSALVQIYELEEHKIETWREIYLDQSFKPLVCISPNASLFDVAVSLIRNKIH 151
Qy 123 RLPVLDPVSGNVHLHILTHKRLKFLHFGSLPPSPFLYRTIQDLGIGTFDRLAVVLETA 182
Db 152 RLPVIDPESGNTLYLTHKRLKFLHFGSLPPSPFLYRTIQDLGIGTFDRLAVVLETA 211
Qy 183 PILTALDIFVDRRVVSALPVVNECGVGLYSRFDVIHLAAQOYTNHLDMSVGEALRQRTL 242
Db 212 PVYVALGIFVQHRVSALPVVDEKGRVVDIYKSDVINLAAEKTNNLNDVSVTKALQHRSH 271
Qy 243 CLEGVLSQCPHESLGEVIDRIAREQVHRLVLDVETQHLGLGVSLSDILOALVLS 296
Db 272 YFEGVLKCYLHETLETIINRLVEAEVHRLVVDVENDVVGKIGVSLSDILOALVLT 325

RESULT 13
US-09-949-016-10881
; Sequence 10881, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
```


Qy 286 LSDILQALVL 295
| | | | : : |
Db 310 LSDILKYILL 319

Search completed: January 24, 2006, 22:16:24
Job time : 26.3836 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 24, 2006, 22:01:17 ; Search time 90.0325 Seconds
(without alignments)
2390.094 Million cell updates/sec

Title: US-10-070-794A-4
Perfect score: 1551
Sequence: 1 MRFMQHCTCDMATSSKLV.....LSDIQLVLSPAGIDALGA 305

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1551	100.0	464	1 AAKG3_HUMAN	Q9ug19 homo sapien
2	1551	100.0	489	2 Q4QG8_HUMAN	Q4qg98 homo sapien
3	1551	100.0	489	2 Q4V779_HUMAN	Q4v779 homo sapien
4	1507	97.2	464	2 Q532T5_PIG	Q532t5 sus scrofa
5	1507	97.2	514	1 AAKG3_PIG	Q9mvp4 sus scrofa
6	1489	96.0	464	2 Q8C341_MOUSE	Q8c341 mus musculus
7	1489	96.0	489	2 Q8BGW7_MOUSE	Q8bgw7 m amp-activ
8	1478.5	95.3	465	2 Q4G3U3_BOVIN	Q4g3u3 bos taurus
9	1478.5	95.3	490	2 Q8WVK8_MOUSE	Q8wvk8 mus musculus
10	1408	90.8	447	2 Q6TEH8_HORSE	Q6teh8 equus caball
11	1376	88.7	440	2 Q6U7S1_HORSE	Q6u7s1 equus caball
12	1250	80.6	363	2 Q4JK38_CHICK	Q4jk38 gallus gall
13	1250	80.6	382	2 Q4JK39_CHICK	Q4jk39 gallus gall
14	1195	77.0	337	2 Q7ZYL2_XENILA	Q7zyl2 xenopus lae
15	1068	68.9	326	2 Q6V7V4_RAT	Q6v7v4 rattus norv
16	1068	68.9	326	2 Q6V7V5_MOUSE	Q6v7v5 mus musculus
17	1068	68.9	448	2 Q4QRB9_RAT	Q4qrb9 rattus norv
18	1067	68.8	413	2 Q8B1Q9_MOUSE	Q8b1q9 mus musculus
19	1067	68.8	566	2 Q91WG5_MOUSE	Q91wg5 mus musculus
20	1064	68.6	328	2 Q53Y07_HUMAN	Q53y07 homo sapien
21	1064	68.6	525	2 Q6NU10_HUMAN	Q6nu10 homo sapien
22	1064	68.6	569	1 AAKG2_HUMAN	Q9ug10 homo sapien
23	1063	68.5	328	2 Q5ZK07_CHICK	Q5zk07 gallus gall
24	1058	68.2	558	2 Q6PA60_XENILA	Q6pa60 xenopus lae
25	1056.5	68.1	343	2 Q4RVG2_TETNG	Q4rvg2 tetraodon n
26	1054	68.0	524	2 Q5R4S0_PONPY	Q5r4s0 pongo pygma
27	1036	66.8	297	2 Q4RTT1_TETNG	Q4rtt1 tetraodon n
28	1026	66.2	330	2 Q6PCS7_BRARE	Q6pcs7 brachydania
29	1015	65.4	323	2 Q4RXW4_TETNG	Q4rxw4 tetraodon n
30	1010	65.1	330	2 Q5PRE8_MOUSE	Q5pre8 mus musculus
31	1009	65.1	330	2 Q6X275_PIG	Q6x275 sus scrofa

32	1009	65.1	331	1 AAKG1_HUMAN	P54619 homo sapien
33	1008	65.0	333	2 Q4S1Z9_TETNG	Q4s1z9 tetraodon n
34	1007	64.9	330	1 AAKG1_RAT	P80385 rattus norv
35	1007	64.9	330	2 Q4QW6_RAT	Q4qw6 rattus norv
36	1005	64.8	330	1 AAKG1_BOVIN	P58108 bos taurus
37	1003	64.7	299	2 Q4RSP4_MACPA	Q4rsp4 macaca fasc
38	994.5	64.1	340	2 Q8N7V9_HUMAN	Q8n7v9 homo sapien
39	991	63.9	334	2 Q6GN94_XENILA	Q6gn94 xenopus lae
40	990	63.8	287	2 Q6U716_RAT	Q6u716 rattus norv
41	989	63.8	330	1 AAKG1_MOUSE	Q54950 mus musculus
42	946	61.0	329	2 Q4RY44_TETNG	Q4ry44 tetraodon n
43	899	58.0	267	2 Q8EM63_MOUSE	Q8em63 mus musculus
44	857	55.3	598	2 Q7PXX4_ANOGA	Q7pxk4 anopheles g
45	854	55.1	594	2 Q5BU45_AEDAE	Q5bu45 aedes aegy

ALIGNMENTS

RESULT 1
ID AAKG3_HUMAN STANDARD; PRT; 464 AA.
AC Q9UG19; Q9NEL1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE 5'-AMP-activated protein kinase, gamma-3 subunit (AMPK gamma-3 chain)
DE (AMPK gamma3).
GN Name-PRKAG3; Synonyms-AMPKG3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20164049; PubMed=10698692; DOI=10.1042/0264-6021:3460659;
RA Cheung P.C.F., Salt I.P., Davies S.P., Hardie D.G., Carling D.;
RT "Characterization of AMP-activated protein kinase gamma-subunit
RT isoforms and their role in AMP binding.";
RL Biochem. J. 346:659-669(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skeletal muscle;
RX MEDLINE=20280150; PubMed=10818001; DOI=10.1126/science.288.5469.1248;
RA Milan D., Jeon J.-T., Looft C., Amarger V., Robic A., Thelander M.,
RA Rogel-Gaillard C., Paul S., Iannuccelli N., Rask L., Ronne H.,
RA Lundstroem K., Reinsch N., Gellin J., Kalm E., Le Roy P., Chardon P.,
RA Andersson L.;
RT "A mutation in PRKAG3 associated with excess glycogen content in pig
RT skeletal muscle.";
RL Science 288:1248-1251(2000).
CC -!- FUNCTION: AMPK is responsible for the regulation of fatty acid
CC synthesis by phosphorylation of acetyl-CoA carboxylase. Also
CC regulates cholesterol synthesis via phosphorylation and
CC inactivation of hydroxymethylglutaryl-CoA reductase and hormone-
CC sensitive lipase. This is a regulatory subunit. It may play a role
CC in the regulation of energy metabolism in skeletal muscle.
CC -!- SUBUNIT: Heterotrimer of an alpha catalytic subunit, a beta and a
CC gamma non-catalytic regulatory subunits.
CC -!- TISSUE SPECIFICITY: Skeletal muscle, with weak expression in heart
CC and pancreas.
CC -!- SIMILARITY: Belongs to the 5'-AMP-activated protein kinase gamma
CC subunit family.
CC -!- SIMILARITY: Contains 4 CBS domains.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AJ249977; CAB65117.1; ALT_INIT; mRNA.


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DR EMBL; AF214519; AAF733987.1; -; mRNA.
DR Ensembl; ENSG00000115592; Homo sapiens.
DR HGNC; HGNC:9387; PRKAG3.
DR MIM; 604976; -.
DR GO; GO:0004679; F:AMP-activated protein kinase activity; TAS.
DR GO; GO:0007243; P:protein kinase cascade; TAS.
DR InterPro; IPR000644; CBS.
DR Pfam; PF00571; CBS; 2.
DR SMART; SM00116; CBS; 4.
KW CBS domain; Fatty acid biosynthesis; Lipid synthesis; Repeat.
FT DOMAIN 147 201 CBS 1.
FT DOMAIN 228 282 CBS 2.
FT DOMAIN 303 356 CBS 3.
FT DOMAIN 375 428 CBS 4.
FT CONFLICT 58 58 T -> A (in Ref. 1).
FT CONFLICT 163 164 MQ -> IE (in Ref. 1).
FT CONFLICT 398 398 Q -> K (in Ref. 1).
FT CONFLICT 461 464 ALGA -> PSGPEKI (in Ref. 1).
SQ SEQUENCE 464 AA; 53985C2C77003A63 CRC64;

Query Match 100.0%; Score 1551; DB 1; Length 464;
Best Local Similarity 100.0%; Pred. No. 1.3e-118;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRFQEHCTCDAMATSSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMLTIT 60
Db 160 MRFQEHCTCDAMATSSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMLTIT 219

Qy 61 DFILVLRHYRSPVLQIYEIQHKTETWREIYLGCCFKPLVISPNDLSFEAVYTLIKNR 120
Db 220 DFILVLRHYRSPVLQIYEIQHKTETWREIYLGCCFKPLVISPNDLSFEAVYTLIKNR 279

Qy 121 IHRPLVLPDPSGVNLHILTHKRLKFLHIFGSLPRPSFLYRTIQDGLGIGTFRDLAVVLE 180
Db 280 IHRPLVLPDPSGVNLHILTHKRLKFLHIFGSLPRPSFLYRTIQDGLGIGTFRDLAVVLE 339

Qy 181 TAPILTALDIFVDRRVSAIPVNECGQVGLYSRFDVIHLAAQOQTYNHLDSVGEALRQR 240
Db 340 TAPILTALDIFVDRRVSAIPVNECGQVGLYSRFDVIHLAAQOQTYNHLDSVGEALRQR 399

Qy 241 TLCLEGVLSQPHESLGEVIDRIAREQVHRLVLDVETQHLGLGVVSLSDILQALVLSAGI 300
Db 400 TLCLEGVLSQPHESLGEVIDRIAREQVHRLVLDVETQHLGLGVVSLSDILQALVLSAGI 459

Qy 301 DALGA 305
Db 460 DALGA 464

RESULT 2
Q4QQG8 HUMAN PRELIMINARY; PRT; 489 AA.
AC Q4QQG8
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE AMP-activated protein kinase, non-catalytic gamma-3 subunit.
GN Name=PRKAG3;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., Kernerman K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RG NIH MGC Project;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC098306; AAH98306.1; -; mRNA.
DR EMBL; BC098255; AAH98255.1; -; mRNA.
KW Kinase.
SQ SEQUENCE 489 AA; 54232 MW; A67D9DEAB76BF0C9 CRC64;

Query Match 100.0%; Score 1551; DB 2; Length 489;
Best Local Similarity 100.0%; Pred. No. 1.4e-118;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRFQEHCTCDAMATSSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMLTIT 60
Db 185 MRFQEHCTCDAMATSSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMLTIT 244

Qy 61 DFILVLRHYRSPVLQIYEIQHKTETWREIYLGCCFKPLVISPNDLSFEAVYTLIKNR 120
Db 245 DFILVLRHYRSPVLQIYEIQHKTETWREIYLGCCFKPLVISPNDLSFEAVYTLIKNR 304

Qy 121 IHRPLVLPDPSGVNLHILTHKRLKFLHIFGSLPRPSFLYRTIQDGLGIGTFRDLAVVLE 180
Db 305 IHRPLVLPDPSGVNLHILTHKRLKFLHIFGSLPRPSFLYRTIQDGLGIGTFRDLAVVLE 364

Qy 181 TAPILTALDIFVDRRVSAIPVNECGQVGLYSRFDVIHLAAQOQTYNHLDSVGEALRQR 240
Db 365 TAPILTALDIFVDRRVSAIPVNECGQVGLYSRFDVIHLAAQOQTYNHLDSVGEALRQR 424

Qy 241 TLCLEGVLSQPHESLGEVIDRIAREQVHRLVLDVETQHLGLGVVSLSDILQALVLSAGI 300
Db 425 TLCLEGVLSQPHESLGEVIDRIAREQVHRLVLDVETQHLGLGVVSLSDILQALVLSAGI 484

Qy 301 DALGA 305
Db 485 DALGA 489

RESULT 3
Q4V779 HUMAN PRELIMINARY; PRT; 489 AA.
AC Q4V779
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE AMP-activated protein kinase, non-catalytic gamma-3 subunit.
GN Name=PRKAG3;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J.J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E., Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=PCR rescued clones;
 RG NIH MGC Project;
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC098102; AAH98102.1; -; mRNA.
 DR EMBL; BC098277; AAH98277.1; -; mRNA.
 KW Kinase.
 SQ SEQUENCE 489 AA; 54258 MW; 0E93E2B5117B328D CRC64;
 Query Match 100.0%; Score 1551; DB 2; Length 489;
 Best Local Similarity 100.0%; Pred. No. 1.4e-118;
 Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRFMQSHCTCYDAMATSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMILTIT 60
 DB 185 MRFMQSHCTCYDAMATSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMILTIT 244
 QY 61 DFLVLHRYRSPVQVIEIQHETWREIYLGCCFKPLVSPNDLSLFEAVYTLIKNR 120
 DB 245 DFLVLHRYRSPVQVIEIQHETWREIYLGCCFKPLVSPNDLSLFEAVYTLIKNR 304
 QY 121 IHRPLVDPVSGNVHLTHKRLKFLHFGSLPRPSFLYRTIQDLGIGTFPRDLAVLVE 180
 DB 305 IHRPLVDPVSGNVHLTHKRLKFLHFGSLPRPSFLYRTIQDLGIGTFPRDLAVLVE 364
 QY 181 TAPILTALDIFVDRRVSALPVVNECCQVGLYSRFDVIHLAAQQTNNHLDMSVGEALRQR 240
 DB 365 TAPILTALDIFVDRRVSALPVVNECCQVGLYSRFDVIHLAAQQTNNHLDMSVGEALRQR 424
 QY 241 TLCLEGLVSCQPHESIGEVIDRIAREQVHRLVLVDETOHLLGVVSLDILQALVLSGAPI 300
 DB 425 TLCLEGLVSCQPHESIGEVIDRIAREQVHRLVLVDETOHLLGVVSLDILQALVLSGAPI 484
 QY 301 DALGA 305
 DB 485 DALGA 489
 RESULT 4
 ID Q53ZT5_PIG PRELIMINARY; PRT; 464 AA.
 AC Q53ZT5;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DE AMP-activated protein kinase gamma subunit.
 GN Name=PRKAG3;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
 OC Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RX PubMed=14970697; DOI=10.1159/000075743;
 RA Amarger V., Eriandsson R., Fieberg G., Jeon J.T., Andersson L.;
 RT "Comparative sequence analysis of the PRKAG3 region between human and pig: evolution of repetitive sequences and potential new exons.";
 RL Cytogenet. Genome Res. 102:163-172(2003).
 DR EMBL; AV264345; AAP12533.1; -; mRNA.
 KW Kinase.
 SQ SEQUENCE 464 AA; 51308 MW; 17638CB12A2BA9DF CRC64;
 Query Match 97.2%; Score 1507; DB 2; Length 464;
 Best Local Similarity 97.0%; Pred. No. 5.3e-115;
 Matches 296; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 QY 1 MRFMQSHCTCYDAMATSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMILTIT 60
 DB 160 MRFMQSHCTCYDAMATSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMILTIT 219
 QY 61 DFLVLHRYRSPVQVIEIQHETWREIYLGCCFKPLVSPNDLSLFEAVYTLIKNR 120
 DB 220 DFLVLHRYRSPVQVIEIQHETWREIYLGCCFKPLVSPNDLSLFEAVYTLIKNR 279
 QY 121 IHRPLVDPVSGNVHLTHKRLKFLHFGSLPRPSFLYRTIQDLGIGTFPRDLAVLVE 180
 DB 280 IHRPLVDPVSGNVHLTHKRLKFLHFGSLPRPSFLYRTIQDLGIGTFPRDLAVLVE 339
 QY 181 TAPILTALDIFVDRRVSALPVVNECCQVGLYSRFDVIHLAAQQTNNHLDMSVGEALRQR 240
 DB 340 TAPILTALDIFVDRRVSALPVVNECCQVGLYSRFDVIHLAAQQTNNHLDMSVGEALRQR 399
 QY 241 TLCLEGLVSCQPHESIGEVIDRIAREQVHRLVLVDETOHLLGVVSLDILQALVLSGAPI 300
 DB 400 TLCLEGLVSCQPHETIGLDRIVREQVHRLVLVDETOHLLGVVSLDILQALVLSGAPI 459
 QY 301 DALGA 305
 DB 460 DALGA 464
 RESULT 5
 ID AAKG3_PIG STANDARD; PRT; 514 AA.
 AC Q9WYP4; Q6WZ89;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE 5'-AMP-activated protein kinase, gamma-3 subunit (AMPK gamma-3 chain) (AMPK gamma3).
 DE (AMPK gamma3).
 GN Name=PRKAG3;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
 OC Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP NUCLEOTIDE SEQUENCE (ISOFORM 1), AND VARIANT RN(-) GLN-250.
 RC TISSUE=Skeletal muscle;
 RX MEDLINE=20280150; PubMed=10818001; DOI=10.1126/science.288.5469.1248;
 RA Milan D., Jeon J.-T., Looft C., Amarger V., Robic A., Thelander M., Rogel-Gaillard C., Paul S., Iannucelli N., Rask L., Ronne H., Lundstroem K., Reinsch N., Gellin J., Kalm E., Le Roy P., Chardon P., Andersson L.;
 RT "A mutation in PRKAG3 associated with excess glycogen content in pig skeletal muscle.";
 RL Science 288:1248-1251(2000).
 RN [2]
 RP NUCLEOTIDE SEQUENCE (ISOFORM 2).
 RC TISSUE=Skeletal muscle;
 RA Milan D., Jeon J.-T., Looft C., Amarger V., Robic A., Thelander M., Rogel-Gaillard C., Paul S., Gellin J., Lundstrom K., Reinsch N., Kalm E., Le Roy P., Chardon P., Andersson L.;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE (ISOFORM 1).

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RX PubMed=14970697; DOI=10.1159/000075743;
RA Amarger V., Erlandsson R., Pielberg G., Jeon J.T., Andersson L.;
RT "Comparative sequence analysis of the PRKAG3 region between human and
RT pig: evolution of repetitive sequences and potential new exons.";
RL Cytogenet. Genome Res. 102:163-172(2003).
CC -1- FUNCTION: AMPK is responsible for the regulation of fatty acid
CC synthesis by phosphorylation of acetyl-CoA carboxylase. Also
CC regulates cholesterol synthesis via phosphorylation and
CC inactivation of hydroxymethylglutaryl-CoA reductase and hormone-
CC sensitive lipase. This is a regulatory subunit. It may play a role
CC in the regulation of energy metabolism in skeletal muscle.
CC -1- SUBUNIT: Heterotrimer of an alpha catalytic subunit, a beta and a
CC gamma non-catalytic regulatory subunits.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=2;
CC IsoId=Q9MYP4-1; Sequence=Displayed;
CC Name=1;
CC IsoId=Q9MYP4-2; Sequence=VSP_008059;
CC -1- TISSUE SPECIFICITY: Muscle.
CC -1- DISEASE: Defects in PRKAG3 are the cause of the RN- phenotype
CC which is associated with excess glycogen content (about 70%) in
CC skeletal muscle. This mutation originated in the Hampshire breed
CC pigs and has beneficial effects on meat content but detrimental
CC effects on processing yield. Thus, this mutation is of
CC considerable economic significance in the pig breeding industry.
CC -1- SIMILARITY: Belongs to the 5'-AMP-activated protein kinase gamma
CC subunit family.
CC -1- SIMILARITY: Contains 4 CBS domains.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AF214520; AAF73988.2; -; mRNA.
CC EMBL; AF214521; AAF73989.1; -; Genomic DNA.
CC EMBL; AY263454; AAP14907.1; -; Genomic DNA.
CC InterPro; IPR000644; CBS.
CC Pfam; PF00571; CBS; 2.
CC Alternative splicing; CBS domain; Disease mutation;
CC Fatty acid biosynthesis; Lipid synthesis; Repeat.
CC FT DOMAIN 222 276 CBS 1.
CC FT DOMAIN 303 357 CBS 2.
CC FT DOMAIN 378 431 CBS 3.
CC FT DOMAIN 450 503 CBS 4.
CC FT VARSPLIC 1 50 Missing (in isoform 1).
CC FT VARIANT 250 250 R -> Q (in RN-).
CC FT CONFLICT 418 418 V -> E (in Ref. 3).
CC FT CONFLICT 441 441 N -> S (in Ref. 3).
CC SQ SEQUENCE 514 AA; 56790 MW; 8CE025FBBF93E4AE CRC64;

Query Match 97.2%; Score 1507; DB 1; Length 514;
Best Local Similarity 97.0%; Pred. No. 6e-115;
Matches 296; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MRFQHTCYDAMATSSKLVIFDTMLEIKKAFPAFFALVANGVRAAPLWDSKKQSFVGMLTIT 60
Db 210 MHFQHTCYDAMATSSKLVIFDTMLEIKKAFPAFFALVANGVRAAPLWDSKKQSFVGMLTIT 269

Qy 61 DFILVLHRYRSPVQIYEIEBHQKIETWREIYLOGCFKPLVSI SPNDSLFEAVYTLIKNR 120
Db 270 DFILVLHRYRSPVQIYEIEBHQKIETWREIYLOGCFKPLVSI SPNDSLFEAVYTLIKNR 329

Qy 121 IHRPLVLPDPSGNVLHILTHKRLKFLHIFGSLPRSPFLYRTIQDLGIGTFRDLAVVLE 180
Db 330 IHRPLVLPDPSGNVLHILTHKRLKFLHIFGSLPRSPFLYRTIQDLGIGTFRDLAVVLE 389

Qy 181 TAPILTALDIFVDRVSALPVVNECGVVGYSRFDVHIHAAQQTYNHLDMSVGEALRQR 240
Db 390 TAPILTALDIFVDRVSALPVVNECGVVGYSRFDVHIHAAQQTYNHLDMSVGEALRQR 449

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Qy 241 TLCLEGVLSQPHESLGEVIDRIAREQVHRLVLDVETQHLGVVSLDILQALVLSPAGI 300
Db 450 TLCLEGVLSQPHETIGEVIDRIAREQVHRLVLDVETQHLGVVSLDILQALVLSPAGI 509

Qy 301 DALGA 305
Db 510 DALGA 514

RESULT 6
Q8CJ41_MOUSE PRELIMINARY; PRT; 464 AA.
AC Q8CJ41_MOUSE PRELIMINARY; PRT; 464 AA.
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, last annotation update)
DE AMP-activated protein kinase gamma 3 subunit short form.
GN Name=Prkg3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE
RC STRAIN=BALB/c; TISSUE=Skeletal muscle;
RX PubMed=14512293; DOI=10.1152/ajpcell.00319.2003;
RA Yu H., Fujii N., Hirshman M.F., Pomerleau L.J.;
RT "Cloning and characterization of mouse 5'-AMP-activated protein kinase
RT gamma3 subunit.";
RL Am. J. Physiol. Cell Physiol. 286:C283-C292(2004).
DR EMBL; AF255501; AAM47138.1; -; mRNA.
DR MGI; MGI:1891343; Prkg3.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR InterPro; IPR000644; CBS.
DR Pfam; PF00571; CBS; 2.
DR SMART; SMO0116; CBS; 4.
KW Kinase.
SQ SEQUENCE 464 AA; 51116 MW; CEC324A5855C3F2E CRC64;

Query Match 96.0%; Score 1489; DB 2; Length 464;
Best Local Similarity 96.1%; Pred. No. 1.6e-113;
Matches 293; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MRFQHTCYDAMATSSKLVIFDTMLEIKKAFPAFFALVANGVRAAPLWDSKKQSFVGMLTIT 60
Db 160 MHFQHTCYDAMATSSKLVIFDTMLEIKKAFPAFFALVANGVRAAPLWDSKKQSFVGMLTIT 219

Qy 61 DFILVLHRYRSPVQIYEIEBHQKIETWREIYLOGCFKPLVSI SPNDSLFEAVYTLIKNR 120
Db 220 DFILVLHRYRSPVQIYEIEBHQKIETWREIYLOGCFKPLVSI SPNDSLFEAVYTLIKNR 279

Qy 121 IHRPLVLPDPSGNVLHILTHKRLKFLHIFGSLPRSPFLYRTIQDLGIGTFRDLAVVLE 180
Db 280 IHRPLVLPDPSGNVLHILTHKRLKFLHIFGSLPRSPFLYRTIQDLGIGTFRDLAVVLE 339

Qy 181 TAPILTALDIFVDRVSALPVVNECGVVGYSRFDVHIHAAQQTYNHLDMSVGEALRQR 240
Db 340 TAPILTALDIFVDRVSALPVVNECGVVGYSRFDVHIHAAQQTYNHLDMSVGEALRQR 399

Qy 241 TLCLEGVLSQPHESLGEVIDRIAREQVHRLVLDVETQHLGVVSLDILQALVLSPAGI 300
Db 400 TLCLEGVLSQPHESLGEVIDRIAREQVHRLVLDVETQHLGVVSLDILQALVLSPAGI 459

Qy 301 DALGA 305
Db 460 DALGA 464

RESULT 7
Q8BGW7_MOUSE

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ID AC Q8BGM7_MOUSE PRELIMINARY; PRT; 489 AA.
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE AMP-activated protein kinase gamma 3 subunit long form (Mus musculus
 DE adult male bone cDNA, RIKEN full-length enriched library,
 DE clone:9830138C07 product:5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-3
 DE SUBUNIT (AMPK GAMMA-3 CHAIN) (AMPK GAMMA3) homolog).
 GN Name=Prkg3;
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=BALB/C; TISSUE=Muscle;
 RX PubMed=14512293; DOI=10.1152/ajpcell.00319.2003;
 RA Yu H., Fujii N., Hirshman M.F., Pomerleau J.M., Goodyear L.J.;
 RT "Cloning and characterization of mouse 5'-AMP-activated protein kinase
 gamma3 subunit".
 RL Am. J. Physiol. Cell Physiol. 286:C283-C292(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Bone;
 RX MEDLINE=92279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning".
 RL Meth. Enzymol. 303:19-44(1999).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Bone;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischnann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Straubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Bone;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nakado I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Bruic V., Ciothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagaehima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tonita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs".
 RL Nature 420:563-573(2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Bone;
 RX MEDLINE=20493374; PubMed=11076861; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Suganara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes".
 RL Genome Res. 10:1617-1630(2000).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Bone;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hatama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multiplexed capillary sequencer".
 RL Genome Res. 10:1757-1771(2000).
 RN [7]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Bone;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akashira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF525500; AAN47137.1; -; mRNA.
 DR EMBL; AK036585; BAC29492.1; -; mRNA.
 DR Ensembl; ENSMUSG0000006542; Mus musculus.
 DR MGI; MGI:1891343; Prkg3.
 DR GO; GO:0016301; P-kinase activity; IEA.
 DR GO; GO:0006633; P-fatty acid biosynthesis; IEA.
 DR InterPro; IPR000644; CBS.
 DR Pfam; PF00571; CBS; 2.
 DR SMART; SM00116; CBS; 4.
 KW Kinase.
 SQ SEQUENCE 489 AA; 53848 MW; 85C9F71D8BDBDA5D CRC64;
 Query Match 36.0%; Score 1489; DB 2; Length 489;
 Best Local Similarity 96.1%; Pred. No. 1.7e-113;
 Matches 293; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
 QY 1 MRPMQSHCTCDAMATSKLVIPDTMLEIKKAPFALVGRAPLWDSKKQSFVGLMTIT 60
 DB 185 MRPMQSHCTCDAMATSKLVIPDTMLEIKKAPFALVGRAPLWDSKKQSFVGLMTIT 244
 QY 61 DFTLVHLHYRSPVLPVQIYIEQHKIETWREIYLQCGCFKPLVSPNSDLSPEAVYTLIKNR 120

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Db 245 DFILVLRHYRSPVQIYEIEEHKIEIETWREIYLGCCFKPLVSPNDLSLFEAVYALIKNR 304
Qy 121 IHRPLVLDVPSGVNLHILTHKRLKFLHIFGSLPLPRPSFLYRTIQDGLIGTFRDLAVL 180
Db 305 IHRPLVLDVPSGVTLVYILTHKRLKFLHIFGALLPRPSFLCRTIQDGLIGTFRDLAVL 364
Qy 181 TAPILTALDIFVDRVSALPVNCEGVGLYSRFDVHILAAQOTYNHLDMSVGEALRQ 240
Db 365 TAPILTALDIFVDRVSALPVNCEGVGLYSRFDVHILAAQOTYNHLDMSVGEALRQ 424
Qy 241 TLCLEGLVSCQPHESELGEVIDRIAREQVHRLVLVDETHQLLGVVSLSDIILQALVLS 300
Db 425 TLCLEGLVSCQPHESELGEVIDRIAREQVHRLVLVDETHQLLGVVSLSDIILQALV 484
Qy 301 DALGA 305
Db 485 DALSA 489

RESULT 8
Q4G3U3_BOVIN
ID Q4G3U3_BOVIN PRELIMINARY; PRT; 465 AA.
AC Q4G3U3;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE AMP-activated protein kinase gamma subunit.
GN Name=PRKAG3;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Stelatal muscle;
RA Yu S.L., Kim J.E., Jung K.C., Lee J.H., Choi I.H., Yoon D.H.,
RT "Cloning and characterization of bovine AMP-activated protein kinase
gamma subunit (PRKAG3) gene."
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY692035; AAV87666.1; -; Genomic_DNA.
KW Kinase.
SQ SEQUENCE 465 AA; 51523 MW; 35C8BC32C901D565 CRC64;

Query Match 95.3%; Score 1478.5; DB 2; Length 465;
Best Local Similarity 95.4%; Pred. No. 1.2e-112;
Matches 292; Conservative 8; Mismatches 5; Indels 1; Gaps 1;

Qy 1 MRFQEHCTCYDAMATSSKLVIFDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGM 60
Db 160 MHFQEHCTCYDAMATSSKLVIFDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGM 219
Qy 61 DFILVLRHYRSPVQIYEIEEHKIEIETWREIYLGCCFKPLVSPNDLSLFEAVYALIKNR 120
Db 220 DFILVLRHYRSPVQIYEIEEHKIEIETWREIYLGCCFKPLVSPNDLSLFEAVYALIKNR 279
Qy 121 IHRPLVLDVPSGVNLHILTHKRLKFLHIFGSLPLPRPSFLYRTIQDGLIGTFRDLAVL 179
Db 280 IHRPLVLDVPSGVNLHILTHKRLKFLHIFGSLPLPRPSFLYRTIQDGLIGTFRDLAVL 339
Qy 180 ETAPILTALDIFVDRVSALPVNCEGVGLYSRFDVHILAAQOTYNHLDMSVGEALRQ 239
Db 340 ETAPILTALDIFVDRVSALPVNCEGVGLYSRFDVHILAAQOTYNHLDMSVGEALR 399
Qy 240 TLCLEGLVSCQPHESELGEVIDRIAREQVHRLVLVDETHQLLGVVSLSDIILQALVLS 299
Db 400 TLCLEGLVSCQPHESELGEVIDRIAREQVHRLVLVDETHQLLGVVSLSDIILQALV 459
Qy 300 IDALGA 305
Db 460 IDALSA 465

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RESULT 9

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Q80WK8_MOUSE
ID Q80WK8_MOUSE PRELIMINARY; PRT; 490 AA.
AC Q80WK8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE AMP-activated protein kinase gamma subunit.
GN Name=Prkag3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14970697; DOI=10.1159/000075743;
RA Amarger V., Erlandsson R., Pielberg G., Jeon J.T., Andersson L.;
RT "Comparative sequence analysis of the PRKAG3 region between human and
pig: evolution of repetitive sequences and potential new exons.";
RL Cytogenet. Genome Res. 102:163-172(2003).
DR EMBL; AY263402; AAP22981.1; -; Genomic DNA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR InterPro; IPR000644; CBS.
DR Pfam; PF00571; CBS; 2.
DR SMART; SM00116; CBS; 4.
KW Kinase.
SQ SEQUENCE 490 AA; 53948 MW; DBFEF917B67D4CD5 CRC64;

Query Match 95.3%; Score 1478.5; DB 2; Length 490;
Best Local Similarity 95.8%; Pred. No. 1.2e-112;
Matches 293; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

Qy 1 MRFQEHCTCYDAMATSSKLVIFDTMLEIKKAFALVANGVRAAPLWDSKKQSFVGM 60
Db 185 MHFQEHCTCYDAMATSSKLVIFDTMLEIKKAFAMVANGVRAAPLWDSKKQSFVGM 244
Qy 61 DFILVLRHYRSPVQIYEIEEHKIEIETWREIYLGCCFKPLVSPNDLSLFEAVYALIKNR 120
Db 245 DFILVLRHYRSPVQIYEIEEHKIEIETWREIYLGCCFKPLVSPNDLSLFEAVYALIKNR 304
Qy 121 IHRPLVLDVPSGVNLHILTHKRLKFLHIFGSLPLPRPSFLYRTIQDGLIGTFRDLAVL 180
Db 305 IHRPLVLDVPSGVTLVYILTHKRLKFLHIFGALLPRPSFLCRTIQDGLIGTFRDLAVL 364
Qy 181 TAPILTALDIFVDRVSALPVNCEGVGLYSRFDVHILAAQOTYNHLDMSVGEALRQ 239
Db 365 TAPILTALDIFVDRVSALPVNCEGVGLYSRFDVHILAAQOTYNHLDMSVGEALR 424
Qy 240 TLCLEGLVSCQPHESELGEVIDRIAREQVHRLVLVDETHQLLGVVSLSDIILQALVLS 299
Db 425 TLCLEGLVSCQPHESELGEVIDRIAREQVHRLVLVDETHQLLGVVSLSDIILQALV 484
Qy 300 IDALGA 305
Db 485 IDALSA 490

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RESULT 10

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Q6TEH8_HORSE
ID Q6TEH8_HORSE PRELIMINARY; PRT; 447 AA.
AC Q6TEH8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE AMP-activated protein kinase gamma subunit 3 (Fragment).
GN Name=prkag3;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.

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OX NCBI_TaxID=9796;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14970705; DOI=10.1159/000075751;
RA Park H.B., Marklund S., Jeon J.T., Mickelson J.R., Valberg S.J.,
RT Sandberg K., Andersson L.;
RT "Molecular characterization and mutational screening of the PRKAG3
RT gene in the horse.";
RL Cytogenet. Genome Res. 102:211-216(2003).
DR EMBL; AY423273; AAR03832.1; -; Genomic DNA.
DR EMBL; AY423271; AAR03832.1; JOINED; Genomic DNA.
DR EMBL; AY423272; AAR03832.1; JOINED; Genomic DNA.
DR GO; GO:0016301; P:kinase activity; IEA.
DR InterPro; IPR000644; CBS.
DR Pfam; PF00571; CBS; 2.
DR SMART; SM00116; CBS; 4.
KW Kinase.
FT NON_TER 447 447
FT SEQUENCE 447 AA; 49219 MW; 3BB4E70BA6F93C3E CRC64;

Query Match 90.8%; Score 1408; DB 2; Length 447;
Best Local Similarity 95.8%; Pred. No. 6.7e-107;
Matches 276; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MRFMOEHTCYDAMATSSKLVIFDTMLEIKKAFPAFVALVANGVRAAPLWDSKKQSFVGMLTIT 60
Db 160 MHFMOEHTCYDAMATSSKLVIFDTMLEIKKAFPAFVALVANGVRAAPLWDSKKQSFVGMLTIT 219

Qy 61 DFILVLRHYRSPVLQVYEIOHKIETWREIYLOGCFKPLVSPNDLSLFEAVVTLIKNR 120
Db 220 DFILVLRHYRSPVLQVYEIOHKIETWREIYLOGCFKPLVSPNDLSLFEAVVTLIKNR 279

Qy 121 IHRPLVLPDPSGVNLHILTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 180
Db 280 IHRPLVLPDPSGVNLHILTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 339

Qy 181 TAPILTALDIFVDRRVSALPVNVECGVGLYSRFDVIHLAAQOQYTNHLDMSVGEALRQR 240
Db 340 TAPILTALDIFVDRRVSALPVNVECGVGLYSRFDVIHLAAQOQYTNHLDMSVGEALRQR 399

Qy 241 TLCLEGVLSQPHESLGEVIDRIAREQVHRLVLVDETOHLL 281
Db 400 TVCLEGVLSQPHESLGEVIDRIAREQVHRLVLVDETOHLL 447

RESULT 11
Q6U7S1_HORSE PRELIMINARY; PRT; 440 AA.
AC Q6U7S1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE AMP-activated protein kinase gamma subunit 3 (Fragment).
GN Name=Prkag3;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
OC NCBI_TaxID=9796;
RN [1]
RP NUCLEOTIDE SEQUENCE
RX PubMed=14970705; DOI=10.1159/000075751;
RA Park H.B., Marklund S., Jeon J.T., Mickelson J.R., Valberg S.J.,
RT Sandberg K., Andersson L.;
RT "Molecular characterization and mutational screening of the PRKAG3
RT gene in the horse.";
RL Cytogenet. Genome Res. 102:211-216(2003).
DR EMBL; AY376689; AAR03583.1; -; mRNA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR InterPro; IPR000644; CBS.
DR Pfam; PF00571; CBS; 2.
DR SMART; SM00116; CBS; 3.
KW Kinase.
FT NON_TER 440 440

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SQ SEQUENCE 440 AA; 48561 MW; CB6C706D98E4A66A CRC64;

Query Match 88.7%; Score 1376; DB 2; Length 440;
Best Local Similarity 95.7%; Pred. No. 2.8e-104;
Matches 269; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MRFMOEHTCYDAMATSSKLVIFDTMLEIKKAFPAFVALVANGVRAAPLWDSKKQSFVGMLTIT 60
Db 160 MHFMOEHTCYDAMATSSKLVIFDTMLEIKKAFPAFVALVANGVRAAPLWDSKKQSFVGMLTIT 219

Qy 61 DFILVLRHYRSPVLQVYEIOHKIETWREIYLOGCFKPLVSPNDLSLFEAVVTLIKNR 120
Db 220 DFILVLRHYRSPVLQVYEIOHKIETWREIYLOGCFKPLVSPNDLSLFEAVVTLIKNR 279

Qy 121 IHRPLVLPDPSGVNLHILTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 180
Db 280 IHRPLVLPDPSGVNLHILTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 339

Qy 181 TAPILTALDIFVDRRVSALPVNVECGVGLYSRFDVIHLAAQOQYTNHLDMSVGEALRQR 240
Db 340 TAPILTALDIFVDRRVSALPVNVECGVGLYSRFDVIHLAAQOQYTNHLDMSVGEALRQR 399

Qy 241 TLCLEGVLSQPHESLGEVIDRIAREQVHRLVLVDETOHLL 281
Db 400 TVCLEGVLSQPHESLGEVIDRIAREQVHRLVLVDETOHLL 440

RESULT 12
Q4JK38_CHICK PRELIMINARY; PRT; 363 AA.
AC Q4JK38;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE 5'-AMP-activated protein kinase gamma-3 non-catalytic subunit short
DE form.
GN Name=PRKAG3;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skeletal muscle;
RA Proszkowiec-Weglarz M., Richards M.P., Poch S.M.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; DQ079815; AAY86042.1; -; mRNA.
KW Kinase.
SQ SEQUENCE 363 AA; 41151 MW; 06FCD94FCC3AEDC CRC64;

Query Match 80.6%; Score 1250; DB 2; Length 363;
Best Local Similarity 77.4%; Pred. No. 4.7e-94;
Matches 236; Conservative 39; Mismatches 30; Indels 0; Gaps 0;

Qy 1 MRFMOEHTCYDAMATSSKLVIFDTMLEIKKAFPAFVALVANGVRAAPLWDSKKQSFVGMLTIT 60
Db 59 MHFMRSHCCYDAVPTSKLVVFTTLEIKKAFVALVANGVRAAPLWDSKKQSFVGMLTIT 118

Qy 61 DFILVLRHYRSPVLQVYEIOHKIETWREIYLOGCFKPLVSPNDLSLFEAVVTLIKNR 120
Db 119 DFILVLRHYRSPVLQVYEIOHKIETWREIYLOGCFKPLVSPNDLSLFEAVVTLIKNR 178

Qy 121 IHRPLVLPDPSGVNLHILTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 180
Db 179 IHRPLVLPDPSGVNLHILTHKRLKFLHIFGSLPRPSFLYRTIQDLGIGTFRDLAVVLE 238

Qy 181 TAPILTALDIFVDRRVSALPVNVECGVGLYSRFDVIHLAAQOQYTNHLDMSVGEALRQR 240
Db 239 NAFVAALEIFVDRRVSALPVNVECGVGLYSRFDVIHLAAQOQYTNHLDMSVGEALRQR 298

Qy 241 TLCLEGVLSQPHESLGEVIDRIAREQVHRLVLVDETOHLLGVVSLSDIIOALVLSPAGI 300

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Db 299 TVCLEGVLTCPYHETMEDIIDRITTEQVHRLVLDENYPRGIVSLSDILOALVLTGAGI 358
Qy 301 DALGA 305
   ||| :
Db 359 DALNS 363

RESULT 13
Q4JK39 CHICK
ID Q4JK39 CHICK PRELIMINARY; PRT; 382 AA.
AC Q4JK39
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE 5'-AMP-activated protein kinase gamma-3 non-catalytic subunit long
DE form.
GN Name=PKAG3;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skeletal muscle;
RA Proszkowiec-Weglarz M., Richards M.P., Poch S.M.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; DQ079814; AAY86041.1; -; mRNA.
KW Kinase.
SQ SEQUENCE 382 AA; 42960 MW; 70988BFF1A2C77A59 CRC64;

Query Match 80.6%; Score 1250; DB 2; Length 382;
Best Local Similarity 77.4%; Pred. No. 5e-94;
Matches 236; Conservative 39; Mismatches 30; Indels 0; Gaps 0;

Qy 1 MRFQHTCYDAMATSSKLVIFDTMLEIKKFAFFALVANGVRAAPLWDSKKQSFVGMILTIT 60
Db 78 MHRSHCCYDAVPTSCKLVVDFDTLEIKKFAFFALVANGVRAAPLWDSKKQSFVGMILTIT 137

Qy 61 DFILVHLRYRSPVQIYEIBQHKIETWREIYLGQCFKPLVSI SPNDSLSFPAVYTLIKNR 120
Db 138 DFILVHLRYRSPVQIYEVEEHKIEIWRVYLGQSFKPLVSI SPNDSLSFPAVYTLIKHK 197

Qy 121 IHRPLVLDPSGVNLHILTHKRLKFLHI FGSLLPRSPFLYRTTODIGIGTFRDLAVYLE 180
Db 198 IHRPLVPIEPISGVNLHILTHKRLKFLHI FGSLLPRSPFLYRTTODIGIGTFRDLAVYLE 257

Qy 181 TAPILTALDIFVDRVSALPVVNECGVGLYSRFDVTHLAAQQTYNHLDMSVGEALRQR 240
Db 258 NAPVYALAEI FVDRVSALPVVNAAGVGLYSRFDVTHLAAQQTYNHLDMSVGEALRQR 317

Qy 241 TLCLEGVLSQCPHESLGEVIDRIAREQVHRLVLDVDETQHLLGVVSLSDILOALVLTGAGI 300
Db 318 TVCLEGVLTCPYHETMEDIIDRITTEQVHRLVLDENYPRGIVSLSDILOALVLTGAGI 377

Qy 301 DALGA 305
   ||| :
Db 378 DALNS 382

RESULT 14
Q7ZY12 XENLA
ID Q7ZY12 XENLA PRELIMINARY; PRT; 337 AA.
AC Q7ZY12;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Prkag3-prov protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
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RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Embryo;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative."
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC043738; AAH43738.1; -; mRNA.
DR InterPro; IPR00644; CBS.
DR Pfam; PF00571; CBS; 2.
DR SMART; SM00116; CBS; 4.
SQ SEQUENCE 337 AA; 38325 MW; BPF4AE102D6F1DC4 CRC64;

Query Match 77.0%; Score 1195; DB 2; Length 337;
Best Local Similarity 75.4%; Pred. No. 1.4e-89;
Matches 227; Conservative 39; Mismatches 35; Indels 0; Gaps 0;

Qy 1 MRFQHTCYDAMATSSKLVIFDTMLEIKKFAFFALVANGVRAAPLWDSKKQSFVGMILTIT 60
Db 33 MEFMKKCCYNAITPSCKLVVDFDTLQIKKFAFFALVANGVRAAPLWDSKKQSFVGMILTIT 92

Qy 61 DFILVHLRYRSPVQIYEIBQHKIETWREIYLGQCFKPLVSI SPNDSLSFPAVYTLIKNR 120
Db 93 DFILVHLRYRSPVQIYEVEEHKIEIWRVYLGQSFKPLVSI SPNDSLSFPAVYTLIKNK 152

Qy 121 IHRPLVLDPSGVNLHILTHKRLKFLHI FGSLLPRSPFLYRTTODIGIGTFRDLAVYLE 180
Db 153 IHRPLVMDPSGVNLHILTHKRLKFLHI FGSLLPRSPFLYRTTODIGIGTFRDLAVYQD 212

Qy 181 TAPILTALDIFVDRVSALPVVNECGVGLYSRFDVTHLAAQQTYNHLDMSVGEALRQR 240
Db 213 TSSVNALEIFVDRVSALPVVNECGVGLYSRFDVTHLAAQQTYNHLDMSVGEALRQR 272

Qy 241 TLCLEGVLSQCPHESLGEVIDRIAREQVHRLVLDVDETQHLLGVVSLSDILOALVLTGAGI 300
Db 273 SLCEGVLMCPHESLGEVIDRIAREQVHRLVLDVDEERRRPLGIVSLSDILOALVLTGAGI 332

Qy 301 D 301
Db 333 D 333
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